

PATENT SEQUENCE ALIGNMENT

Query	361	GTGTACCAGGCTATGATTTCTCTTGCATTAAAAATGTATTATTATT	405
Sbjct	361	GTGTACCAGGCTATGATTTCTCTTGCATTAAAAATGTATTATTATT	405

Sequence 108 matched with Sequence 2

Query= Sequence ID - 108
Length=550

nt: 550

SEQ ID NO: 2

nt: 550

ALIGNMENTS

Identities = 550/550 (100%), Gaps = 0/550 (0%)

Query	1	GGCTTTGACAGAGTGCAAGACGATGACTTGCAAAATGTCGCATCTGGAACGCAACATAGA	60
Sbjct	1	GGCTTTGACAGAGTGCAAGACGATGACTTGCAAAATGTCGCATCTGGAACGCAACATAGA	60
Query	61	NACCATCATCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAA	120
Sbjct	61	NACCATCATCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAA	120
Query	121	CCAGGGGGAATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGGAGAA	180
Sbjct	121	CCAGGGGGAATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGGAGAA	180
Query	181	TAAGAATGAAAAGGTCATAGAACACATCATGGAGGACCTGGACACAAATGCAGACAAGCA	240
Sbjct	181	TAAGAATGAAAAGGTCATAGAACACATCATGGAGGACCTGGACACAAATGCAGACAAGCA	240
Query	241	GCTGAGCTTCGAGGAGTTCATCATGCTGATGGCGAGGCTAACCTGGGCCTCCACGAGAA	300
Sbjct	241	GCTGAGCTTCGAGGAGTTCATCATGCTGATGGCGAGGCTAACCTGGGCCTCCACGAGAA	300
Query	301	GATGCACGAGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAGGCCTCGGGGAGGGCAC	360
Sbjct	301	GATGCACGAGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAGGCCTCGGGGAGGGCAC	360
Query	361	CCCCTAAGACCACAGTGGCCAAGATCACAGTGGCCACGGCCACGGCCACAGTCATGGTGG	420
Sbjct	361	CCCCTAAGACCACAGTGGCCAAGATCACAGTGGCCACGGCCACGGCCACAGTCATGGTGG	420
Query	421	CCACGGCCACAGCCACTAATCAGGAGGCCAGGCCACCCTGCCTNTACCCAACCAGGGCCC	480
Sbjct	421	CCACGGCCACAGCCACTAATCAGGAGGCCAGGCCACCCTGCCTNTACCCAACCAGGGCCC	480

PATENT SEQUENCE ALIGNMENT

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Query  481  CGGGGCCTGTTATGTCAAACGTCTTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CGGGGCCTGTTATGTCAAACGTCTTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAGT  540

Query  541  CTCTTTCTCC  550
          ||||||||
Sbjct  541  CTCTTTCTCC  550
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Sequence 110 matched with Sequence 3

Query= Sequence ID 110

Length=423

SEQ ID NO: 3

ALIGNMENTS

Identities = 423/423 (100%), Gaps = 0/423 (0%)

Query	1	ACGAAGACAGACATCTGTGGAATGATTCACATCCTCTCAAGTTAGGAGGATGGAGGCCTG	60
Sbjct	1	ACGAAGACAGACATCTGTGGAATGATTCACATCCTCTCAAGTTAGGAGGATGGAGGCCTG	60
Query	61	CTTCATTAAGAAGCTgggggtagggtagggtagggAGAACACTTAACAACATGGGGACC	120
Sbjct	61	CTTCATTAAGAAGCTGGGGGTAGGGTGGGGTGGGGAGAACACTTAACAACATGGGGACC	120
Query	121	AGTCAGGGGAATCCCCTTATTTCTGTTTTGCATATGAGGAACCCTAGAGCAGCCAGGTGA	180
Sbjct	121	AGTCAGGGGAATCCCCTTATTTCTGTTTTGCATATGAGGAACCCTAGAGCAGCCAGGTGA	180
Query	181	GGCTCTCTAGTTTAATAAAAAATCATGGAAAGACTCTTAATGCAGACTCTTCTTAAGTGTT	240
Sbjct	181	GGCTCTCTAGTTTAATAAAAAATCATGGAAAGACTCTTAATGCAGACTCTTCTTAAGTGTT	240
Query	241	AATAGGGATTTTTTCAGCTTATTTTGGTTGCAGTTTCCAATTTTAAAAATGTTGAGGTA	300
Sbjct	241	AATAGGGATTTTTTCAGCTTATTTTGGTTGCAGTTTCCAATTTTAAAAATGTTGAGGTA	300
Query	301	ATCTTTCCACCTTCCCAAACCTAATTCTTGTAGATGCATTAGTGTTGAACCAATGCTTT	360
Sbjct	301	ATCTTTCCACCTTCCCAAACCTAATTCTTGTAGATGCATTAGTGTTGAACCAATGCTTT	360
Query	361	CTCATGTCTCAATTCTTTGTATATGCATTCTTTTCAGATGTATTAAACAAACAAAAACCC	420
Sbjct	361	CTCATGTCTCAATTCTTTGTATATGCATTCTTTTCAGATGTATTAAACAAACAAAAACCC	420
Query	421	TTC	423
Sbjct	421	TTC	423

Sequence 192 matched with Sequence 4

Query= Sequence ID - 192 nt: 286
Length=286

SEQ ID NO: 4 nt: 286

ALIGNMENTS

Identities = 286/286 (100%), Gaps = 0/286 (0%)

Query	1	CCGGTAATAGAATAGAAAAGGGAGAGTGTCTTCATGCAATGTGGCATCCTGGATTGGGTC	60
Sbjct	1	CCGGTAATAGAATAGAAAAGGGAGAGTGTCTTCATGCAATGTGGCATCCTGGATTGGGTC	60
Query	61	TCGNNACAAAAACAGGACATTAGTGGGAAAATTGGAAATCTGAAAAAAGTCTGAATTTTA	120
Sbjct	61	TCGNNACAAAAACAGGACATTAGTGGGAAAATTGGAAATCTGAAAAAAGTCTGAATTTTA	120
Query	121	GTTAATATACCAATTTTCAGTCTCTTGTTTTGACAGATGTACCATGGTGATGTAAGATGT	180
Sbjct	121	GTTAATATACCAATTTTCAGTCTCTTGTTTTGACAGATGTACCATGGTGATGTAAGATGT	180
Query	181	TGACCTTGGGGTAGGCTGGGTGAAGGGTATACAGGAACTCTTTGTACTATCTCTGCAACT	240
Sbjct	181	TGACCTTGGGGTAGGCTGGGTGAAGGGTATACAGGAACTCTTTGTACTATCTCTGCAACT	240
Query	241	TCTCTGTAAATCTAGTATCATTCCAAAATAAAAGTTTATTTAATTT	286
Sbjct	241	TCTCTGTAAATCTAGTATCATTCCAAAATAAAAGTTTATTTAATTT	286

Sequence 250 matched with Sequence 5

Query= Sequence ID 250
Length=545

SEQ ID NO: 5

ALIGNMENTS

Identities = 545/545 (100%), Gaps = 0/545 (0%)

Query	1	GTGGAAGTGACATCGTCTTTAAACCTGCGTGGCAATCCCTGACGCACCGCCGTGATGCC	60
Sbjct	1	GTGGAAGTGACATCGTCTTTAAACCTGCGTGGCAATCCCTGACGCACCGCCGTGATGCC	60
Query	61	CAGGGAAGACAGGGCGACCTGGAAGTCCAACACTACTTCCTTAAGATCATCCAACATTGGA	120
Sbjct	61	CAGGGAAGACAGGGCGACCTGGAAGTCCAACACTACTTCCTTAAGATCATCCAACATTGGA	120
Query	121	TGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCA	180
Sbjct	121	TGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCA	180
Query	181	GATCCGCATGTCCCTTCGCGGGAAGGCTGTGGTGCTGATGGGCAAGAACACCATGATGCG	240
Sbjct	181	GATCCGCATGTCCCTTCGCGGGAAGGCTGTGGTGCTGATGGGCAAGAACACCATGATGCG	240
Query	241	CAAGGCCATCCGAGGGCACCTGGAAAAACAACCCAGCTCTGGAGAAACTGCTGCCTCATAT	300
Sbjct	241	CAAGGCCATCCGAGGGCACCTGGAAAAACAACCCAGCTCTGGAGAAACTGCTGCCTCATAT	300
Query	301	CCGGGGGAATGTGGGCTTTGTGTTACCAAGGAGGACCTCACTGAGATCAGGGACATGTT	360
Sbjct	301	CCGGGGGAATGTGGGCTTTGTGTTACCAAGGAGGACCTCACTGAGATCAGGGACATGTT	360
Query	361	GCTGGCCAATAAGGTGCCAGCTGCTGCCCCTGCTGGTGCCATTGCCCCATGTGAAGTCAC	420
Sbjct	361	GCTGGCCAATAAGGTGCCAGCTGCTGCCCCTGCTGGTGCCATTGCCCCATGTGAAGTCAC	420
Query	421	TGTGCCAGCCCAGAACACTGGTCTCGGGCCCGAGAAGACCTCCTTTTTCCAGGCTTTAGG	480
Sbjct	421	TGTGCCAGCCCAGAACACTGGTCTCGGGCCCGAGAAGACCTCCTTTTTCCAGGCTTTAGG	480

PATENT SEQUENCE ALIGNMENT

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Query  481  TATCACCCTAAAATCTCCAGGGGCACCATTGAAATCCTGAGTGATGTGCACTGATCAAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TATCACCCTAAAATCTCCAGGGGCACCATTGAAATCCTGAGTGATGTGCACTGATCAAG  540

Query  541  ACTGG  545
          |||||
Sbjct  541  ACTGG  545
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Sequence 299 matched with Sequence 6

Query= Sequence ID 299

Length=591

SEQ ID NO: 6

ALIGNMENTS

Identities = 591/591 (100%), Gaps = 0/591 (0%)

Query	1	CAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGtttt	60
Sbjct	1	CAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTT	60
Query	61	tttCTCTTTGAAAGATAGAGATTGNTACAACCTACTTAAAAAATATAGTCAATAGGTTACT	120
Sbjct	61	TTTCTCTTTGAAAGATAGAGATTGNTACAACCTACTTAAAAAATATAGTCAATAGGTTACT	120
Query	121	AAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAA	180
Sbjct	121	AAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAA	180
Query	181	AATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATG	240
Sbjct	181	AATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATG	240
Query	241	ACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGA	300
Sbjct	241	ACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGA	300
Query	301	GAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAAT	360
Sbjct	301	GAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAAT	360
Query	361	GAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTG	420
Sbjct	361	GAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTG	420
Query	421	AAGGCGATCTTTTAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGA	480
Sbjct	421	AAGGCGATCTTTTAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGA	480

PATENT SEQUENCE ALIGNMENT

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Query  481  CGCANGGAGAATTGCGCATTTAAAGCCTAGTTACGCATTTACTAAACGCAGACGAAAATG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CGCANGGAGAATTGCGCATTTAAAGCCTAGTTACGCATTTACTAAACGCAGACGAAAATG  540

Query  541  GGAAGATTAATTGGGAGTGGTAGGATGAAACAATTTTGGAGAAGATAGAAG  591
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GGAAGATTAATTGGGAGTGGTAGGATGAAACAATTTTGGAGAAGATAGAAG  591
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Sequence 300 matched with Sequence 7

Query= Sequence ID 300
Length=297

SEQ ID NO: 7

ALIGNMENTS

Identities = 297/297 (100%), Gaps = 0/297 (0%)

Query	1	CTCAAAGGAGaaaaaaaccttgtaaaaaaagcaaaaatgacaacagaaaaCAATCTTA	60
Sbjct	1	CTCAAAGGAGAAAAAAACCTTGTAaaaaaAGCAAAAATGACAACAGAAAAACAATCTTA	60
Query	61	TTCCGAGCATTCAGTAACCTTTTTGTGTATGTACTTAGCTGTACTATAAGTAGTTGGTT	120
Sbjct	61	TTCCGAGCATTCAGTAACCTTTTTGTGTATGTACTTAGCTGTACTATAAGTAGTTGGTT	120
Query	121	TGTATGAGATGGTTAAAAAGGCCAAAGATAAAAGGTTTCtttttttttccttttttgtct	180
Sbjct	121	TGTATGAGATGGTTAAAAAGGCCAAAGATAAAAGGTTTCCTTTTTTTTCCTTTTTTTGTCT	180
Query	181	atgaagttgctgtttattttttttGGCCTGTTTGATGTATGTGTGAAACAATGTTGTCCA	240
Sbjct	181	ATGAAGTTGCTGTTTATTTTTTTTGGCCTGTTTGATGTATGTGTGAAACAATGTTGTCCA	240
Query	241	ACAATAAACAGGAATTTTATTTTGCTGAGTTGTTCTaaaaaaaaaaaaaaaaaaaaa	297
Sbjct	241	ACAATAAACAGGAATTTTATTTTGCTGAGTTGTTCTAAAAAAAAAAAAAAAAAAAAA	297

Sequence 302 matched with Sequence 8

Query= Sequence ID 302
Length=282

SEQ ID NO: 8

ALIGNMENTS

Identities = 282/282 (100%), Gaps = 0/282 (0%)

Query	1	AGTAGAGACGGGGTTTCACTGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATC	60
Sbjct	1	AGTAGAGACGGGGTTTCACTGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATC	60
Query	61	CGGCCACCTCGGCCTCCCGAAAGTGCTGGGATTACAGGCGTGAGCCACGGCGCCCAGCCC	120
Sbjct	61	CGGCCACCTCGGCCTCCCGAAAGTGCTGGGATTACAGGCGTGAGCCACGGCGCCCAGCCC	120
Query	121	CAGCCTGTCACTTAAACTGATAAACGACAGATTAACAGTAGAAAAATTTATTTTGCATA	180
Sbjct	121	CAGCCTGTCACTTAAACTGATAAACGACAGATTAACAGTAGAAAAATTTATTTTGCATA	180
Query	181	CATAATGAGGCTTCACAAAAGAGAAGTGAAAACCCAAGTAGGAGTTTAGGGCTGGGGGCT	240
Sbjct	181	CATAATGAGGCTTCACAAAAGAGAAGTGAAAACCCAAGTAGGAGTTTAGGGCTGGGGGCT	240
Query	241	TATATACCATTTAACAAGGGGTGATAAATTGTAAGAGAATAG	282
Sbjct	241	TATATACCATTTAACAAGGGGTGATAAATTGTAAGAGAATAG	282

Sequence 304 matched with Sequence 9

Query= Sequence ID 304
Length=619

SEQ ID NO: 9

ALIGNMENTS

Identities = 619/619 (100%), Gaps = 0/619 (0%)

Query	1	TCCTTGGTTTCGATTTGTGGCAACAATCCAGTCTtttttgtttttttCAGGGATACCATAT	60
Sbjct	1	TCCTTGGTTTCGATTTGTGGCAACAATCCAGTCTTTTTGTTTTTTCAGGGATACCATAT	60
Query	61	GTAACAGGTGCCATTGTTACTGTAACTTTTCACACATGCCTTCAGTTTGATGTCAAAGTC	120
Sbjct	61	GTAACAGGTGCCATTGTTACTGTAACTTTTCACACATGCCTTCAGTTTGATGTCAAAGTC	120
Query	121	ATCATTTAGTGTAACAGCAAGTTATCTGTTAGGCTGCACATCATGAACTTTACTTTTAG	180
Sbjct	121	ATCATTTAGTGTAACAGCAAGTTATCTGTTAGGCTGCACATCATGAACTTTACTTTTAG	180
Query	181	AAAGTCTTATCTTTTATGCCACAGAAATAGCATTGGCTATTAGTCATGGATGGCAAAGA	240
Sbjct	181	AAAGTCTTATCTTTTATGCCACAGAAATAGCATTGGCTATTAGTCATGGATGGCAAAGA	240
Query	241	AATTAATTTTGAGTTGTTTGGATAAAAAATGTTTCAGTTGACTGTAGTGTGTATTGAGAGA	300
Sbjct	241	AATTAATTTTGAGTTGTTTGGATAAAAAATGTTTCAGTTGACTGTAGTGTGTATTGAGAGA	300
Query	301	CACTGCCAGTAAACAAACTCTCTTGGTAGGTGGAAATCCCCTAGAAGTTACAGAAAATTG	360
Sbjct	301	CACTGCCAGTAAACAAACTCTCTTGGTAGGTGGAAATCCCCTAGAAGTTACAGAAAATTG	360
Query	361	GGAGGAGGTGAACTTAATTAAATAACTTGAATTGTTTAGACATATTCAGAGCTTCTTATG	420
Sbjct	361	GGAGGAGGTGAACTTAATTAAATAACTTGAATTGTTTAGACATATTCAGAGCTTCTTATG	420
Query	421	ACCTTGAAGAAATCACCCAACTTCAAAAGACCTCGGTTTCTTCATTTGTAAAATTAGGGA	480
Sbjct	421	ACCTTGAAGAAATCACCCAACTTCAAAAGACCTCGGTTTCTTCATTTGTAAAATTAGGGA	480

PATENT SEQUENCE ALIGNMENT

Query	481	GTTTGA	CTAGAT	GTGTAA	ATCTAG	TTGTTA	GTAACT	TCTAAG	ATGTAAAA	ACCCTC	TTG	540	
Sbjct	481	GTTTGA	CTAGAT	GTGTAA	ATCTAG	TTGTTA	GTAACT	TCTAAG	ATGTAAAA	ACCCTC	TTG	540	
Query	541	TTTAACA	AAAAAC	CTACA	AGATCA	AGTTG	CTTATC	TGAAAT	C	TTTATG	AATCA	AACTAG	600
Sbjct	541	TTTAACA	AAAAAC	CTACA	AGATCA	AGTTG	CTTATC	TGAAAT	C	TTTATG	AATCA	AACTAG	600
Query	601	CACTAAG	TCTAG	CTCG	ACC	619							
Sbjct	601	CACTAAG	TCTAG	CTCG	ACC	619							

Sequence 306 matched with Sequence 10

Query= Sequence ID 306

Length=536

SEQ ID NO: 10

ALIGNMENTS

Identities = 536/536 (100%), Gaps = 0/536 (0%)

Query	1	CTTTTCCTCCCGCTGTCCCCACGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGTG	60
Sbjct	1	CTTTTCCTCCCGCTGTCCCCACGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGTG	60
Query	61	AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCTG	120
Sbjct	61	AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCTG	120
Query	121	GGAAGTGTTTTTGAGAAGTCTCGGTCCGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA	180
Sbjct	121	GGAAGTGTTTTTGAGAAGTCTCGGTCCGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA	180
Query	181	ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGTC	240
Sbjct	181	ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGTC	240
Query	241	AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA	300
Sbjct	241	AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA	300
Query	301	AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACTA	360
Sbjct	301	AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACTA	360
Query	361	TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCTACAACAGTGTCTGG	420
Sbjct	361	TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCTACAACAGTGTCTGG	420
Query	421	GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG	480
Sbjct	421	GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG	480

Query	481	CTGACCAAGAATGTGGATTTTGTGAAGGATGCNCATGAANAAATGGACNAGCTGTG	536
Sbjct	481	CTGACCAAGAATGTGGATTTTGTGAAGGATGCNCATGAANAAATGGACNAGCTGTG	536

Sequence 308 matched with Sequence 11

Query= Sequence ID - 308
Length=373

nt: 373

SEQ ID NO: 11

nt: 373

ALIGNMENTS

Identities = 371/371 (100%), Gaps = 0/371 (0%)

Query	1	AAGTGGGTCTTGCCATCCCTGAACTGNAATCATCCCTAACATATTCATACCTGTTTTTCAT	60
Sbjct	1	AAGTGGGTCTTGCCATCCCTGAACTGNAATCATCCCTAACATATTCATACCTGTTTTTCAT	60
Query	61	TTTAAAAGTTGGGTCAGtttttttATTAGTACATGTATTTCTATCCTACTGATTTATTTG	120
Sbjct	61	TTTAAAAGTTGGGTCAGTTTTTTTATTAGTACATGTATTTCTATCCTACTGATTTATTTG	120
Query	121	CTATATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGTCCTGTATGGAGA	180
Sbjct	121	CTATATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGTCCTGTATGGAGA	180
Query	181	CCTAGCTCTTCTCAGTGTCTACTATTATAAACAATGCTACAGTGAATATTGGTGNATAAA	240
Sbjct	181	CCTAGCTCTTCTCAGTGTCTACTATTATAAACAATGCTACAGTGAATATTGGTGNATAAA	240
Query	241	TCCATACNCACCACGTACATATCTTAAGTTCTGGAAGAGATATTGCTAAACCAGAAGATA	300
Sbjct	241	TCCATACNCACCACGTACATATCTTAAGTTCTGGAAGAGATATTGCTAAACCAGAAGATA	300
Query	301	ACCTGCATTTAAAATTTGACTGCTAGGGNCAGGGNCACATTTAATTAAATTAGAACAAANG	360
Sbjct	301	ACCTGCATTTAAAATTTGACTGCTAGGGNCAGGGNCACATTTAATTAAATTAGAACAAANG	360
Query	361	AATGCATAATG 371	
Sbjct	361	AATGCATAATG 371	

Sequence 309 matched with Sequence 12

Query= Sequence ID 309
Length=796

SEQ ID NO: 12

ALIGNMENTS

Identities = 796/796 (100%), Gaps = 0/796 (0%)

Query	1	CCGGAATCGCGGCCGCGTCGACGAAAAATATGTGCCCTGGCCAAC	60
Sbjct	1	CCGGAATCGCGGCCGCGTCGACGAAAAATATGTGCCCTGGCCAAC	60
Query	61	TAGGCAATCTGAAGGAAACCAGAAAAATGTGAATTTCTCTTCCCTCA	120
Sbjct	61	TAGGCAATCTGAAGGAAACCAGAAAAATGTGAATTTCTCTTCCCTCA	120
Query	121	AGTAGTATTTAATATTCAAGTACTTGTAATTTGCAGAACAGTACTTT	180
Sbjct	121	AGTAGTATTTAATATTCAAGTACTTGTAATTTGCAGAACAGTACTTT	180
Query	181	ATGAATTCTATTTAAATTTGTCACTTAATATTTAGCCAAGAAGCAA	240
Sbjct	181	ATGAATTCTATTTAAATTTGTCACTTAATATTTAGCCAAGAAGCAA	240
Query	241	TTTCTGGTTTATTTCTCCAACCTCCTAATAAATAGGGTCACATAt	300
Sbjct	241	TTTCTGGTTTATTTCTCCAACCTCCTAATAAATAGGGTCACATAT	300
Query	301	AATTTGAAAAGTAATACAGGCATATGGTATTTTAAAAATGAAACA	360
Sbjct	301	AATTTGAAAAGTAATACAGGCATATGGTATTTTAAAAATGAAACA	360
Query	361	TTTTGAAAAGTGGTCTTGCCATCCCTGAACTGTAATCATCCCTAAC	420
Sbjct	361	TTTTGAAAAGTGGTCTTGCCATCCCTGAACTGTAATCATCCCTAAC	420
Query	421	TTTCATTTTAAAAGTTGGGTCAGtttttttATTAGTACATGTATTT	480
Sbjct	421	TTTCATTTTAAAAGTTGGGTCAGTTTTTTTATTAGTACATGTATTT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TATTTGCTATATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGTCCTGTA	540
Sbjct	481	TATTTGCTATATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGTCCTGTA	540
Query	541	TGGAGACCTAGCTCTTCTCAGTGTCTACTATTATAAACAATGCTACAGTGAATATTGGTG	600
Sbjct	541	TGGAGACCTAGCTCTTCTCAGTGTCTACTATTATAAACAATGCTACAGTGAATATTGGTG	600
Query	601	NATAAATCCTACACACCACGTAACATATCTTAAGTTCCTGGAAGAGATATTGCTAAACCA	660
Sbjct	601	NATAAATCCTACACACCACGTAACATATCTTAAGTTCCTGGAAGAGATATTGCTAAACCA	660
Query	661	GAAGATAACCTGCATTTAAAATTTGACTGCTAGGGTCAGGGTCACATTTAAATTAAATTA	720
Sbjct	661	GAAGATAACCTGCATTTAAAATTTGACTGCTAGGGTCAGGGTCACATTTAAATTAAATTA	720
Query	721	GAACAAGGAATGCATAATGTCTTCGATAGCAATCTATTCAAGGTGCACCGTGGTCACAAA	780
Sbjct	721	GAACAAGGAATGCATAATGTCTTCGATAGCAATCTATTCAAGGTGCACCGTGGTCACAAA	780
Query	781	GGAAAGCAAAACTGTC	796
Sbjct	781	GGAAAGCAAAACTGTC	796

Sequence 310 matched with Sequence 13

Query= Sequence ID - 310 nt:564

Length=564

SEQ ID NO: 13

nt:564

ALIGNMENTS

Identities = 564/564 (100%), Gaps = 0/564 (0%)

Query	1	CCTGGNCAGAGGCCTCTATCCTGTANTGATAATTGCCATCAAAATTGTCAAAAANGATTT	60
Sbjct	1	CCTGGNCAGAGGCCTCTATCCTGTANTGATAATTGCCATCAAAATTGTCAAAAANGATTT	60
Query	61	AATTTCTATGGGNAATAGTCCTTTTCTTAGCTTCTGCCNNTCACTTGCTTATTTTTTTGTG	120
Sbjct	61	AATTTCTATGGGNAATAGTCCTTTTCTTAGCTTCTGCCNNTCACTTGCTTATTTTTTTGTG	120
Query	121	TGGGAATGGGGTTGGATAAACCAATGAACTTTATTATAAACAAATCCCACCTATATCTAN	180
Sbjct	121	TGGGAATGGGGTTGGATAAACCAATGAACTTTATTATAAACAAATCCCACCTATATCTAN	180
Query	181	CAAATTTATATTTTCGGTGAAATACAGATATTTGCCTTTCTGGAGTANTATAGAAGCTGT	240
Sbjct	181	CAAATTTATATTTTCGGTGAAATACAGATATTTGCCTTTCTGGAGTANTATAGAAGCTGT	240
Query	241	CAATATGTATCTACTGTACAGTACTAAATAGTATTCATTTATGAAATGAGTAGTGTGTTGG	300
Sbjct	241	CAATATGTATCTACTGTACAGTACTAAATAGTATTCATTTATGAAATGAGTAGTGTGTTGG	300
Query	301	GTGGCTGGGGTTAAGGAAAAATGAGACTTGGAATTGTAGCTTTTATCCAAGTTTTGAGTA	360
Sbjct	301	GTGGCTGGGGTTAAGGAAAAATGAGACTTGGAATTGTAGCTTTTATCCAAGTTTTGAGTA	360
Query	361	TAAATAGGGttttgtttgtttttttAACCTAAAACTGAAATGCCATATAGAAAAACA	420
Sbjct	361	TAAATAGGGTTTTGTTTTGTTTTTTAACCTAAAACTGAAATGCCATATAGAAAAACA	420
Query	421	GCATTGTTTTTACAGTTTGTAGTAAGTAACTTTTTAAAGATTTTATCAAAAAGAATTTTG	480
Sbjct	421	GCATTGTTTTTACAGTTTGTAGTAAGTAACTTTTTAAAGATTTTATCAAAAAGAATTTTG	480

PATENT SEQUENCE ALIGNMENT

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Query  481  TCTATNGTGAGTAAAAGAAGTTCTAATAATGGCCTAATCACTGCATTTTAAAAAACAAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TCTATNGTGAGTAAAAGAAGTTCTAATAATGGCCTAATCACTGCATTTTAAAAAACAAA  540

Query  541  GTTCAACACAAATGACATTTGTTT  564
          ||||||||||||||||||
Sbjct  541  GTTCAACACAAATGACATTTGTTT  564
```

Sequence 311 matched with Sequence 14

Query= Sequence ID 311
Length=230

SEQ ID NO: 14

ALIGNMENTS

Identities = 230/230 (100%), Gaps = 0/230 (0%)

Query	1	CCTCTCCTCCATCTAAAGGCAACATTCCTTACCCATTAGTCTCAGAAATTGTCTTAAGCA	60
Sbjct	1	CCTCTCCTCCATCTAAAGGCAACATTCCTTACCCATTAGTCTCAGAAATTGTCTTAAGCA	60
Query	61	ACAGCCCCAAATGCTGGCTGCCCCGGCCAAGCATTGGGGCCGCCATCCTGCCTGGCACT	120
Sbjct	61	ACAGCCCCAAATGCTGGCTGCCCCGGCCAAGCATTGGGGCCGCCATCCTGCCTGGCACT	120
Query	121	GGCTGATGGGCACCTCTGTTGGTTCCATCAGCCAGAGCTCTGCCAAAGGCCCCGCAGTCC	180
Sbjct	121	GGCTGATGGGCACCTCTGTTGGTTCCATCAGCCAGAGCTCTGCCAAAGGCCCCGCAGTCC	180
Query	181	CTCTCCCAGGAGGACCCTAGAGGCAATTAAATGATGTCCTGTTCCATTGG	230
Sbjct	181	CTCTCCCAGGAGGACCCTAGAGGCAATTAAATGATGTCCTGTTCCATTGG	230

Sequence 313 matched with Sequence 15

Query= Sequence ID - 313 nt: 554
Length=554

SEQ ID NO: 15 nt: 554

ALIGNMENTS

Identities = 170/191 (89%), Gaps = 12/191 (6%)

```
Query 112 TATAGATTA-AAGATCTATGGGTTTTTAATATGGATTANAAATCTGTGGGTTTTTGATAT 170
      ||| ||||| || |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 168 TATGGATTANAA-ATCTGTGGGTTTTTAATATGGATTGGAAATCTGTGGGTTTTTAATAT 226

Query 171 GGATT--ANAA-ATCTGTGGGTTTTTAATATGGATTGGAA-ATCTGTGGGTTTTTAATAT 226
      ||||| | || | ||||| ||||| ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct 227 GGATTAAAAAACATCTGTGGGTTTTTAATATGGATT-AAACATCTGTGGGTTTTTAATAT 285

Query 227 GGATTAAAAAACATCTGTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATG 286
      ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 286 GGATT---AAACATC--TGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATG 340

Query 287 GATTAAACATC 297
      | ||||| |||
Sbjct 341 GGTTAAAAATC 351
```

Sequence 314 matched with Sequence 16

Query= Sequence ID 314
Length=610

SEQ ID NO: 16

ALIGNMENTS

Identities = 610/610 (100%), Gaps = 0/610 (0%)

Query	1	CTTTTCCTCCCGCTGTCCCCACGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGTG	60
Sbjct	1	CTTTTCCTCCCGCTGTCCCCACGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGTG	60
Query	61	AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTTCG	120
Sbjct	61	AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTTCG	120
Query	121	GGAAGTGTTTTTGAGAAGTCTCGGTCCGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA	180
Sbjct	121	GGAAGTGTTTTTGAGAAGTCTCGGTCCGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA	180
Query	181	ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCAGATGAGGCAGCTGTGACTGTGTC	240
Sbjct	181	ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCAGATGAGGCAGCTGTGACTGTGTC	240
Query	241	AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA	300
Sbjct	241	AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA	300
Query	301	AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACTA	360
Sbjct	301	AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACTA	360
Query	361	TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCTACAACAGTGTCTGG	420
Sbjct	361	TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCTACAACAGTGTCTGG	420
Query	421	GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG	480
Sbjct	421	GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAA  540
          |||
Sbjct  481  CTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAA  540

Query  541  GAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACCTCTGACAACCAC  600
          |||
Sbjct  541  GAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACCTCTGACAACCAC  600

Query  601  AATCATGAGG  610
          |||
Sbjct  601  AATCATGAGG  610
```

Sequence 315 matched with Sequence 17

Query= Sequence ID 315
Length=359

SEQ ID NO: 17

ALIGNMENTS

Identities = 359/359 (100%), Gaps = 0/359 (0%)

Query	1	TGGTACAGATACAAACTGGACTCTCAGGACAAAACGACACCAGCCAAACCAGCAGCCCCT	60
Sbjct	1	TGGTACAGATACAAACTGGACTCTCAGGACAAAACGACACCAGCCAAACCAGCAGCCCCT	60
Query	61	CAGCATCCAGCAGCATGAGCGGAGGCATTTTCCTTTTCTTCGTGGCCAATGCCATAATCC	120
Sbjct	61	CAGCATCCAGCAGCATGAGCGGAGGCATTTTCCTTTTCTTCGTGGCCAATGCCATAATCC	120
Query	121	ACCTCTTCTGCTTCAGTTGAGGTGACACGTCTCAGCCTTAGCCCTGTGCCCCCTGAAACA	180
Sbjct	121	ACCTCTTCTGCTTCAGTTGAGGTGACACGTCTCAGCCTTAGCCCTGTGCCCCCTGAAACA	180
Query	181	GCTGCCACCATCACTCGCAAGAGAATCCCCTCCATCTTTGGGAGGGGTTGATGCCAGACA	240
Sbjct	181	GCTGCCACCATCACTCGCAAGAGAATCCCCTCCATCTTTGGGAGGGGTTGATGCCAGACA	240
Query	241	TCACCAGGTTGTAGAAGTTGACAGGCAGTGCCATGGGGGCAACAGCCAAAATAGGGGGGT	300
Sbjct	241	TCACCAGGTTGTAGAAGTTGACAGGCAGTGCCATGGGGGCAACAGCCAAAATAGGGGGGT	300
Query	301	AATGATGTACGGGCCAAGCACTGCCCAGCTGGGGGTCAATAAAGTTACCCTTGTA	359
Sbjct	301	AATGATGTACGGGCCAAGCACTGCCCAGCTGGGGGTCAATAAAGTTACCCTTGTA	359

Sequence 321 matched with Sequence 19

Query= Sequence ID 321
Length=661

SEQ ID NO: 19

ALIGNMENTS

Identities = 661/661 (100%), Gaps = 0/661 (0%)

Query	1	CAGAACAGTACTTTTTAATTTGACCCATGAATTCTATTTAAATTTGTCACTTAATATTTA	60
Sbjct	1	CAGAACAGTACTTTTTAATTTGACCCATGAATTCTATTTAAATTTGTCACTTAATATTTA	60
Query	61	GCCAAGAAGCAAACCATCTAAAAAGATTCTGGTTTATTTCTCCAACCTCCTAATAAATAG	120
Sbjct	61	GCCAAGAAGCAAACCATCTAAAAAGATTCTGGTTTATTTCTCCAACCTCCTAATAAATAG	120
Query	121	GGTCACATAttttttaacttttttCTAATTTGAAAAGTAATACAGGCATATGGTATTTTA	180
Sbjct	121	GGTCACATATTTTTTAACTTTTTCTAATTTGAAAAGTAATACAGGCATATGGTATTTTA	180
Query	181	AAAATGAAACAACACAAAGGGATATGTTTTGAAAAGTGGTTCTTGCCATCCCTGAACTGT	240
Sbjct	181	AAAATGAAACAACACAAAGGGATATGTTTTGAAAAGTGGTTCTTGCCATCCCTGAACTGT	240
Query	241	AATCATCCCTAACATATTCATACCTGTTTTCATTTTTAAAAGTTGGGTCAGtttttttATT	300
Sbjct	241	AATCATCCCTAACATATTCATACCTGTTTTCATTTTTAAAAGTTGGGTCAGTTTTTTTATT	300
Query	301	AGTACATGTATTTCTATCCTACTGATTTATTTGCTATATCATCTAATTTAGTTTGAATAT	360
Sbjct	301	AGTACATGTATTTCTATCCTACTGATTTATTTGCTATATCATCTAATTTAGTTTGAATAT	360
Query	361	TCCATAATTTACTTAATTAGTCCTGTATGGAGACCTAGCTCTTCTCAGTGTCTACTATTA	420
Sbjct	361	TCCATAATTTACTTAATTAGTCCTGTATGGAGACCTAGCTCTTCTCAGTGTCTACTATTA	420
Query	421	TAAACAATGCTACAGTGAATATTGGTGTATAAATCCATACACACCACGTAACATATCTTA	480
Sbjct	421	TAAACAATGCTACAGTGAATATTGGTGTATAAATCCATACACACCACGTAACATATCTTA	480

Query	481	AGTTCCTGGAAGAGATATTGCTAAACCAGAAGATAACCTGCATTATAAAATTTTGACTGCT	540
Sbjct	481	AGTTCCTGGAAGAGATATTGCTAAACCAGAAGATAACCTGCATTATAAAATTTTGACTGCT	540
Query	541	AGGGTCAGGGTCACATTTAAATTAAATTAGAACAAGGAATGCATAATGTCTTCGATAGCA	600
Sbjct	541	AGGGTCAGGGTCACATTTAAATTAAATTAGAACAAGGAATGCATAATGTCTTCGATAGCA	600
Query	601	ATCTATTCCAGGTGCACCGTGGTCACAAAGGAAAGCAAACTGTCAATAACTTTCTTCTC	660
Sbjct	601	ATCTATTCCAGGTGCACCGTGGTCACAAAGGAAAGCAAACTGTCAATAACTTTCTTCTC	660
Query	661	A 661	
Sbjct	661	A 661	

Sequence 322 matched with Sequence 20

Query= Sequence ID 322
Length=770

SEQ ID NO: 20

ALIGNMENTS

Identities = 770/770 (100%), Gaps = 0/770 (0%)

Query	1	TAGCATTGGCCTTTTAAACATTTGTTTAttttttttCTGAGAATGGCTAACACACTTT	60
Sbjct	1	TAGCATTGGCCTTTTAAACATTTGTTTATTTTTTTTCTGAGAATGGCTAACACACTTT	60
Query	61	ATTGAGGTCGAAATTAATAAAGAAAATAAAAGAAATGTATCTTCATTCATTCTGTATGT	120
Sbjct	61	ATTGAGGTCGAAATTAATAAAGAAAATAAAAGAAATGTATCTTCATTCATTCTGTATGT	120
Query	121	TAGTGTTTTAATTACCCTTAGAATATATGGATAAAAAATACTATTCTTTGTCTTGGAGAA	180
Sbjct	121	TAGTGTTTTAATTACCCTTAGAATATATGGATAAAAAATACTATTCTTTGTCTTGGAGAA	180
Query	181	GGTAAGAGTCTAGTTAGATGAATAAGGGTTATCTATGTAGAACAACCTAGAGAATGAGAAG	240
Sbjct	181	GGTAAGAGTCTAGTTAGATGAATAAGGGTTATCTATGTAGAACAACCTAGAGAATGAGAAG	240
Query	241	AGAGCTTATGAGATTGAGTACTACGTTATGCAGTAGAGTAGCACGTCATCTGCTACTGAG	300
Sbjct	241	AGAGCTTATGAGATTGAGTACTACGTTATGCAGTAGAGTAGCACGTCATCTGCTACTGAG	300
Query	301	TATGGTGTGATAACATTGTGTAACAGGAAAGTATGATCAATATCTACTTAAAATTAAGGA	360
Sbjct	301	TATGGTGTGATAACATTGTGTAACAGGAAAGTATGATCAATATCTACTTAAAATTAAGGA	360
Query	361	CAATATTAGCACTACATTGCTTTATTTTAAAGTAAAAATTAGAGAACTAAACACAAGCAT	420
Sbjct	361	CAATATTAGCACTACATTGCTTTATTTTAAAGTAAAAATTAGAGAACTAAACACAAGCAT	420
Query	421	TGTAAGTACAATAAAAGCTGATCTTTCTAGTTAAGCAGAATAATACATGTTCAAGCATCT	480
Sbjct	421	TGTAAGTACAATAAAAGCTGATCTTTCTAGTTAAGCAGAATAATACATGTTCAAGCATCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCTAAATCATTAATATAAGAATATAGGGGTTTTCTATAATCTTATTTTCTTTGGAAGAG	540
Sbjct	481	GCTAAATCATTAATATAAGAATATAGGGGTTTTCTATAATCTTATTTTCTTTGGAAGAG	540
Query	541	TACCTCATTTTCAAGANGAGAAGTTTCTAATTGCCACTTCTTTAAAAATAAAACAGGGTT	600
Sbjct	541	TACCTCATTTTCAAGANGAGAAGTTTCTAATTGCCACTTCTTTAAAAATAAAACAGGGTT	600
Query	601	TTAATGTTCCCAGCACAAAAATTAATATCTCTTCAAAAAGTCTCTTGTGATTAAGTTTGA	660
Sbjct	601	TTAATGTTCCCAGCACAAAAATTAATATCTCTTCAAAAAGTCTCTTGTGATTAAGTTTGA	660
Query	661	ATCCCTTGTCACTGCTTCTAATATTGACACTGACCTCCTTAGGTATTTTTCAGGGGTT	720
Sbjct	661	ATCCCTTGTCACTGCTTCTAATATTGACACTGACCTCCTTAGGTATTTTTCAGGGGTT	720
Query	721	ATAATCTTTTCTTAAGGTATCTTTTTTCAAGAATTGGATACCTTGGGCTT	770
Sbjct	721	ATAATCTTTTCTTAAGGTATCTTTTTTCAAGAATTGGATACCTTGGGCTT	770

Sequence 323 matched with Sequence 21

Query= Sequence ID 323
Length=654

SEQ ID NO: 21

ALIGNMENTS

Identities = 654/654 (100%), Gaps = 0/654 (0%)

Query	1	CGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAAGA	60
Sbjct	1	CGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAAGA	60
Query	61	AAGGGTCCAAGACTCCATTAAGTGCCTGGATGAAGGGCACTGCTACAGCAGCTAGTACC	120
Sbjct	61	AAGGGTCCAAGACTCCATTAAGTGCCTGGATGAAGGGCACTGCTACAGCAGCTAGTACC	120
Query	121	AGAGACTCTCCTATCTCACGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGAAT	180
Sbjct	121	AGAGACTCTCCTATCTCACGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGAAT	180
Query	181	GCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCCAG	240
Sbjct	181	GCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCCAG	240
Query	241	TGCAACCCTTGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCTGG	300
Sbjct	241	TGCAACCCTTGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCTGG	300
Query	301	AAACACACCAGCTTCTGCTACCTTCATGCTCATTGTTaaaaaaaGATTAACCAGTGTGAA	360
Sbjct	301	AAACACACCAGCTTCTGCTACCTTCATGCTCATTGTTAAAAAAGATTAACCAGTGTGAA	360
Query	361	CATTCTGATCTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTGGTAGAA	420
Sbjct	361	CATTCTGATCTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTGGTAGAA	420
Query	421	TAACCCCCAAAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAAGA	480
Sbjct	421	TAACCCCCAAAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAAGA	480

Sequence 324 matched with Sequence 22

Query= Sequence ID 324
Length=676

SEQ ID NO: 22

ALIGNMENTS

Identities = 676/676 (100%), Gaps = 0/676 (0%)

Query	1	GTTTGTTACAGGCAGAATTGGATAGATACAGCCCTACAAATGTATATGCCCTCCCCTGaa	60
Sbjct	1	GTTTGTTACAGGCAGAATTGGATAGATACAGCCCTACAAATGTATATGCCCTCCCCTGAA	60
Query	61	aaaaaTTGGATGAAAATCTGCACAGCAAAGTGAAACACACAGATAATAGGAACAAAATGT	120
Sbjct	61	AAAAATTGGATGAAAATCTGCACAGCAAAGTGAAACACACAGATAATAGGAACAAAATGT	120
Query	121	AGTTCCCATGTGCCAAACAAAATAAATGAAATCTCTGCATGTTTGCAGCATATCTGCCTT	180
Sbjct	121	AGTTCCCATGTGCCAAACAAAATAAATGAAATCTCTGCATGTTTGCAGCATATCTGCCTT	180
Query	181	TTGGGAATGTAATCAAGGNATAATCTTTGGCTAGTGTTATGTGCCTGTAttttttAAAA	240
Sbjct	181	TTGGGAATGTAATCAAGGNATAATCTTTGGCTAGTGTTATGTGCCTGTATTTTTTTAAAA	240
Query	241	TGGTACACCAGAAAAGGACTGGCAGTCTACTTCTACCATAGTTAAACTTCACCCTCTTTA	300
Sbjct	241	TGGTACACCAGAAAAGGACTGGCAGTCTACTTCTACCATAGTTAAACTTCACCCTCTTTA	300
Query	301	ATTTCAACATATTCTTTGGAAGCAGGAAGAAATGCTCATAAAGAGGATCAGACCTTCT	360
Sbjct	301	ATTTCAACATATTCTTTGGAAGCAGGAAGAAATGCTCATAAAGAGGATCAGACCTTCT	360
Query	361	TTCCCGTGAAACCAGTATTTGGCGCCATATATAAGCCTGGTTAAATTGGTCATCTAAAGC	420
Sbjct	361	TTCCCGTGAAACCAGTATTTGGCGCCATATATAAGCCTGGTTAAATTGGTCATCTAAAGC	420
Query	421	TGTCAAATAAGACATTCTGTGAAAGGTAAACATCGAAACTGGTTATAAGTAAAACCATCA	480
Sbjct	421	TGTCAAATAAGACATTCTGTGAAAGGTAAACATCGAAACTGGTTATAAGTAAAACCATCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGCCAACAACAGGGTCTTGAGATAACCTTTGAAGCTTATTGTCTGGCCTGCACCAGAAGA	540
Sbjct	481	AGCCAACAACAGGGTCTTGAGATAACCTTTGAAGCTTATTGTCTGGCCTGCACCAGAAGA	540
Query	541	TGTCTGCATTACTCATTGCTAAAAATGTGTACACAGAACTGCACTAGGATTAATTGGTTC	600
Sbjct	541	TGTCTGCATTACTCATTGCTAAAAATGTGTACACAGAACTGCACTAGGATTAATTGGTTC	600
Query	601	AAGAAGAAATTTAAACTTACGTTTGGGTTTCCATACAGCACTCTATTGAATACATGCATC	660
Sbjct	601	AAGAAGAAATTTAAACTTACGTTTGGGTTTCCATACAGCACTCTATTGAATACATGCATC	660
Query	661	TGAATTTAAGTTGCAA	676
Sbjct	661	TGAATTTAAGTTGCAA	676

Sequence 325 matched with Sequence 23

Query= Sequence ID 325
Length=609

SEQ ID NO: 23

ALIGNMENTS

Identities = 609/609 (100%), Gaps = 0/609 (0%)

Query	1	GACCAGTAATGGCTTTTAAGAGTCCATTTTGTTCATTGTCTCCCTAGTTAATTACAGGTGG	60
Sbjct	1	GACCAGTAATGGCTTTTAAGAGTCCATTTTGTTCATTGTCTCCCTAGTTAATTACAGGTGG	60
Query	61	GGGATCTTTTGCCTCTATTCTCTTCATATTGAAATGAATCATACTCATGTTTTGTGGAAC	120
Sbjct	61	GGGATCTTTTGCCTCTATTCTCTTCATATTGAAATGAATCATACTCATGTTTTGTGGAAC	120
Query	121	TCCTTAAAGTTGTAGCTGTCATGATCAGAtttttttttATATTTCCCTCAGCTTAACTCTGC	180
Sbjct	121	TCCTTAAAGTTGTAGCTGTCATGATCAGATTTTTTTTATATTTCCCTCAGCTTAACTCTGC	180
Query	181	TACTTGATTTACAGTGACCCATAACCTACTCATCCTTGGTTTATAGTGACACATAATCTT	240
Sbjct	181	TACTTGATTTACAGTGACCCATAACCTACTCATCCTTGGTTTATAGTGACACATAATCTT	240
Query	241	ATCTCTTTATAGAACCCTTAAATTTTATCATTATTTTCGCTTAGAATACAGCATTTCCTTG	300
Sbjct	241	ATCTCTTTATAGAACCCTTAAATTTTATCATTATTTTCGCTTAGAATACAGCATTTCCTTG	300
Query	301	CTTCTGTTGCTGGTTTGACTTAAGAAATAAGGCAGTAACTCTGATCAATCAATTATCCAT	360
Sbjct	301	CTTCTGTTGCTGGTTTGACTTAAGAAATAAGGCAGTAACTCTGATCAATCAATTATCCAT	360
Query	361	AAGGAAGGGCTTTTCATGGGTTCTATTAATTTGTTAGTACCCTAAGTATATCTGAAAAAT	420
Sbjct	361	AAGGAAGGGCTTTTCATGGGTTCTATTAATTTGTTAGTACCCTAAGTATATCTGAAAAAT	420
Query	421	ATGTCTATTGAGAGAAGATTTTGGCATTCCAGATGGTATAGTCTATATATATTTAAAGTT	480
Sbjct	421	ATGTCTATTGAGAGAAGATTTTGGCATTCCAGATGGTATAGTCTATATATATTTAAAGTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TTGAATTTGCTTATATATACTCAGCTTTCTTTTTCTAGCATTTTGCATTTACCTGTTAA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTGAATTTGCTTATATATACTCAGCTTTCTTTTTCTAGCATTTTGCATTTACCTGTTAA  540

Query  541  TTGAAGTATACCCCCCACATATAAAAGTTCCTCTTAAAGACACTGGACTCTTTCTGGGGG  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TTGAAGTATACCCCCCACATATAAAAGTTCCTCTTAAAGACACTGGACTCTTTCTGGGGG  600

Query  601  GCTAAAATA  609
          ||||||||
Sbjct  601  GCTAAAATA  609
```

Sequence 326 matched with Sequence 24

Query= Sequence ID - 326 nt: 554
Length=554

SEQ ID NO: 24 nt: 554

ALIGNMENTS

Identities = 170/191 (89%), Gaps = 12/191 (6%)

```
Query 112 TATAGATTA-AAGATCTATGGGTTTTTAATATGGATTANAAATCTGTGGGTTTTTGATAT 170
      ||| ||||| || |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 168 TATGGATTANAA-ATCTGTGGGTTTTTAATATGGATTGGAAATCTGTGGGTTTTTAATAT 226

Query 171 GGATT--ANAA-ATCTGTGGGTTTTTAATATGGATTGGAA-ATCTGTGGGTTTTTAATAT 226
      ||||| | || | ||||| ||||| ||||| ||||| || || ||||| ||||| |||||
Sbjct 227 GGATTAAAAAACATCTGTGGGTTTTTAATATGGATT-AAACATCTGTGGGTTTTTAATAT 285

Query 227 GGATTAAAAAACATCTGTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATG 286
      ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 286 GGATT---AAACATC--TGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATG 340

Query 287 GATTAAACATC 297
      | ||||| |||
Sbjct 341 GGTTAAAAATC 351
```

Sequence 327 matched with Sequence 25

Query= Sequence ID 327
Length=674

SEQ ID NO: 25

ALIGNMENTS

Identities = 671/671 (100%), Gaps = 0/671 (0%)

Query	1	CGGCTACCGACAGAAGGACTATTTTCATCGCCACCCAGGGGCCACTGGCACACACGGTTGA	60
Sbjct	1	CGGCTACCGACAGAAGGACTATTTTCATCGCCACCCAGGGGCCACTGGCACACACGGTTGA	60
Query	61	GGACTTCTGGAGGATGATCTGGGAGGGGAAGTCCCACACTATCGTGATGCTGACGGAGGT	120
Sbjct	61	GGACTTCTGGAGGATGATCTGGGAGGGGAAGTCCCACACTATCGTGATGCTGACGGAGGT	120
Query	121	GCAGGAGAGAGAGCAGGATAAATGCTACCAAGTATTGGCCAACCGAGGGCTCAGTTACTCA	180
Sbjct	121	GCAGGAGAGAGAGCAGGATAAATGCTACCAAGTATTGGCCAACCGAGGGCTCAGTTACTCA	180
Query	181	TGGAGAAATAACGATTGAGATAAAGAATGATACCCTTTTCTCAGAAGCCATCAGTATACGAGA	240
Sbjct	181	TGGAGAAATAACGATTGAGATAAAGAATGATACCCTTTTCTCAGAAGCCATCAGTATACGAGA	240
Query	241	CTTTCTGGTCACTCTCAATCAGCCCCAGGCCCGCCAGGAGGAGCAGGTCCGAGTAGTGCG	300
Sbjct	241	CTTTCTGGTCACTCTCAATCAGCCCCAGGCCCGCCAGGAGGAGCAGGTCCGAGTAGTGCG	300
Query	301	CCAGTTTCACTTCCACGGCTGGCCTGAGATCGGGATTCCCGCCGAGGGCAAAGGCATGAT	360
Sbjct	301	CCAGTTTCACTTCCACGGCTGGCCTGAGATCGGGATTCCCGCCGAGGGCAAAGGCATGAT	360
Query	361	TGACCTCATCGCAGCCGTGCAGAAGCANCAGCAGCAGACAGGCAACCACCCCATCACCGT	420
Sbjct	361	TGACCTCATCGCAGCCGTGCAGAAGCANCAGCAGCAGACAGGCAACCACCCCATCACCGT	420
Query	421	GCACTGCAGTGCCGGAGCTGGGCGAACAGGTACATTCATAGCCCTCAGCAACATTTTGGGA	480
Sbjct	421	GCACTGCAGTGCCGGAGCTGGGCGAACAGGTACATTCATAGCCCTCAGCAACATTTTGGGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GCGAGTAAAAGCCGAGGGACTTTTANATGTATTTCAAGCTGTGAAGAGTTTACGACTTCA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GCGAGTAAAAGCCGAGGGACTTTTANATGTATTTCAAGCTGTGAAGAGTTTACGACTTCA  540

Query  541  GAGACCACATATGGTGCAACCCTGGAACAGTATGAAATGTGCTACAAAGTGGTACAAGAT  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GAGACCACATATGGTGCAACCCTGGAACAGTATGAAATGTGCTACAAAGTGGTACAAGAT  600

Query  601  TTATTGATATATTTCTGATTATGCTAATTTCAATGAAGATCCTGCCTTAAATATTTTTTA  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TTATTGATATATTTCTGATTATGCTAATTTCAATGAAGATCCTGCCTTAAATATTTTTTA  660

Query  661  ATTTAATGGCA  671
          |||||||||
Sbjct  661  ATTTAATGGCA  671
```

Sequence 328 matched with Sequence 26

Query= Sequence ID 328

Length=609

SEQ ID NO: 26

ALIGNMENTS

Identities = 609/609 (100%), Gaps = 0/609 (0%)

Query	1	CAAGACTCCATCTCaaaaaaaaaaaaaaaaaTCTACAGTGCTGAGTATATAAAATTATTAAC	60
Sbjct	1	CAAGACTCCATCTCAAAAAAAAAAAAAAAAAATCTACAGTGCTGAGTATATAAAATTATTAAC	60
Query	61	ACATTTTACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAACAGGTAAT	120
Sbjct	61	ACATTTTACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAACAGGTAAT	120
Query	121	TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT	180
Sbjct	121	TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT	180
Query	181	GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT	240
Sbjct	181	GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT	240
Query	241	TTGTTCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT	300
Sbjct	241	TTGTTCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT	300
Query	301	GCCAAATATGGGTAAATAAGGGAAAAATTTGTTTAAATATTTAGTCCTTCTGAGATGGCTT	360
Sbjct	301	GCCAAATATGGGTAAATAAGGGAAAAATTTGTTTAAATATTTAGTCCTTCTGAGATGGCTT	360
Query	361	GAATATTTGAATTTTGTGTTGACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA	420
Sbjct	361	GAATATTTGAATTTTGTGTTGACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA	420
Query	421	GAGGAAAGATGGATTTTCAGTCTGTATTTTAAACATCATTTATTTTAAATCTGGTGCTGA	480
Sbjct	421	GAGGAAAGATGGATTTTCAGTCTGTATTTTAAACATCATTTATTTTAAATCTGGTGCTGA	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 AAAATAAGaaaaaaTTAAACTGCATTCTGCTGTTCTTCTTTANAAGCATTCTGCGTAA 540
          |||
Sbjct 481 AAAATAAGAAAAAAATTAAGTGCATTCTGCTGTTCTTCTTTANAAGCATTCTGCGTAA 540

Query 541 ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA 600
          |||
Sbjct 541 ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA 600

Query 601 GTGGTTTTT 609
          |||
Sbjct 601 GTGGTTTTT 609
```

Sequence 330 matched with Sequence 27

Query= Sequence ID 330
Length=383

SEQ ID NO: 27

ALIGNMENTS

Identities = 383/383 (100%), Gaps = 0/383 (0%)

Query	1	GCGGGAATCGCGGCCCGCGTCGACCTCAAAGGAGaaaaaaaaaccttgtaaaaaagcaaa	60
Sbjct	1	GCGGGAATCGCGGCCCGCGTCGACCTCAAAGGAGAAAAAAACCTTGTAaaaaAAGCAAA	60
Query	61	aatgacaacagaaaaaCAATCTTATTCCGAGCATTCCAGTAACTTTTTGTGTATGTACT	120
Sbjct	61	AATGACAACAGAAAAACAATCTTATTCCGAGCATTCCAGTAACTTTTTGTGTATGTACT	120
Query	121	TAGCTGTACTATAAGTAGTTGGTTTGTATGAGATGGTTAAAAAGGCCAAAGATAAAAGGT	180
Sbjct	121	TAGCTGTACTATAAGTAGTTGGTTTGTATGAGATGGTTAAAAAGGCCAAAGATAAAAGGT	180
Query	181	TTCtttttttttcccttttttgtctatgaagttgctgtttattttttttGGCCTGTTTGAT	240
Sbjct	181	TTCTTTTTTTTCCTTTTTTGTCTATGAAGTTGCTGTTTATTTTTTTTGGCCTGTTTGAT	240
Query	241	GTATGTGTGAAACAATGTTGTCCAACAATAAACAGGAATTTTATTTTGCTGAGTTGTTCT	300
Sbjct	241	GTATGTGTGAAACAATGTTGTCCAACAATAAACAGGAATTTTATTTTGCTGAGTTGTTCT	300
Query	301	aattttaaaatt	360
Sbjct	301	AAATTTTAAATTT	360
Query	361	ttttaaataaaaaCCCTTGTTTAT	383
Sbjct	361	TTTAAATAAAACCCTTGTTTAT	383

Sequence 331 matched with Sequence 28

Query= Sequence ID 331

Length=729

SEQ ID NO: 28

ALIGNMENTS

Identities = 729/729 (100%), Gaps = 0/729 (0%)

Query	1	GCCGCGTCGACCTGCATGAGCCACAGTTTCTTGA	60
Sbjct	1	GCCGCGTCGACCTGCATGAGCCACAGTTTCTTGA	60
Query	61	AGGCCTTGTTCTGAGCCCTGACATGTGCTTGGGCA	120
Sbjct	61	AGGCCTTGTTCTGAGCCCTGACATGTGCTTGGGCA	120
Query	121	GCCTCCTGCCCTGATCAGGGACCCTCCCCGCTTTC	180
Sbjct	121	GCCTCCTGCCCTGATCAGGGACCCTCCCCGCTTTC	180
Query	181	GCAAAACAAAGGCAGTTTTATATGAAAGATTANA	240
Sbjct	181	GCAAAACAAAGGCAGTTTTATATGAAAGATTANA	240
Query	241	TGATGTAATTCCCACTGTAATAGCATAGGGATTTT	300
Sbjct	241	TGATGTAATTCCCACTGTAATAGCATAGGGATTTT	300
Query	301	CATCANTGGGGCCAAGGGTTCTCTGTCCCTGGTT	360
Sbjct	301	CATCANTGGGGCCAAGGGTTCTCTGTCCCTGGTT	360
Query	361	TTTCCTGGTGATGCCTTGTTTGGGGTTCTGTGGG	420
Sbjct	361	TTTCCTGGTGATGCCTTGTTTGGGGTTCTGTGGG	420
Query	421	TGAATGTAACCTGCTAGCTCTCCGAAGCCCTGCG	480
Sbjct	421	TGAATGTAACCTGCTAGCTCTCCGAAGCCCTGCG	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 AGTGGTGGCCGCGCTGTGCCTGCTCGTGTTGCCTACATGTCCCTGGCTTGTTGAGGCGCT 540
          |||
Sbjct 481 AGTGGTGGCCGCGCTGTGCCTGCTCGTGTTGCCTACATGTCCCTGGCTTGTTGAGGCGCT 540

Query 541 GCTTCAACCTGCACCCCTCCTTGTCTCATAGATGCTCCTTTTGACCTTTTCAAAATTAAT 600
          |||
Sbjct 541 GCTTCAACCTGCACCCCTCCTTGTCTCATAGATGCTCCTTTTGACCTTTTCAAAATTAAT 600

Query 601 ATGGATGGGAAAGCTCCTATGCCTTTTGGCTTCCTGGTAGAAGGCGGGATGCCCAAGGGT 660
          |||
Sbjct 601 ATGGATGGGAAAGCTCCTATGCCTTTTGGCTTCCTGGTAGAAGGCGGGATGCCCAAGGGT 660

Query 661 CTGCCTGGGTGTGGATTGGATGCTTGGGGTGTGGGGGTTGGAAACTGTCTTGTGGCCCAC 720
          |||
Sbjct 661 CTGCCTGGGTGTGGATTGGATGCTTGGGGTGTGGGGGTTGGAAACTGTCTTGTGGCCCAC 720

Query 721 TTGGGCCCC 729
          |||
Sbjct 721 TTGGGCCCC 729
```

Sequence 335 matched with Sequence 29

Query= Sequence ID 335
Length=552

SEQ ID NO: 29

ALIGNMENTS

Identities = 552/552 (100%), Gaps = 0/552 (0%)

Query	1	CCCGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAA	60
Sbjct	1	CCCGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAA	60
Query	61	GAAAGGGTCCAAGACTCCATTAAGTGCCTGGATGAAGGGCACTGCTACAGCAGCTAGTA	120
Sbjct	61	GAAAGGGTCCAAGACTCCATTAAGTGCCTGGATGAAGGGCACTGCTACAGCAGCTAGTA	120
Query	121	CCAGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGA	180
Sbjct	121	CCAGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGA	180
Query	181	ATGCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCC	240
Sbjct	181	ATGCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCC	240
Query	241	AGTGCAACCCTTGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCT	300
Sbjct	241	AGTGCAACCCTTGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCT	300
Query	301	GGAAACACACCAGCTTCTGCTACCTTCATGCTCATTGTTaaaaaaaGATTAACCAGTGTG	360
Sbjct	301	GGAAACACACCAGCTTCTGCTACCTTCATGCTCATTGTTAAAAAAGATTAACCAGTGTG	360
Query	361	AACATTCTGATCTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTGGTAG	420
Sbjct	361	AACATTCTGATCTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTGGTAG	420
Query	421	AATAACCCCCAAAAGCTCAAAGCTAAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAA	480
Sbjct	421	AATAACCCCCAAAAGCTCAAAGCTAAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GAATGGACTGGCGGCGTGGGTGAGCTGATTGGAAGAACTGCCCTTCTGCAAAAAACACTG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAATGGACTGGCGGCGTGGGTGAGCTGATTGGAAGAACTGCCCTTCTGCAAAAAACACTG  540

Query  541  GCCTGCTTTCCA  552
          |||||||||
Sbjct  541  GCCTGCTTTCCA  552
```

Sequence 337 matched with Sequence 30

Query= Sequence ID 337
Length=606

SEQ ID NO: 30

ALIGNMENTS

Identities = 606/606 (100%), Gaps = 0/606 (0%)

Query	1	CAAGACTCCATCTCaaaaaaaaaaaaaaaaTCTACAGTGCTGAGTATATAAAATTATTAAC	60
Sbjct	1	CAAGACTCCATCTCAAAAAAAAAAAAAAAAAATCTACAGTGCTGAGTATATAAAATTATTAAC	60
Query	61	ACATTTTCAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAACAGGTAAT	120
Sbjct	61	ACATTTTCAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAACAGGTAAT	120
Query	121	TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT	180
Sbjct	121	TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT	180
Query	181	GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT	240
Sbjct	181	GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT	240
Query	241	TTGTTCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT	300
Sbjct	241	TTGTTCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT	300
Query	301	GCCAAATATGGGTAAATAAGGGAAAAATTTGTTTAAATATTTAGTCCTTCTGAGATGGCTT	360
Sbjct	301	GCCAAATATGGGTAAATAAGGGAAAAATTTGTTTAAATATTTAGTCCTTCTGAGATGGCTT	360
Query	361	GAATATTTGAATTTTGTGTTGACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA	420
Sbjct	361	GAATATTTGAATTTTGTGTTGACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA	420
Query	421	GAGGAAAGATGGATTTTCAGTCTGTATTTTAAACATCATTTATTTTAAATCTGGTGCTGA	480
Sbjct	421	GAGGAAAGATGGATTTTCAGTCTGTATTTTAAACATCATTTATTTTAAATCTGGTGCTGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AAAATAAGaaaaaaTTAAACTGCATTCTGCTGTTCTTCTTTAGAACGATTCCTGCGTAA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AAAATAAGAAAAAAATTAAGTGCATTCTGCTGTTCTTCTTTAGAACGATTCCTGCGTAA  540

Query  541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA  600

Query  601  GTGGTT  606
          |||||
Sbjct  601  GTGGTT  606
```

Sequence 338 matched with Sequence 31

Query= Sequence ID 338

Length=734

SEQ ID NO: 31

ALIGNMENTS

Identities = 734/734 (100%), Gaps = 0/734 (0%)

Query	1	CTGGACTGCATGACCAGATCTGATGGGTGAGACTCAGGTGGCATGGAAGAGCCGAAAGAG	60
Sbjct	1	CTGGACTGCATGACCAGATCTGATGGGTGAGACTCAGGTGGCATGGAAGAGCCGAAAGAG	60
Query	61	GATACCATATGTGGGTGCCgggggggATAGGTGAGAAGTACTAGAAGGCGGAATGGAAGG	120
Sbjct	61	GATACCATATGTGGGTGCCGGGGGGGATAGGTGAGAAGTACTAGAAGGCGGAATGGAAGG	120
Query	121	ACACTTCTGCTCAGCTCTGTGACACGGGCAGGGACCCTGCAGGGCTCAGGTCCTTTAACA	180
Sbjct	121	ACACTTCTGCTCAGCTCTGTGACACGGGCAGGGACCCTGCAGGGCTCAGGTCCTTTAACA	180
Query	181	CAGCAGCTTCATTCTAACACCAGCAGCGTTGGAACACACGTACAAGTATGCAGACTAAGC	240
Sbjct	181	CAGCAGCTTCATTCTAACACCAGCAGCGTTGGAACACACGTACAAGTATGCAGACTAAGC	240
Query	241	TCTTGCTTGGCTGATACGGCTTTTTGGGTTTTTAGAGAACATGCATATATGTTCTCATTC	300
Sbjct	241	TCTTGCTTGGCTGATACGGCTTTTTGGGTTTTTAGAGAACATGCATATATGTTCTCATTC	300
Query	301	ATGGTACATGAACTCAGAAGCCTTACTGCCTATTTTTGTTAATACTTCTGGGCAAACATT	360
Sbjct	301	ATGGTACATGAACTCAGAAGCCTTACTGCCTATTTTTGTTAATACTTCTGGGCAAACATT	360
Query	361	ACCACTTACAACCTCACACCAGTTAGAAATCATTTGTAAAATGTTATTTAATAAAGCCAAA	420
Sbjct	361	ACCACTTACAACCTCACACCAGTTAGAAATCATTTGTAAAATGTTATTTAATAAAGCCAAA	420
Query	421	GAACTAAATCATATTTATTTTCCAAGNTTTCTAAGATCTCTGAAACTAATGAGGTTTTT	480
Sbjct	421	GAACTAAATCATATTTATTTTCCAAGNTTTCTAAGATCTCTGAAACTAATGAGGTTTTT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TAAATCCCCATTAAGTACTCATCACTGCTAGTAAAAGCAGTTGTCTTTACCTTTAATTCC	540
Sbjct	481	TAAATCCCCATTAAGTACTCATCACTGCTAGTAAAAGCAGTTGTCTTTACCTTTAATTCC	540
Query	541	AGTGAGTCCCCTTAAATTTATTTTTTATTATCTTTGGCTACATTGCCTTAGACAAAATGT	600
Sbjct	541	AGTGAGTCCCCTTAAATTTATTTTTTATTATCTTTGGCTACATTGCCTTAGACAAAATGT	600
Query	601	GGTCACCCTAATTTAANGGATAAAATTCACATCCTCACAGATTTCTTATTAAGAGGGTCT	660
Sbjct	601	GGTCACCCTAATTTAANGGATAAAATTCACATCCTCACAGATTTCTTATTAAGAGGGTCT	660
Query	661	AANCCTTGAATAATCANCAGTGGAAATGGAAGTCTTCTTTACTGGNTTNNATCCTTTCCC	720
Sbjct	661	AANCCTTGAATAATCANCAGTGGAAATGGAAGTCTTCTTTACTGGNTTNNATCCTTTCCC	720
Query	721	TTTTTTATCCCATG	734
Sbjct	721	TTTTTTATCCCATG	734

Sequence 339 matched with Sequence 32

Query= Sequence ID 339
Length=517

SEQ ID NO: 32

ALIGNMENTS

Identities = 517/517 (100%), Gaps = 0/517 (0%)

Query	1	tttttttttAAATAAAGCTGTCGGCACTCAAGGGTAATTTTCATATCAGTGTGNTCTACAA	60
Sbjct	1	TTTTTTTTTAAATAAAGCTGTCGGCACTCAAGGGTAATTTTCATATCAGTGTGNTCTACAA	60
Query	61	GCTGGGGGAAAATGAGTTCTAATTGTCANAGCTACCAAATCCTTCACCTTTAGCATAAAG	120
Sbjct	61	GCTGGGGGAAAATGAGTTCTAATTGTCANAGCTACCAAATCCTTCACCTTTAGCATAAAG	120
Query	121	GTTTAAAGATATCACAAAGATGCCAAGTGATTAATAATGTTTTAAACCACCCCTTTTTCT	180
Sbjct	121	GTTTAAAGATATCACAAAGATGCCAAGTGATTAATAATGTTTTAAACCACCCCTTTTTCT	180
Query	181	GTCTGAAAAAACAACATAAACAATATTACAACAGTATAGTTACAGAAGGGTTCTATTTTC	240
Sbjct	181	GTCTGAAAAAACAACATAAACAATATTACAACAGTATAGTTACAGAAGGGTTCTATTTTC	240
Query	241	ATATGTTTTATGCACACTGTGCCTCAAAGGTACTATTTAAATATATATACTTTTGAGGGG	300
Sbjct	241	ATATGTTTTATGCACACTGTGCCTCAAAGGTACTATTTAAATATATATACTTTTGAGGGG	300
Query	301	GTGGCTAATGCAGAAACACCCAAGACCTAAGGAAGATACAACCCCATTTCTAGGTGTGAG	360
Sbjct	301	GTGGCTAATGCAGAAACACCCAAGACCTAAGGAAGATACAACCCCATTTCTAGGTGTGAG	360
Query	361	GTCTAAATGCTTCACACACCCACTTGTGACCTTTTTTCATGAAGAATCATAACACTGTGC	420
Sbjct	361	GTCTAAATGCTTCACACACCCACTTGTGACCTTTTTTCATGAAGAATCATAACACTGTGC	420
Query	421	AGTGAGAAACAGTGGCAAAGCAATACTGAAAGCATTTTAAATTATTTACTAGGTTAAAAG	480
Sbjct	421	AGTGAGAAACAGTGGCAAAGCAATACTGAAAGCATTTTAAATTATTTACTAGGTTAAAAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	GGTGAAGTGAAGCTTTTAAATACATCAAATTCATCAT	517
Sbjct	481	GGTGAAGTGAAGCTTTTAAATACATCAAATTCATCAT	517

Sequence 360 matched with Sequence 33

Query= Sequence ID 360
Length=536

SEQ ID NO: 33

ALIGNMENTS

Identities = 536/536 (100%), Gaps = 0/536 (0%)

Query	1	GCAAGTGAGAGCCGGACGGGCACTGGGCGACTCTGTGCCTCGCTGAGGAAAAATAACTAA	60
Sbjct	1	GCAAGTGAGAGCCGGACGGGCACTGGGCGACTCTGTGCCTCGCTGAGGAAAAATAACTAA	60
Query	61	ACATGGGCAAAGGAGATCCTAAGAAGCCGAGAGGCCAAATGTCATCATATGCATTTTTTTG	120
Sbjct	61	ACATGGGCAAAGGAGATCCTAAGAAGCCGAGAGGCCAAATGTCATCATATGCATTTTTTTG	120
Query	121	TGCAAACTTGTCGGGAGGAGCATAAGAAGAAGCACCCAGATGCTTCAGTCAACTTCTCAG	180
Sbjct	121	TGCAAACTTGTCGGGAGGAGCATAAGAAGAAGCACCCAGATGCTTCAGTCAACTTCTCAG	180
Query	181	AGTTTTCTAAGAAGTGCTCAGAGAGGTGGAAGACCATGTCTGCTAAAGAGAAAGGAAAAT	240
Sbjct	181	AGTTTTCTAAGAAGTGCTCAGAGAGGTGGAAGACCATGTCTGCTAAAGAGAAAGGAAAAT	240
Query	241	TTGAAGATATGGCAAAGCGGACAAGGCCCGTTATGAAAGAGAAATGAAAACCTATATCC	300
Sbjct	241	TTGAAGATATGGCAAAGCGGACAAGGCCCGTTATGAAAGAGAAATGAAAACCTATATCC	300
Query	301	CTCCCAAAGGGGAGACAAAAAGAAGTTCAAGGATCCCAATGCACCCAAGAGGCCTCCTT	360
Sbjct	301	CTCCCAAAGGGGAGACAAAAAGAAGTTCAAGGATCCCAATGCACCCAAGAGGCCTCCTT	360
Query	361	CGGCCTTCTTCCTCTTCTGCTCTGAGTATCGCCAAAAATCAAAGGAGAACATCCTGGCC	420
Sbjct	361	CGGCCTTCTTCCTCTTCTGCTCTGAGTATCGCCAAAAATCAAAGGAGAACATCCTGGCC	420
Query	421	TGTCCATTGGTGATGTTGCGAAGAAACTGGGAGAGATGTGGAATAACACTGCTGCAGATG	480
Sbjct	421	TGTCCATTGGTGATGTTGCGAAGAAACTGGGAGAGATGTGGAATAACACTGCTGCAGATG	480

Sequence 361 matched with Sequence 34

Query= Sequence ID - 361
Length=622

nt: 622

SEQ ID NO: 34

nt: 622

ALIGNMENTS

Identities = 622/622 (100%), Gaps = 0/622 (0%)

Query	1	CTGTNATNGAATCTGCTTGTNACTNAAATGCTAAACTCAATTCTGTAATTCAATAGGTGC	60
Sbjct	1	CTGTNATNGAATCTGCTTGTNACTNAAATGCTAAACTCAATTCTGTAATTCAATAGGTGC	60
Query	61	ACCTNTCTGAGAAACATANNAGACAATGAGGAAAAGGATTCANCATTCCGTGGAATTTGT	120
Sbjct	61	ACCTNTCTGAGAAACATANNAGACAATGAGGAAAAGGATTCANCATTCCGTGGAATTTGT	120
Query	121	ACCATGATCAGTGTGAATCCANTGGCGTAATCCAAGTAAGATGTTACAAAAGATTTGTT	180
Sbjct	121	ACCATGATCAGTGTGAATCCANTGGCGTAATCCAAGTAAGATGTTACAAAAGATTTGTT	180
Query	181	TTTAATGTCTAATTAATAAAAATTTTAAAGGAAGAAACATTCTAATACTTTAATTATAAAA	240
Sbjct	181	TTTAATGTCTAATTAATAAAAATTTTAAAGGAAGAAACATTCTAATACTTTAATTATAAAA	240
Query	241	AGTTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCTTTAAAATGTATATTTCTTAA	300
Sbjct	241	AGTTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCTTTAAAATGTATATTTCTTAA	300
Query	301	TATCTTGAAATTGTAATGCCtttttttttctctaaattttttttGTCATGAAATGAGATA	360
Sbjct	301	TATCTTGAAATTGTAATGCCTTTTTTTTTCTCTAAATTTTTTTTGTGTCATGAAATGAGATA	360
Query	361	GTAACAGCAGATTGGGACAACAAGGTTATATTCTTGTCTTGAATCAGGCCATGGCTTCTT	420
Sbjct	361	GTAACAGCAGATTGGGACAACAAGGTTATATTCTTGTCTTGAATCAGGCCATGGCTTCTT	420
Query	421	TCATCCAAATTTTCAGACCTCATTTATTTACTTTGTCCCTGCCTCCCATCCCTGGATATCA	480
Sbjct	421	TCATCCAAATTTTCAGACCTCATTTATTTACTTTGTCCCTGCCTCCCATCCCTGGATATCA	480

Sequence 363 matched with Sequence 35

Query= Sequence ID - 363
Length=628

nt: 628

SEQ ID NO: 35

nt: 628

ALIGNMENTS

Identities = 628/628 (100%), Gaps = 0/628 (0%)

Query	1	ATCACNTGAGGCAAGAGTTTGAGCCAGCCTAGCTAACATGGTGAAACCCCATCTCTACAA	60
Sbjct	1	ATCACNTGAGGCAAGAGTTTGAGCCAGCCTAGCTAACATGGTGAAACCCCATCTCTACAA	60
Query	61	AAATATAAAAAATTAGCCTGGGTGGTGATGGGCACCTGTAACCCAGCTACTCGGGAGGCT	120
Sbjct	61	AAATATAAAAAATTAGCCTGGGTGGTGATGGGCACCTGTAACCCAGCTACTCGGGAGGCT	120
Query	121	GAGGTAGGAGAATCACTTGAACCCGGGAGATGGAGGTTGCAGTGAGCCAAGATCGTGCCA	180
Sbjct	121	GAGGTAGGAGAATCACTTGAACCCGGGAGATGGAGGTTGCAGTGAGCCAAGATCGTGCCA	180
Query	181	CTGCACTCCAGCCTGTGTGACAGAACAAGACTCTGTCTCaaaaaaaaataataataataa	240
Sbjct	181	CTGCACTCCAGCCTGTGTGACAGAACAAGACTCTGTCTCAAAAAAAAAATAATAATAATAA	240
Query	241	taataataaaaaaggaataacatagctaggaataaatTTAATCAAAGAGGTGAAAGACTTA	300
Sbjct	241	TAATAATAAAAAAGGAATAACATAGCTAGGAATAAATTTAATCAAAGAGGTGAAAGACTTA	300
Query	301	TACACTTAAAACTACaaaaaaaaaTCACTGAAGGAATTATAGACCCaaataaaaaataaa	360
Sbjct	301	TACACTTAAAACTACAAAAAAAAAATCACTGAAGGAATTATAGACCCAAATAAAAAATAAA	360
Query	361	taaaaaGACATTCTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTA	420
Sbjct	361	TAAAAAGACATTCTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTA	420
Query	421	CCCAAAGTGATCTACAGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTA	480
Sbjct	421	CCCAAAGTGATCTACAGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTA	480

nt: 528

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nt:      528
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Identities = 524/524 (100%), Gaps = 0/524 (0%)

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PATENT SEQUENCE ALIGNMENT

Query	481	TAATCCCAGCACTTTGGAGCCTGGGGCGGGCGGATCACTTGAGG	524
Sbjct	481	TAATCCCAGCACTTTGGAGCCTGGGGCGGGCGGATCACTTGAGG	524

Sequence 365 matched with Sequence 37

Query= Sequence ID 365
Length=403

SEQ ID NO: 37

ALIGNMENTS

Identities = 403/403 (100%), Gaps = 0/403 (0%)

Query	1	GTCCCGGAATCGCGGCCGCGTCGACCTTTTCTATGCCTGCTATATAAACAGTACCTTGCA	60
Sbjct	1	GTCCCGGAATCGCGGCCGCGTCGACCTTTTCTATGCCTGCTATATAAACAGTACCTTGCA	60
Query	61	AGATGTCCTGTCTGATATCCACAAAGGGGTATTGTCAACCCCAAGTTCAGACAGCTTTGT	120
Sbjct	61	AGATGTCCTGTCTGATATCCACAAAGGGGTATTGTCAACCCCAAGTTCAGACAGCTTTGT	120
Query	121	ATTCTTCTGTCCCTGGATACATGAATTACTGCCATCTTTACACAGCGCCCTAAAATACCA	180
Sbjct	121	ATTCTTCTGTCCCTGGATACATGAATTACTGCCATCTTTACACAGCGCCCTAAAATACCA	180
Query	181	ACGCGAAGTTACCTGCTCAGCTTGAAGCTGCGCTGTACCCTGGAACCAGCACTTCTGCTG	240
Sbjct	181	ACGCGAAGTTACCTGCTCAGCTTGAAGCTGCGCTGTACCCTGGAACCAGCACTTCTGCTG	240
Query	241	AATGACTCAGGATGAAGCCTCGACTTCTCCTTCCCATCCCATGCCAGACCCAGTGGCT	300
Sbjct	241	AATGACTCAGGATGAAGCCTCGACTTCTCCTTCCCATCCCATGCCAGACCCAGTGGCT	300
Query	301	CCTTTCCCAATCTGATCCAGTGACTTTAAGTCCAGCTGTTGCAACCTGGGCATGAGGAGG	360
Sbjct	301	CCTTTCCCAATCTGATCCAGTGACTTTAAGTCCAGCTGTTGCAACCTGGGCATGAGGAGG	360
Query	361	AGTGCAAGATGGCTTTGTCCTACCTGGAAAAGAGGCTTTCTGGA	403
Sbjct	361	AGTGCAAGATGGCTTTGTCCTACCTGGAAAAGAGGCTTTCTGGA	403

Sequence 366 matched with Sequence 38

Query= Sequence ID 366
Length=111

SEQ ID NO: 38

ALIGNMENTS

Identities = 111/111 (100%), Gaps = 0/111 (0%)

Query	1	CACCATTACACACAGTGGGTCCTTGAATAGCATCGTTTTATTCAATGTCATTTGTTAT	60
Sbjct	1	CACCATTACACACAGTGGGTCCTTGAATAGCATCGTTTTATTCAATGTCATTTGTTAT	60
Query	61	AACATTGAGaaaaaaATTGATTCCCGGCTGGGGCCACTGTCTGTGCACCGT	111
Sbjct	61	AACATTGAGAAAAAAATTGATTCCCGGCTGGGGCCACTGTCTGTGCACCGT	111

Sequence 368 matched with Sequence 39

Query= Sequence ID - 368
Length=329

nt: 329

SEQ ID NO: 39

nt: 329

ALIGNMENTS

Identities = 329/329 (100%), Gaps = 0/329 (0%)

Query	1	GAAAGATCTAAAATCGACACCCTAACATCACAATTTAAAGAACTAGAGAAGCAAGAGCAA	60
Sbjct	1	GAAAGATCTAAAATCGACACCCTAACATCACAATTTAAAGAACTAGAGAAGCAAGAGCAA	60
Query	61	ATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG	120
Sbjct	61	ATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG	120
Query	121	AGACACAAAAAACCATTCaaaaaaaCAATGAATCCAGGAGtttttttttAAAAAGAT	180
Sbjct	121	AGACACAAAAAACCATTCAAAAAAAACAATGAATCCAGGAGTTTTTTTTTTAAAAAGAT	180
Query	181	CAACAGAATTGACAGACTGCTAGCAAGACTAATAAAGAAGAGAGAAGCATCAAATAGACT	240
Sbjct	181	CAACAGAATTGACAGACTGCTAGCAAGACTAATAAAGAAGAGAGAAGCATCAAATAGACT	240
Query	241	CAATAAAAAATGATAAAGGGGATATCACCACCAATCCCACAGAAATACAACTACCATCA	300
Sbjct	241	CAATAAAAAATGATAAAGGGGATATCACCACCAATCCCACAGAAATACAACTACCATCA	300
Query	301	GAGAACACTATAAACACCTCTATGCAAAT	329
Sbjct	301	GAGAACACTATAAACACCTCTATGCAAAT	329

Sequence 369 matched with Sequence 40

Query= Sequence ID 369
Length=341

SEQ ID NO: 40

ALIGNMENTS

Identities = 341/341 (100%), Gaps = 0/341 (0%)

Query	1	GAAAGATCTAAAATCGACACCCTAACATCACAATTTAAAGAACTAGAGAAGCAAGAGCAA	60
Sbjct	1	GAAAGATCTAAAATCGACACCCTAACATCACAATTTAAAGAACTAGAGAAGCAAGAGCAA	60
Query	61	ATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG	120
Sbjct	61	ATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG	120
Query	121	AGACACAAAAAACCATTCaaaaaaaCAATGAATCCAGGAGTTTTTTTTTAAAAAGAT	180
Sbjct	121	AGACACAAAAAACCATTCAAAAAAAACAATGAATCCAGGAGTTTTTTTTTAAAAAGAT	180
Query	181	CAACAGAATTGACAGACTGCTAGCAAGACTAATAAAGAAGAGAGAAGCATCAAATAGACT	240
Sbjct	181	CAACAGAATTGACAGACTGCTAGCAAGACTAATAAAGAAGAGAGAAGCATCAAATAGACT	240
Query	241	CAATAAAAAATGATAAAGGGGATATCACCACCAATCCCACAGAAATACAACTACCATCA	300
Sbjct	241	CAATAAAAAATGATAAAGGGGATATCACCACCAATCCCACAGAAATACAACTACCATCA	300
Query	301	GAGAACACTATAAACACCTCTATGCAAATAAACTAGAAAAT	341
Sbjct	301	GAGAACACTATAAACACCTCTATGCAAATAAACTAGAAAAT	341

Sequence 370 matched with Sequence 41

Query= Sequence ID 370
Length=185

SEQ ID NO: 41

ALIGNMENTS

Identities = 185/185 (100%), Gaps = 0/185 (0%)

Query	1	GAAAGATCTAAAATCGACACCCTAACATCACAATTTAAAGAACTAGAGAAGCAAGAGCAA	60
Sbjct	1	GAAAGATCTAAAATCGACACCCTAACATCACAATTTAAAGAACTAGAGAAGCAAGAGCAA	60
Query	61	ATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG	120
Sbjct	61	ATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG	120
Query	121	AGACACAAAAAACCATTCAaaaaaaaaCAATGAATCCAGGAGTTTTTTTTTTAAAAAGAT	180
Sbjct	121	AGACACAAAAAACCATTCAAAAAAAAAACAATGAATCCAGGAGTTTTTTTTTTAAAAAGAT	180
Query	181	CAACA 185	
Sbjct	181	CAACA 185	

Sequence 371 matched with Sequence 42

Query= Sequence ID 371
Length=553

SEQ ID NO: 42

ALIGNMENTS

Identities = 553/553 (100%), Gaps = 0/553 (0%)

Query	1	GCCCGGAATCGCGCCGCGTCGACGTAAGCTCGGCTGAATCCACGGTTCAAGAACAGGAA	60
Sbjct	1	GCCCGGAATCGCGCCGCGTCGACGTAAGCTCGGCTGAATCCACGGTTCAAGAACAGGAA	60
Query	61	AGAAGGCCAAGGCATAGGGAGTGGGGCAGTTGGGTGAATATTAGTACCTTTCCCTCAGNT	120
Sbjct	61	AGAAGGCCAAGGCATAGGGAGTGGGGCAGTTGGGTGAATATTAGTACCTTTCCCTCAGNT	120
Query	121	NCATTAATTACCCCTGCCTACTCTGCACAAAAGGATNTAACAACAGTTTCCTTTTAAATG	180
Sbjct	121	NCATTAATTACCCCTGCCTACTCTGCACAAAAGGATNTAACAACAGTTTCCTTTTAAATG	180
Query	181	GCCAGGTACAGCTGCTTATATGGANGGGCATTNTNTNAATGATATCCTTNATCACTGTCTT	240
Sbjct	181	GCCAGGTACAGCTGCTTATATGGANGGGCATTNTNTNAATGATATCCTTNATCACTGTCTT	240
Query	241	AATCATCACATNCTTAAACAATCACTTTATTGTGTTAAGGAAGATAAAAAATGGCTGGGT	300
Sbjct	241	AATCATCACATNCTTAAACAATCACTTTATTGTGTTAAGGAAGATAAAAAATGGCTGGGT	300
Query	301	TCAATTTCCGTTCTGGAAGAAATCGANTNAAAAGGTAACCATTTAATAATGCANAGGGCA	360
Sbjct	301	TCAATTTCCGTTCTGGAAGAAATCGANTNAAAAGGTAACCATTTAATAATGCANAGGGCA	360
Query	361	NTTTCAGTGCAGACCCTAATACTGGAAATTTTTAAAAACAAATGAAAACTTCTACTTTT	420
Sbjct	361	NTTTCAGTGCAGACCCTAATACTGGAAATTTTTAAAAACAAATGAAAACTTCTACTTTT	420
Query	421	TCTTCTAAGCTTACTTAACCACCCAAATTTTCCAGCCACATATCTTCCTAGTCTACAAC	480
Sbjct	421	TCTTCTAAGCTTACTTAACCACCCAAATTTTCCAGCCACATATCTTCCTAGTCTACAAC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GCCTTTAACTTTAAGAGATGCTCaaaaaaTGTAATTCTCAAATACATTCTTATTACAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GCCTTTAACTTTAAGAGATGCTCAAAAAAATGTAAATTCTCAAATACATTCTTATTACAA  540

Query  541  TTAGTGCTAACCT  553
          ||||||||||||
Sbjct  541  TTAGTGCTAACCT  553
```

Sequence 373 matched with Sequence 43

Query= Sequence ID 373
Length=510

SEQ ID NO: 43

ALIGNMENTS

Identities = 510/510 (100%), Gaps = 0/510 (0%)

Query	1	CCAGTGTGCTGGGATTACAGGCATGAGCCCTGCACCCAGCCTCTTAAACTGATCATATGA	60
Sbjct	1	CCAGTGTGCTGGGATTACAGGCATGAGCCCTGCACCCAGCCTCTTAAACTGATCATATGA	60
Query	61	TATTGGTTCTCAACCAAGGGTGACTTTGCCCCCAGAGGATACTTGGCAATGTCTGGAGAT	120
Sbjct	61	TATTGGTTCTCAACCAAGGGTGACTTTGCCCCCAGAGGATACTTGGCAATGTCTGGAGAT	120
Query	121	ACTCAGTTGTCATGACTTGGACAGGTGCTACTGTCACCCAGTGGGTAGAGGTCAGGGATG	180
Sbjct	121	ACTCAGTTGTCATGACTTGGACAGGTGCTACTGTCACCCAGTGGGTAGAGGTCAGGGATG	180
Query	181	GTGCTAAACATAGGACAGCTGTCAAGAGAAAAGAATGTACCCAGCCCCAAATGTCAGTAG	240
Sbjct	181	GTGCTAAACATAGGACAGCTGTCAAGAGAAAAGAATGTACCCAGCCCCAAATGTCAGTAG	240
Query	241	GGCTGAGGTTGAGAAACCCAGCTGTAGCTGACGTGTGAAGGACAGACTGGCCTGGAAGTG	300
Sbjct	241	GGCTGAGGTTGAGAAACCCAGCTGTAGCTGACGTGTGAAGGACAGACTGGCCTGGAAGTG	300
Query	301	TGTTTTCTGCCCCTTTCCACCCCTGCATATTAGTTAAGGCCAAAGGAAAAAAGGAATGCA	360
Sbjct	301	TGTTTTCTGCCCCTTTCCACCCCTGCATATTAGTTAAGGCCAAAGGAAAAAAGGAATGCA	360
Query	361	GGAAATGCCCGTTAAAAATCTTCAAAACAATATAAAATGATCAATTCCACTAAAACCCTT	420
Sbjct	361	GGAAATGCCCGTTAAAAATCTTCAAAACAATATAAAATGATCAATTCCACTAAAACCCTT	420
Query	421	TACACATTTAAGTATAAAGGTATTGGTAGGAAAATTTGTTATTCACTGCTTTTCTCAGTG	480
Sbjct	421	TACACATTTAAGTATAAAGGTATTGGTAGGAAAATTTGTTATTCACTGCTTTTCTCAGTG	480

```
Query 481 TCATGAAATAATTATTTCTGCTGTCAGTTT 510
          |||
Sbjct 481 TCATGAAATAATTATTTCTGCTGTCAGTTT 510
```

Sequence 374 matched with Sequence 44

Query= Sequence ID 374
Length=335

SEQ ID NO: 44

ALIGNMENTS

Identities = 335/335 (100%), Gaps = 0/335 (0%)

Query	1	aaaaaaaaaTCACTGAAGGAATTATAGACCCaaataaaaaataataaaaaGACATTCTG	60
Sbjct	1	AAAAAAAAAATCACTGAAGGAATTATAGACCCAAATAAAAATAAATAAAAAAGACATTCTG	60
Query	61	TGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAGTGATCTAC	120
Sbjct	61	TGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAGTGATCTAC	120
Query	121	AGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAATGGAAAAGCCA	180
Sbjct	121	AGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAATGGAAAAGCCA	180
Query	181	ATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAAACAATCTTGGGGaaa	240
Sbjct	181	ATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAAACAATCTTGGGGAAA	240
Query	241	aaaaacaaaaaacaaaGTCAAAGAACTCACACTTCTCTATTTATAATTTACTACAAAGTT	300
Sbjct	241	AAAAACAAAAAACAAAGTCAAAGAACTCACACTTCTCTATTTATAATTTACTACAAAGTT	300
Query	301	ATAGTAATCAAAGTCGACGCGGCCGCGATTCCGGG	335
Sbjct	301	ATAGTAATCAAAGTCGACGCGGCCGCGATTCCGGG	335

Sequence 378 matched with Sequence 45

Query= Sequence ID 378
Length=314

SEQ ID NO: 45

ALIGNMENTS

Identities = 314/314 (100%), Gaps = 0/314 (0%)

Query	1	CGACTGCGGCTCTTCCTCGGGCAGCGGAAGCGGCGGCGGTCGGAGAAGTGGCCTAAAA	60
Sbjct	1	CGACTGCGGCTCTTCCTCGGGCAGCGGAAGCGGCGGCGGTCGGAGAAGTGGCCTAAAA	60
Query	61	CTTCGGCGTTGGGTGAAAGAAAATGGCCCGAACCAAGCAGACTGCTCGTAAGTCCACCGG	120
Sbjct	61	CTTCGGCGTTGGGTGAAAGAAAATGGCCCGAACCAAGCAGACTGCTCGTAAGTCCACCGG	120
Query	121	TGGGAAAGCCCCCGCAAACAGCTGGCCACGAAAGCCGCCAGGAAAAGCGCTCCCTCTAC	180
Sbjct	121	TGGGAAAGCCCCCGCAAACAGCTGGCCACGAAAGCCGCCAGGAAAAGCGCTCCCTCTAC	180
Query	181	CGGCGGGGTGAAGAAGCCTCATCGCTACAGGCCCGGGACCGTGGCGCTTCGAGAGATTCTG	240
Sbjct	181	CGGCGGGGTGAAGAAGCCTCATCGCTACAGGCCCGGGACCGTGGCGCTTCGAGAGATTCTG	240
Query	241	TCGTTATCAGAAGTCGACCGAGCTGCTCATCCGGAAGCTGCCCTTCCAGAGGTTGGTGAG	300
Sbjct	241	TCGTTATCAGAAGTCGACCGAGCTGCTCATCCGGAAGCTGCCCTTCCAGAGGTTGGTGAG	300
Query	301	GGANATCGCCCAGG	314
Sbjct	301	GGANATCGCCCAGG	314

Sequence 380 matched with Sequence 46

Query= Sequence ID 380

Length=537

SEQ ID NO: 46

ALIGNMENTS

Identities = 537/537 (100%), Gaps = 0/537 (0%)

Query	1	GCAATTTAATTTTAAATAACAAAGATACTGTATTTTAACATGGTGAAATATACTTGGCTA	60
Sbjct	1	GCAATTTAATTTTAAATAACAAAGATACTGTATTTTAACATGGTGAAATATACTTGGCTA	60
Query	61	AGTCCAGATTaaaaaaaGTATCTAGCCCAACAGTACAATTATACAGCTTTGTACAG	120
Sbjct	61	AGTCCAGATTAAAAAAAAAAGTATCTAGCCCAACAGTACAATTATACAGCTTTGTACAG	120
Query	121	AACATTCCATAGATCAACAGAAAATACATTTGAGCGCaaaaataaaaaTATTTAAGGAG	180
Sbjct	121	AACATTCCATAGATCAACAGAAAATACATTTGAGCGCAAAAATAAAAAATATTTAAGGAG	180
Query	181	AATCTCTAAGCAGCATTTTATTTCTGCAAAAGACATATCTTGTCTGATTAAATATCTACA	240
Sbjct	181	AATCTCTAAGCAGCATTTTATTTCTGCAAAAGACATATCTTGTCTGATTAAATATCTACA	240
Query	241	AGTGCTTTTCCTTTCAAAAATACATATATTCTTAATAGACTAAGTCATTAACAATGACCT	300
Sbjct	241	AGTGCTTTTCCTTTCAAAAATACATATATTCTTAATAGACTAAGTCATTAACAATGACCT	300
Query	301	GGTAATTCTTTCACTTCAATTTGAATGATTTATAAGCTAAATCTTCAACCACAAAAAGGT	360
Sbjct	301	GGTAATTCTTTCACTTCAATTTGAATGATTTATAAGCTAAATCTTCAACCACAAAAAGGT	360
Query	361	TTTTATTTGTATTAAGATGTTACCACTTTTGACAAAAAGCTTAAATATTTTATATTTCA	420
Sbjct	361	TTTTATTTGTATTAAGATGTTACCACTTTTGACAAAAAGCTTAAATATTTTATATTTCA	420
Query	421	AAGGAAAAATTAGCAACATAACTTTACAATATATTCTATGATATTTTGATTGTGAGGGCTA	480
Sbjct	421	AAGGAAAAATTAGCAACATAACTTTACAATATATTCTATGATATTTTGATTGTGAGGGCTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CTCTATTTAAAACTGATGATCTCTGTTGTGTTGCTCAGATGCAGGAAAGCAGCAAAA	537
Sbjct	481	CTCTATTTAAAACTGATGATCTCTGTTGTGTTGCTCAGATGCAGGAAAGCAGCAAAA	537

Sequence 381 matched with Sequence 47

Query= Sequence ID - 381
Length=534

nt: 534

SEQ ID NO: 47

nt: 534

ALIGNMENTS

Identities = 534/534 (100%), Gaps = 0/534 (0%)

Query	1	GACTTANATCTAAATGGACCACATTCTCTACTTaaaaaaTGCTATTAACCATGTGATCT	60
Sbjct	1	GACTTANATCTAAATGGACCACATTCTCTACTTAAAAAATGCTATTAACCATGTGATCT	60
Query	61	TCTCAGTCATGAGGTAATCTGGTGACTACCCTTCCTCAAAGCCAGTTGGGATATTCTTTG	120
Sbjct	61	TCTCAGTCATGAGGTAATCTGGTGACTACCCTTCCTCAAAGCCAGTTGGGATATTCTTTG	120
Query	121	AATAGAGTAAACAGTGTTTCTAGGCTGGGAGACACCAGACATAGTTGAGGACAGAGGTG	180
Sbjct	121	AATAGAGTAAACAGTGTTTCTAGGCTGGGAGACACCAGACATAGTTGAGGACAGAGGTG	180
Query	181	CTAGAAAATAGGAAGTTTAAAGCATGTGCGGTGATGCTCAGAGGAGGTAAACCCACCC	240
Sbjct	181	CTAGAAAATAGGAAGTTTAAAGCATGTGCGGTGATGCTCAGAGGAGGTAAACCCACCC	240
Query	241	TCATGCTCATAGCTTCCAATCATTTTCTCTAGTTCTTAACTCTTAAATGTGAGAAATGCT	300
Sbjct	241	TCATGCTCATAGCTTCCAATCATTTTCTCTAGTTCTTAACTCTTAAATGTGAGAAATGCT	300
Query	301	TGAAGATTCTAGTCATCTGAAGAAAGTCTCTTTATTAAAGATTTTCATAAAAGAGACCAA	360
Sbjct	301	TGAAGATTCTAGTCATCTGAAGAAAGTCTCTTTATTAAAGATTTTCATAAAAGAGACCAA	360
Query	361	AGCAGACAAACAGAAAAAGACATCTTGGGGaaaaaaaCAAGGATAATGGGAAGAGAAGGA	420
Sbjct	361	AGCAGACAAACAGAAAAAGACATCTTGGGGAAAAAACAAGGATAATGGGAAGAGAAGGA	420
Query	421	AAGTTTTAAAAATTATCAATATCCTCAGGGGGACAAAATATTATATCCTATAAAGACAGA	480
Sbjct	421	AAGTTTTAAAAATTATCAATATCCTCAGGGGGACAAAATATTATATCCTATAAAGACAGA	480

Sequence 382 matched with Sequence 48

Query= Sequence ID - 382 nt: 444
Length=444

SEQ ID NO: 48 nt: 444

ALIGNMENTS

Identities = 444/444 (100%), Gaps = 0/444 (0%)

Query	1	GTTAAGGAAGTCAGCACTTACATTAAGAAAATTGGCTACAACCCCGACACAGTAGCATT	60
Sbjct	1	GTTAAGGAAGTCAGCACTTACATTAAGAAAATTGGCTACAACCCCGACACAGTAGCATT	60
Query	61	GTGCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACATGCCTTGG	120
Sbjct	61	GTGCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACATGCCTTGG	120
Query	121	TTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGGAACCACGCTGCTTGAG	180
Sbjct	121	TTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGGAACCACGCTGCTTGAG	180
Query	181	GCTCTGGA CTGCATCCTACCACCAACTCGTCCAACTGACAAGCCCTTGCGCCTGCCTCTC	240
Sbjct	181	GCTCTGGA CTGCATCCTACCACCAACTCGTCCAACTGACAAGCCCTTGCGCCTGCCTCTC	240
Query	241	CAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCTGTTGGCCGAGTGGAGACTGGT	300
Sbjct	241	CAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCTGTTGGCCGAGTGGAGACTGGT	300
Query	301	GTTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAACGGAAGTAAAA	360
Sbjct	301	GTTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAACGGAAGTAAAA	360
Query	361	TCTGTGCGAAATGCACCATGAAGCTTTGAGTGAAGCTTTTCCTGGGGACAATGTGGGCTTC	420
Sbjct	361	TCTGTGCGAAATGCACCATGAAGCTTTGAGTGAAGCTTTTCCTGGGGACAATGTGGGCTTC	420
Query	421	AATGTCAAGAATGTGTCTGTCAAG	444
Sbjct	421	AATGTCAAGAATGTGTCTGTCAAG	444

Sequence 383 matched with Sequence 49

Query= Sequence ID - 383
Length=566

nt: 566

SEQ ID NO: 49

nt: 566

ALIGNMENTS

Identities = 566/566 (100%), Gaps = 0/566 (0%)

Query	1	CTTTGAAGAACTTTGCCAAATACTTTCTTACCAATCTCATGAGGAGAGGGAACATGCTGA	60
Sbjct	1	CTTTGAAGAACTTTGCCAAATACTTTCTTACCAATCTCATGAGGAGAGGGAACATGCTGA	60
Query	61	GAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAA	120
Sbjct	61	GAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAA	120
Query	121	ACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTTGGa	180
Sbjct	121	ACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTTGGA	180
Query	181	aaaaaaTGTGAATCAGTCACTACTGGAAGTGCACAACTGGCCACTGACAAAAATGACCC	240
Sbjct	181	AAAAAATGTGAATCAGTCACTACTGGAAGTGCACAACTGGCCACTGACAAAAATGACCC	240
Query	241	CCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGA	300
Sbjct	241	CCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGA	300
Query	301	ATTGGGTGACCACGTGACCAACTTGCGCAAGATGGGAGCGCCCGAATCTGGCTTGGCGGA	360
Sbjct	301	ATTGGGTGACCACGTGACCAACTTGCGCAAGATGGGAGCGCCCGAATCTGGCTTGGCGGA	360
Query	361	ATATCTCTTTGACAAGCACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTA	420
Sbjct	361	ATATCTCTTTGACAAGCACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTA	420
Query	421	ATTTCCCCATAGCCGTGGGGTGACTTCCCTGGTCACCAAGGCAGTGCATGCATGTTGGGG	480
Sbjct	421	ATTTCCCCATAGCCGTGGGGTGACTTCCCTGGTCACCAAGGCAGTGCATGCATGTTGGGG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TTCCTTTACCTTTTCTATAAGTTGTACCAAAACATCCACTTAAGTTCTTTGATTTGTCC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTCCTTTACCTTTTCTATAAGTTGTACCAAAACATCCACTTAAGTTCTTTGATTTGTCC  540

Query  541  ATTCCTTCAAATAAAGAAATTTGGTA  566
          ||||||||||||||||||||
Sbjct  541  ATTCCTTCAAATAAAGAAATTTGGTA  566
```

Sequence 384 matched with Sequence 50

Query= Sequence ID 384
Length=400

SEQ ID NO: 50

ALIGNMENTS

Identities = 400/400 (100%), Gaps = 0/400 (0%)

Query	1	TTTTGGGGTTTATATATAAGCCTGGTTCTTGCTGAAACTGCTTATGTTGATAACCAGTTA	60
Sbjct	1	TTTTGGGGTTTATATATAAGCCTGGTTCTTGCTGAAACTGCTTATGTTGATAACCAGTTA	60
Query	61	GTGAGTTCCTCTCTATTGACTTGCTGGGAAGTTTATAGAGACATTTTTTATGCATTTCAGA	120
Sbjct	61	GTGAGTTCCTCTCTATTGACTTGCTGGGAAGTTTATAGAGACATTTTTTATGCATTTCAGA	120
Query	121	GATTTTCAGTACAAATCTTGAAAAAGGGACATTTAGGCCGGGCGCGGTGGCTCACATCTGT	180
Sbjct	121	GATTTTCAGTACAAATCTTGAAAAAGGGACATTTAGGCCGGGCGCGGTGGCTCACATCTGT	180
Query	181	AACCCTAGCACTCTGGGAGGCTGAGGTGGGTGGATCATGAAGTCAAGAGATAGAGACCAT	240
Sbjct	181	AACCCTAGCACTCTGGGAGGCTGAGGTGGGTGGATCATGAAGTCAAGAGATAGAGACCAT	240
Query	241	CCTGGCAAAAATTAGCTGGGCGTGGTGGGGTGCGCCCGTAGTCCCAGCTACTCGGGAGGC	300
Sbjct	241	CCTGGCAAAAATTAGCTGGGCGTGGTGGGGTGCGCCCGTAGTCCCAGCTACTCGGGAGGC	300
Query	301	TGAGGCAGGAGAATTGCTTGAGCCCGGGAGGCGGAGGTTTCATTGAGCCGAGATAGTGCC	360
Sbjct	301	TGAGGCAGGAGAATTGCTTGAGCCCGGGAGGCGGAGGTTTCATTGAGCCGAGATAGTGCC	360
Query	361	ACTGCACTCCAGCCTGGACAACAGAGCGGAGACTGTGTCTT	400
Sbjct	361	ACTGCACTCCAGCCTGGACAACAGAGCGGAGACTGTGTCTT	400

Sequence 386 matched with Sequence 51

Query= Sequence ID 386
Length=562

SEQ ID NO: 51

ALIGNMENTS

Identities = 562/562 (100%), Gaps = 0/562 (0%)

Query	1	CTAAGGGTTTAAAGATGGAAGAGGCATTGATGAACAGCTGGGGAAGGAGTAGTTTGAGG	60
Sbjct	1	CTAAGGGTTTAAAGATGGAAGAGGCATTGATGAACAGCTGGGGAAGGAGTAGTTTGAGG	60
Query	61	TAGATGTGCAGATGGAATGAAGAGAAGGTCTCAAGAAGAGGGTGGAGCCAAAGAGGGCTG	120
Sbjct	61	TAGATGTGCAGATGGAATGAAGAGAAGGTCTCAAGAAGAGGGTGGAGCCAAAGAGGGCTG	120
Query	121	CAGATTTAGAAGGCTAAAGTCTTTAGATGGCTTTGGATAGCCTGTTGTATCTTGGACCAT	180
Sbjct	121	CAGATTTAGAAGGCTAAAGTCTTTAGATGGCTTTGGATAGCCTGTTGTATCTTGGACCAT	180
Query	181	GCAGGTTACAGTGGAGCATGGAGTGGGGACAGAAGTGGAGGAAGGAACCAGGGAACATGG	240
Sbjct	181	GCAGGTTACAGTGGAGCATGGAGTGGGGACAGAAGTGGAGGAAGGAACCAGGGAACATGG	240
Query	241	AGTGAGAAGCTAAAGGAAAGTGATGCAGTAGATACATGGCTCTAAAGTACTCAGGACTTT	300
Sbjct	241	AGTGAGAAGCTAAAGGAAAGTGATGCAGTAGATACATGGCTCTAAAGTACTCAGGACTTT	300
Query	301	CAGAGGCTTAAACATAGGGTGACCAACTATCCCACTATGCCTGATACTAAGGGCATTCCC	360
Sbjct	301	CAGAGGCTTAAACATAGGGTGACCAACTATCCCACTATGCCTGATACTAAGGGCATTCCC	360
Query	361	TGGATGTGGACCTTTCATTCCCCAAATTAGGAAAGTCTTGGGCATACCAAGACAAGTTGG	420
Sbjct	361	TGGATGTGGACCTTTCATTCCCCAAATTAGGAAAGTCTTGGGCATACCAAGACAAGTTGG	420
Query	421	CCACCCTACTCAAAAGTATGTAAGCTAACATATCTGTTCTCTAAGAGGTTAAAGCTGGAT	480
Sbjct	421	CCACCCTACTCAAAAGTATGTAAGCTAACATATCTGTTCTCTAAGAGGTTAAAGCTGGAT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGGGATACCAGATGTATGTACGTGATGCAGTTAAACAGCAATACAAGGGGGCAAGTCTAC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGGGATACCAGATGTATGTACGTGATGCAGTTAAACAGCAATACAAGGGGGCAAGTCTAC  540

Query  541  CTGATCGGCCAATTCAATGGGA  562
          ||||||||||||||||
Sbjct  541  CTGATCGGCCAATTCAATGGGA  562
```


Sequence 387 matched with Sequence 52

Query= Sequence ID 387

Length=614

SEQ ID NO: 52

ALIGNMENTS

Identities = 614/614 (100%), Gaps = 0/614 (0%)

Query	1	GAAGCCAAACCAAAGGAGCTTCTACTTCATGATGCCATTTATGTAAAGTTCAGGCAGAGA	60
Sbjct	1	GAAGCCAAACCAAAGGAGCTTCTACTTCATGATGCCATTTATGTAAAGTTCAGGCAGAGA	60
Query	61	AAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCAACTGGAAGA	120
Sbjct	61	AAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCAACTGGAAGA	120
Query	121	AGTCATGATTGGGATTTCTGGGTCCTAATAGTGCTCTGTGTCTTGATCTGAGTGCCGACT	180
Sbjct	121	AGTCATGATTGGGATTTCTGGGTCCTAATAGTGCTCTGTGTCTTGATCTGAGTGCCGACT	180
Query	181	ACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTTAATGGTGTGTCTTATT	240
Sbjct	181	ACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTTAATGGTGTGTCTTATT	240
Query	241	AGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACTGAGTAATCAGCTAGGCCAGT	300
Sbjct	241	AGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACTGAGTAATCAGCTAGGCCAGT	300
Query	301	CACTAGGTGAACAACTTACTGCTCCAATCAGCCTTAGAGCAGGAATCAAACCTCATGTCTC	360
Sbjct	301	CACTAGGTGAACAACTTACTGCTCCAATCAGCCTTAGAGCAGGAATCAAACCTCATGTCTC	360
Query	361	AGAAAAGTTATTAATTCAGCTTGTCTTGGGACTTCCTTCAGAGTCACTCTTGAATAGCTG	420
Sbjct	361	AGAAAAGTTATTAATTCAGCTTGTCTTGGGACTTCCTTCAGAGTCACTCTTGAATAGCTG	420
Query	421	AAATAGTAAATGTAAATCTGTGGATGCAAGTGTGTAAATTATTTTAGTCATCAGCTCTA	480
Sbjct	421	AAATAGTAAATGTAAATCTGTGGATGCAAGTGTGTAAATTATTTTAGTCATCAGCTCTA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATAAGATGGCCTTTGGGGAAATGAGTATAAGGTCACGAAAATGAAATGGCAAGAAGGAGG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATAAGATGGCCTTTGGGGAAATGAGTATAAGGTCACGAAAATGAAATGGCAAGAAGGAGG  540

Query  541  TCTACTATTTCTTCTGTAATACTGATTTTACCCCATCAGGGTCAGTCCCCAGAGGTTGT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TCTACTATTTCTTCTGTAATACTGATTTTACCCCATCAGGGTCAGTCCCCAGAGGTTGT  600

Query  601  AAATGTGAAGCTTG  614
          ||||||||||||
Sbjct  601  AAATGTGAAGCTTG  614
```

Sequence 388 matched with Sequence 53

Query= Sequence ID 388
Length=685

SEQ ID NO: 53

ALIGNMENTS

Identities = 685/685 (100%), Gaps = 0/685 (0%)

Query	1	CTTTGGACACTAGGAAAAACCTTGTAGAGAGAGTAAAAATTTAACACCCATAGTAGGC	60
Sbjct	1	CTTTGGACACTAGGAAAAACCTTGTAGAGAGAGTAAAAATTTAACACCCATAGTAGGC	60
Query	61	CTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAATCC	120
Sbjct	61	CTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAATCC	120
Query	121	CAAACATATAACTGAACTCCTCACACCCAATTGGACCAATCTATCACCTATAGAAGAAC	180
Sbjct	121	CAAACATATAACTGAACTCCTCACACCCAATTGGACCAATCTATCACCTATAGAAGAAC	180
Query	181	TAATGTTAGTATAAGTAACATGAAAACATTCTCCTCCGCATAAGCCTGCGTCAGATTAAA	240
Sbjct	181	TAATGTTAGTATAAGTAACATGAAAACATTCTCCTCCGCATAAGCCTGCGTCAGATTAAA	240
Query	241	ACACTGAACTGACAATTAACAGCCCAATATCTACAATCAACCAACAAGTCATTATTACCC	300
Sbjct	241	ACACTGAACTGACAATTAACAGCCCAATATCTACAATCAACCAACAAGTCATTATTACCC	300
Query	301	TCACTGTCAACCCAACACAGGCATGCTCATAAGGAAAGGTTaaaaaaaGTAAAGGAACT	360
Sbjct	301	TCACTGTCAACCCAACACAGGCATGCTCATAAGGAAAGGTTAAAAAAGTAAAGGAACT	360
Query	361	CGGCAAATCTTACCCCGCCTGTTTACCAAAAACATCACCTCTAGCATCACCAGTATTAGA	420
Sbjct	361	CGGCAAATCTTACCCCGCCTGTTTACCAAAAACATCACCTCTAGCATCACCAGTATTAGA	420
Query	421	GGCACCGCCTGCCAGTGACACATGTTTAAACGGCCGCGGTACCCTAACCGTGCAAAGGTA	480
Sbjct	421	GGCACCGCCTGCCAGTGACACATGTTTAAACGGCCGCGGTACCCTAACCGTGCAAAGGTA	480

Sequence 389 matched with Sequence 54

Query= Sequence ID 389
Length=533

SEQ ID NO: 54

ALIGNMENTS

Identities = 533/533 (100%), Gaps = 0/533 (0%)

Query	1	CGACCCGGAATTCGCGCCGCGTCGACTGAGTTCTTGACAAGAGTGTTTTCCCTTCCCG	60
Sbjct	1	CGACCCGGAATTCGCGCCGCGTCGACTGAGTTCTTGACAAGAGTGTTTTCCCTTCCCG	60
Query	61	TCACAGAGTGGGCCCAACGACCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTC	120
Sbjct	61	TCACAGAGTGGGCCCAACGACCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTC	120
Query	121	CCCAACTCCATTGGCAAGTCCCCTGACAGCGTCCTCGTCACAGCCAGCGTCAAGGAAGCT	180
Sbjct	121	CCCAACTCCATTGGCAAGTCCCCTGACAGCGTCCTCGTCACAGCCAGCGTCAAGGAAGCT	180
Query	181	GCCGAGGCTTTCCTAGGCTTTTCCTATGCGCCTCCACGGACTCTTTCCTCTGAACCCTG	240
Sbjct	181	GCCGAGGCTTTCCTAGGCTTTTCCTATGCGCCTCCACGGACTCTTTCCTCTGAACCCTG	240
Query	241	TTAGGGCTTGTTTTAAAGGATTTTATGTGTGTTTCCGAATGTTTTAGTTAGCCTTTTGG	300
Sbjct	241	TTAGGGCTTGTTTTAAAGGATTTTATGTGTGTTTCCGAATGTTTTAGTTAGCCTTTTGG	300
Query	301	TGGAGCCGCCAGCTGACAGGACATCTTACAAGAGAATTTGCACATCTCTGGAAGCTTAGC	360
Sbjct	301	TGGAGCCGCCAGCTGACAGGACATCTTACAAGAGAATTTGCACATCTCTGGAAGCTTAGC	360
Query	361	AATCTTATTGCACACTGTTTCGCTGGAAGCTTTTTGAAGAGCACATTCTCCTCAGTGAGCT	420
Sbjct	361	AATCTTATTGCACACTGTTTCGCTGGAAGCTTTTTGAAGAGCACATTCTCCTCAGTGAGCT	420
Query	421	CATGAGGTTTTCATTTTTATTCTTCCTTCCAACGTGGTGCTATCTCTGAAACGAGCGTTA	480
Sbjct	421	CATGAGGTTTTCATTTTTATTCTTCCTTCCAACGTGGTGCTATCTCTGAAACGAGCGTTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	GAGTGCCGCCTTAGACGGAGGCAGGAGTTTCGTTAGAAAGCGGACGCTGTTCT	533
Sbjct	481	GAGTGCCGCCTTAGACGGAGGCAGGAGTTTCGTTAGAAAGCGGACGCTGTTCT	533

Sequence 390 matched with Sequence 55

Query= Sequence ID - 390
Length=523

nt: 523

SEQ ID NO: 55

nt: 523

ALIGNMENTS

Identities = 523/523 (100%), Gaps = 0/523 (0%)

Query	1	GAATCCCTAGAAAAAGAGAATTCCCAACTTGATGAGGAAAACCTAGAACTGCGAAGGAAT	60
Sbjct	1	GAATCCCTAGAAAAAGAGAATTCCCAACTTGATGAGGAAAACCTAGAACTGCGAAGGAAT	60
Query	61	GTAGAATCTTTGAAGTGTGCAAGCATGAAAATGGCTCAGCTACAGCTAGAAAACAAAGAA	120
Sbjct	61	GTAGAATCTTTGAAGTGTGCAAGCATGAAAATGGCTCAGCTACAGCTAGAAAACAAAGAA	120
Query	121	CTGGAAAGTGAAAAAGAGCAACTTAAGAAGGGTTTGGAGCTCCTGAAAGCATCTTTCAAG	180
Sbjct	121	CTGGAAAGTGAAAAAGAGCAACTTAAGAAGGGTTTGGAGCTCCTGAAAGCATCTTTCAAG	180
Query	181	AAAACAGAACGCTTAGAAGTTAGCTACCAGGGTTTAGATATAGAAAATCAAAGACTGCAA	240
Sbjct	181	AAAACAGAACGCTTAGAAGTTAGCTACCAGGGTTTAGATATAGAAAATCAAAGACTGCAA	240
Query	241	AAAACCTTTAGAGAACAGCAATAaaaaaaTCCAGCAATTAGAGAGTGAAGTACAAGACTTA	300
Sbjct	241	AAAACCTTTAGAGAACAGCAATAAAAAAATCCAGCAATTAGAGAGTGAAGTACAAGACTTA	300
Query	301	GAGATGGAAAAATCAAACATTGCagaaaaacctagaagaactaaaaatatctagcaaaaga	360
Sbjct	301	GAGATGGAAAAATCAAACATTGCAGAAAAACCTAGAAGAACTAAAAATATCTAGCAAAAGA	360
Query	361	ctagaacagctggaaaaagaaaataaaTCATTAGAGCAAGAGACTTCTCAACTGGAAAAG	420
Sbjct	361	CTAGAACAGCTGGAAAAAGAAAATAAATCATTAGAGCAAGAGACTTCTCAACTGGAAAAG	420
Query	421	GATAAGAAACAATTGGAGAAGGAAAAATAAGAGACTCCGACANCAAGCAGAAATTAAAGAT	480
Sbjct	421	GATAAGAAACAATTGGAGAAGGAAAAATAAGAGACTCCGACANCAAGCAGAAATTAAAGAT	480

```
Query    481  CCACATTGAAGAAATAATGTGAAGATTGGAAATTTGAAAA  523
        |||
Sbjct    481  CCACATTGAAGAAATAATGTGAAGATTGGAAATTTGAAAA  523
```


nt: 566

```
nt:      566
```

Identities = 566/566 (100%), Gaps = 0/566 (0%)

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PATENT SEQUENCE ALIGNMENT

```
Query  481  TTCCTTTACCTTTTCTATAAGTTGTACCAAAACATCCACTTAAGTTCTTTGATTTGTCC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTCCTTTACCTTTTCTATAAGTTGTACCAAAACATCCACTTAAGTTCTTTGATTTGTCC  540

Query  541  ATTCCTTCAAATAAAGAAATTTGGTA  566
          ||||||||||||||||||||
Sbjct  541  ATTCCTTCAAATAAAGAAATTTGGTA  566
```

Sequence 394 matched with Sequence 57

Query= Sequence ID 394

Length=616

SEQ ID NO: 57

ALIGNMENTS

Identities = 616/616 (100%), Gaps = 0/616 (0%)

Query	1	GACCCGGAATCGCGGCCGCGTCGACCATTTTAGCCAAGGTGCCTCTATAGGGGTCAAGAC	60
Sbjct	1	GACCCGGAATCGCGGCCGCGTCGACCATTTTAGCCAAGGTGCCTCTATAGGGGTCAAGAC	60
Query	61	ATCATGTGCCCAGACCTAAGGTCAGGAATGTCATATTTTTCTGTAAAAATCATTTTATTT	120
Sbjct	61	ATCATGTGCCCAGACCTAAGGTCAGGAATGTCATATTTTTCTGTAAAAATCATTTTATTT	120
Query	121	CTGTGTATCTTACCTTTAAATCATTGTGGTTTACTCTGAGATTCTGTAGTCCTAATATTG	180
Sbjct	121	CTGTGTATCTTACCTTTAAATCATTGTGGTTTACTCTGAGATTCTGTAGTCCTAATATTG	180
Query	181	TATCATTGTGCTGTCTGCAAAACAACCTGAATCTATTTTGTGTCATCTTTTGTTACATG	240
Sbjct	181	TATCATTGTGCTGTCTGCAAAACAACCTGAATCTATTTTGTGTCATCTTTTGTTACATG	240
Query	241	TAACGCAGCTGTACTTTATGTTCTTTGCAACTGTTTCCATTATGAGAACGCTGTGCTATT	300
Sbjct	241	TAACGCAGCTGTACTTTATGTTCTTTGCAACTGTTTCCATTATGAGAACGCTGTGCTATT	300
Query	301	TACAAGGTTACATTTTTCTTGGCCAGGCGAGGTGGTCATGCCTGTGATCCCAGCACTTTG	360
Sbjct	301	TACAAGGTTACATTTTTCTTGGCCAGGCGAGGTGGTCATGCCTGTGATCCCAGCACTTTG	360
Query	361	GGAGGCCAAGGTGGGCGGATCACTTGAGGTAAAGAGTTGAGACCAGCCTGGCTAGCATGG	420
Sbjct	361	GGAGGCCAAGGTGGGCGGATCACTTGAGGTAAAGAGTTGAGACCAGCCTGGCTAGCATGG	420
Query	421	CGAAGCCCAGTCTCTACTAAAAATACAAAAATTGGCCGGGTGAAATTAGCCGGGCGTGGT	480
Sbjct	421	CGAAGCCCAGTCTCTACTAAAAATACAAAAATTGGCCGGGTGAAATTAGCCGGGCGTGGT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGTGTGTGCTTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAATCCG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGTGTGTGCTTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAATCCG  540

Query  541  GGAGGCAGAGGTTGCAGTGAGCCAAGATCANGCCACTGCACTCCACCTCGGGGTCAAGAG  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GGAGGCAGAGGTTGCAGTGAGCCAAGATCANGCCACTGCACTCCACCTCGGGGTCAAGAG  600

Query  601  CGAAACTCTGTCTCAA  616
          |||||||||||||||
Sbjct  601  CGAAACTCTGTCTCAA  616
```

Sequence 395 matched with Sequence 58

Query= Sequence ID 395
Length=598

SEQ ID NO: 58

ALIGNMENTS

Identities = 598/598 (100%), Gaps = 0/598 (0%)

Query	1	CCGTTTTAGTCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCTGCCTCGGCCTCCC	60
Sbjct	1	CCGTTTTAGTCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCTGCCTCGGCCTCCC	60
Query	61	AAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGTAAATCAGGTTTTTTAAATG	120
Sbjct	61	AAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGTAAATCAGGTTTTTTAAATG	120
Query	121	TTTGCCAAACCTTATCACTGACTTTTATAACAAAATTATTTACTATAATCATTAGGGAAT	180
Sbjct	121	TTTGCCAAACCTTATCACTGACTTTTATAACAAAATTATTTACTATAATCATTAGGGAAT	180
Query	181	ATTTAAGTTCTGCTAATACTTAAAATTGCAGAGTGCTAAAACCAGCAGTGAGTTTAGAAT	240
Sbjct	181	ATTTAAGTTCTGCTAATACTTAAAATTGCAGAGTGCTAAAACCAGCAGTGAGTTTAGAAT	240
Query	241	CAAGCTAAGCTTTATTGTTGCTACTATTTGAGGCATATTAGTTGACTGGTGTTTCATATGC	300
Sbjct	241	CAAGCTAAGCTTTATTGTTGCTACTATTTGAGGCATATTAGTTGACTGGTGTTTCATATGC	300
Query	301	AAGGCAGTCTACTGGGTGCAACAAGGGTTAGAAGGATATTTTAAAAAACTGACCCTATT	360
Sbjct	301	AAGGCAGTCTACTGGGTGCAACAAGGGTTAGAAGGATATTTTAAAAAACTGACCCTATT	360
Query	361	CTCAGGATGAAAATAATACTAGTAATAGTCTGCTCTGTTGGTTAACTCCTCGTAAGGA	420
Sbjct	361	CTCAGGATGAAAATAATACTAGTAATAGTCTGCTCTGTTGGTTAACTCCTCGTAAGGA	420
Query	421	GGTCAATTAAAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAAGAATCATATTCCTTCACT	480
Sbjct	421	GGTCAATTAAAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAAGAATCATATTCCTTCACT	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 AGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTGAAGGATTGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTGAAGGATTGGT 540

Query 541 AAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATTTATTGCAT 598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 AAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATTTATTGCAT 598
```

Length=524

Identities = 524/524 (100%), Gaps = 0/524 (0%)

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```
Query    481  ttttatTTTTTtaaaaaaTAGAAAGCAAAACAAGCTCCTAAAAA  524
        |||
Sbjct    481  TTTTATTTTTTAAAAAAATAGAAAGCAAAACAAGCTCCTAAAAA  524
```


Sequence 397 matched with Sequence 60

Query= Sequence ID - 397
Length=534

nt: 534

SEQ ID NO: 60

nt: 534

ALIGNMENTS

Identities = 534/534 (100%), Gaps = 0/534 (0%)

Query	1	GACCCGGAATCGCGGCCGCTCGACGGAAGCTCCTGCCCTCCTAAAGCTGAAGCCAAAG	60
Sbjct	1	GACCCGGAATCGCGGCCGCTCGACGGAAGCTCCTGCCCTCCTAAAGCTGAAGCCAAAG	60
Query	61	CGAAGGCTTTAAAGGCCAAGAAGGCAGTGTTGAAAGGTGTCCACAGCCACAAAAGAAGG	120
Sbjct	61	CGAAGGCTTTAAAGGCCAAGAAGGCAGTGTTGAAAGGTGTCCACAGCCACAAAAGAAGG	120
Query	121	AGATCCGCACGTCACCCACCTTCCGGCGGCCGAAGACACTGCGACTCCGGAGACAGCCCA	180
Sbjct	121	AGATCCGCACGTCACCCACCTTCCGGCGGCCGAAGACACTGCGACTCCGGAGACAGCCCA	180
Query	181	AATATCCTCGGAAGAGCGCTCCCAGGAGAAACAAGCTTGACCACTATGCTATCATCAAGT	240
Sbjct	181	AATATCCTCGGAAGAGCGCTCCCAGGAGAAACAAGCTTGACCACTATGCTATCATCAAGT	240
Query	241	TTCCGCTGACCACTGAGTCTGCCATGAAGAAGATAGAAGACAACAACACACTTGTGTTCA	300
Sbjct	241	TTCCGCTGACCACTGAGTCTGCCATGAAGAAGATAGAAGACAACAACACACTTGTGTTCA	300
Query	301	TTGTGGATGTTAAAGCCAACAAGCACCAGATTAAACAGGCTGTGAAGAAGCTGTATGACA	360
Sbjct	301	TTGTGGATGTTAAAGCCAACAAGCACCAGATTAAACAGGCTGTGAAGAAGCTGTATGACA	360
Query	361	TTGATGTGGCCAAGGTCAACACCCTGATTCGGCCTGATGGAGAGAAGAAGGCATATGTTC	420
Sbjct	361	TTGATGTGGCCAAGGTCAACACCCTGATTCGGCCTGATGGAGAGAAGAAGGCATATGTTC	420
Query	421	GACTGGCTCCTGATTACGATGCTTTGGATGTTGCCAACAAAATTGGGATCATTTAAACTG	480
Sbjct	421	GACTGGCTCCTGATTACGATGCTTTGGATGTTGCCAACAAAATTGGGATCATTTAAACTG	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGTCCAGCTGCCTAATTCTGAatatatatatatatatatatCTTTTCACCATAA	534
Sbjct	481	AGTCCAGCTGCCTAATTCTGAATATATATATATATATATATCTTTTCACCATAA	534

Sequence 398 matched with Sequence 61

Query= Sequence ID - 398
Length=512

nt: 512

SEQ ID NO: 61

nt: 512

ALIGNMENTS

Identities = 512/512 (100%), Gaps = 0/512 (0%)

Query	1	GGGGAGCCCCCTCTTCCCTCAGTTGTTCCCTACTCAGACTGTTGCACTCTAAACCTAGGGA	60
Sbjct	1	GGGGAGCCCCCTCTTCCCTCAGTTGTTCCCTACTCAGACTGTTGCACTCTAAACCTAGGGA	60
Query	61	GGTTGAAGAATGAGACCCTTAGGTTTTAACACGAATCCTGACACCACCATCTATAGGGTC	120
Sbjct	61	GGTTGAAGAATGAGACCCTTAGGTTTTAACACGAATCCTGACACCACCATCTATAGGGTC	120
Query	121	CCAACTTGGTTATTGTAGGCAACCTTCCCTCTCTCCTTGGTGAAGAACATCCCAAGCCAG	180
Sbjct	121	CCAACTTGGTTATTGTAGGCAACCTTCCCTCTCTCCTTGGTGAAGAACATCCCAAGCCAG	180
Query	181	AAAGAAGTTAACTACAGTGTTTTCTTTGCACCGATCCCCACCCCAATTCAATCCCGGAA	240
Sbjct	181	AAAGAAGTTAACTACAGTGTTTTCTTTGCACCGATCCCCACCCCAATTCAATCCCGGAA	240
Query	241	GGGACTTACTTAGGAAACCCTTCTTTACTAGATATCCTGGCCCCCTGGGCTTGTGAACAC	300
Sbjct	241	GGGACTTACTTAGGAAACCCTTCTTTACTAGATATCCTGGCCCCCTGGGCTTGTGAACAC	300
Query	301	CTCCTAGCCACATCACTACAGTACAGTGAGTGACCCCAGCCTCCTGCCTACCCCAAGATG	360
Sbjct	301	CTCCTAGCCACATCACTACAGTACAGTGAGTGACCCCAGCCTCCTGCCTACCCCAAGATG	360
Query	361	CCCCTCCCCACCCTGACCGTGCTAACTGTGTGTACATATATATTCTACATATATGTATAT	420
Sbjct	361	CCCCTCCCCACCCTGACCGTGCTAACTGTGTGTACATATATATTCTACATATATGTATAT	420
Query	421	TAAAACTGCACTGCCATGTCTGCCCTTTTTTGTGGTGTCTAGCATTAACTTATTGTCTAG	480
Sbjct	421	TAAAACTGCACTGCCATGTCTGCCCTTTTTTGTGGTGTCTAGCATTAACTTATTGTCTAG	480

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Query    481  GCCAAAGCGGGGGTGGGAGGGGAATGCCACAG  512
        |||
Sbjct    481  GCCAAAGCGGGGGTGGGAGGGGAATGCCACAG  512
```

Sequence 399 matched with Sequence 62

Query= Sequence ID 399
Length=642

SEQ ID NO: 62

ALIGNMENTS

Identities = 642/642 (100%), Gaps = 0/642 (0%)

Query	1	TTTTGGCATTACTTAATCCAATTATAAAAACTGAATTTTAAAAAACAGCACTTGTTTTT	60
Sbjct	1	TTTTGGCATTACTTAATCCAATTATAAAAACTGAATTTTAAAAAACAGCACTTGTTTTT	60
Query	61	TCTTCCAAGATTAATTTGAAttttttATGGACATTAGAAAACATTGCAGTTTAGTCATA	120
Sbjct	61	TCTTCCAAGATTAATTTGAATTTTTTATGGACATTAGAAAACATTGCAGTTTAGTCATA	120
Query	121	ATCAAAAATAAATCTTGAGGCTGGTAGAGCAGCTTTGTTGCTGTTTATATTTTTATTGCT	180
Sbjct	121	ATCAAAAATAAATCTTGAGGCTGGTAGAGCAGCTTTGTTGCTGTTTATATTTTTATTGCT	180
Query	181	TACTGGATTTCAGTGTTACCTAGTGCCATCAGTTTGGTATTTTGCCACCTTGCACATTCA	240
Sbjct	181	TACTGGATTTCAGTGTTACCTAGTGCCATCAGTTTGGTATTTTGCCACCTTGCACATTCA	240
Query	241	GTGATGTTTGATtttttcttttccctttttCATATTACTTTTAAATCCTGAATAGTTTG	300
Sbjct	241	GTGATGTTTGATTTTTCTTTTCCTTTTTTCATATTACTTTTAAATCCTGAATAGTTTG	300
Query	301	TGGCAGCTGGAGATCACCTAGTCCACCACTGTCCAACATGGCAATGGTAAGTAATATTGA	360
Sbjct	301	TGGCAGCTGGAGATCACCTAGTCCACCACTGTCCAACATGGCAATGGTAAGTAATATTGA	360
Query	361	GTAAAGAATAGAAAATTAGTAAATGCATGGCTTCAGAATTATAGCAATTTGCAAAATAG	420
Sbjct	361	GTAAAGAATAGAAAATTAGTAAATGCATGGCTTCAGAATTATAGCAATTTGCAAAATAG	420
Query	421	GTTAATGGATGAAAATTAGAATGACCAGTTTAACTTTCCCCCAGCAGATTCTTCTGTTA	480
Sbjct	421	GTTAATGGATGAAAATTAGAATGACCAGTTTAACTTTCCCCCAGCAGATTCTTCTGTTA	480

Query	481	AACAATGCCCTTCAAATAAAGGAAGAACAAGTGGGTGTTATACCTATGTTATTTGGCT	540
Sbjct	481	AACAATGCCCTTCAAATAAAGGAAGAACAAGTGGGTGTTATACCTATGTTATTTGGCT	540
Query	541	ATGTTAGCACAAATATGATGGACTAATTTGAGAAAAAGCATTTACTTCCTTTACTATTACT	600
Sbjct	541	ATGTTAGCACAAATATGATGGACTAATTTGAGAAAAAGCATTTACTTCCTTTACTATTACT	600
Query	601	TCTTTTCTTTATAGGGCTAAGTCTGCCTTCTGGGTCTTTGAA	642
Sbjct	601	TCTTTTCTTTATAGGGCTAAGTCTGCCTTCTGGGTCTTTGAA	642

Sequence 400 matched with Sequence 63

Query= Sequence ID 400

Length=446

SEQ ID NO: 63

ALIGNMENTS

Identities = 446/446 (100%), Gaps = 0/446 (0%)

Query	1	GAAGAAGCGCGAAGAGCCGTTAGTCATGCCGGTGTGGTGGCGGCGGCGGAGACTGCGGGC	60
Sbjct	1	GAAGAAGCGCGAAGAGCCGTTAGTCATGCCGGTGTGGTGGCGGCGGCGGAGACTGCGGGC	60
Query	61	CCGTAGCTGGGCTCTGCGAGGTGCAAGAAAGCCTTTGAGGTGAAGGTGTATGAAAGTCAT	120
Sbjct	61	CCGTAGCTGGGCTCTGCGAGGTGCAAGAAAGCCTTTGAGGTGAAGGTGTATGAAAGTCAT	120
Query	121	CATAACAGATGTTTTCCAAAACTTGTAGAAGGTTGTGAAAAAATACTAGGATCACGCG	180
Sbjct	121	CATAACAGATGTTTTCCAAAACTTGTAGAAGGTTGTGAAAAAATACTAGGATCACGCG	180
Query	181	GCATGTATTGAGCATATAGGTTGCTGTAGATGAATGTTCTTAGCTGTCATGTTTAAAAAT	240
Sbjct	181	GCATGTATTGAGCATATAGGTTGCTGTAGATGAATGTTCTTAGCTGTCATGTTTAAAAAT	240
Query	241	ACTTCTGCTTCGTTACCTCAAGTGTGGCATGCAGCATTTTGGAAGGAAAATTGAAGACGT	300
Sbjct	241	ACTTCTGCTTCGTTACCTCAAGTGTGGCATGCAGCATTTTGGAAGGAAAATTGAAGACGT	300
Query	301	GTTCAAGAAAACATGAACAGAAGCAAATGATGAAAATGAGCATTTTACTTGATGTTGATA	360
Sbjct	301	GTTCAAGAAAACATGAACAGAAGCAAATGATGAAAATGAGCATTTTACTTGATGTTGATA	360
Query	361	ACATCACAATAAATTATGGAGAAAAATACATATTTGGCTAACTTTTAATTGCTGAACAAT	420
Sbjct	361	ACATCACAATAAATTATGGAGAAAAATACATATTTGGCTAACTTTTAATTGCTGAACAAT	420
Query	421	AAAGTGTTTTCTTTTAAATCNAAAAAA	446
Sbjct	421	AAAGTGTTTTCTTTTAAATCNAAAAAA	446

Sequence 401 matched with Sequence 64

Query= Sequence ID 401
Length=629

SEQ ID NO: 64

ALIGNMENTS

Identities = 629/629 (100%), Gaps = 0/629 (0%)

Query	1	GAAGCCAAACCAAAGGGAGCTTCTACTTCATGATGCCATTTATGTAAAGTTCAGGCAGAG	60
Sbjct	1	GAAGCCAAACCAAAGGGAGCTTCTACTTCATGATGCCATTTATGTAAAGTTCAGGCAGAG	60
Query	61	AAAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCAACTGGAAG	120
Sbjct	61	AAAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCAACTGGAAG	120
Query	121	AAGTCATGATTGGGATTTCTGGGTCTAATAGTGCTCTGTGTCTTGATCTGAGTGCCGAC	180
Sbjct	121	AAGTCATGATTGGGATTTCTGGGTCTAATAGTGCTCTGTGTCTTGATCTGAGTGCCGAC	180
Query	181	TACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTTAATGGTGTGTCTTAT	240
Sbjct	181	TACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTTAATGGTGTGTCTTAT	240
Query	241	TAGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACTGAGTAATCAGCTAGGCCAG	300
Sbjct	241	TAGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACTGAGTAATCAGCTAGGCCAG	300
Query	301	TCACTAGGTGAACAACTTACTGCTACCAATCAGCCTTAGAGCAGGAATCAAACCTCATGTC	360
Sbjct	301	TCACTAGGTGAACAACTTACTGCTACCAATCAGCCTTAGAGCAGGAATCAAACCTCATGTC	360
Query	361	TCAGAAAAGTTATTAATTCAGCTTGTCTTGGGACTTCCTTCAGAGTCACTCTTGAATAGC	420
Sbjct	361	TCAGAAAAGTTATTAATTCAGCTTGTCTTGGGACTTCCTTCAGAGTCACTCTTGAATAGC	420
Query	421	TGAAATAGTAAATGTAAATCTGTGGATGCAAGTGTGTAAATTATTTTAGTCATCAGCTC	480
Sbjct	421	TGAAATAGTAAATGTAAATCTGTGGATGCAAGTGTGTAAATTATTTTAGTCATCAGCTC	480

PATENT SEQUENCE ALIGNMENT

Query	481	TAATAAGATGGCCTTTGGGGAAATGAGTATAAGGTCACGAAAATGAAATGGCAAGAAGGA	540
Sbjct	481	TAATAAGATGGCCTTTGGGGAAATGAGTATAAGGTCACGAAAATGAAATGGCAAGAAGGA	540
Query	541	GGTCTACTATTTCTTCTGTAATACTGATTTTACCCCATCAGGGTCAGTCCCCAAAGGTT	600
Sbjct	541	GGTCTACTATTTCTTCTGTAATACTGATTTTACCCCATCAGGGTCAGTCCCCAAAGGTT	600
Query	601	GTAAATGTGAAGCTTGGTCTTTTTCTTTA	629
Sbjct	601	GTAAATGTGAAGCTTGGTCTTTTTCTTTA	629

Sequence 402 matched with Sequence 65

Query= Sequence ID 402
Length=366

SEQ ID NO: 65

ALIGNMENTS

Identities = 366/366 (100%), Gaps = 0/366 (0%)

Query	1	GACCCTATTCTCAGGATGAAAATAATACTAGTAATAGTCTGCTCTGTTGGTTAACTCC	60
Sbjct	1	GACCCTATTCTCAGGATGAAAATAATACTAGTAATAGTCTGCTCTGTTGGTTAACTCC	60
Query	61	TCGTAAGGAGGTACAATTAATAATGCTGTAGTGTGCAAGGGAAGGAGAGGAAGAATCATA	120
Sbjct	61	TCGTAAGGAGGTACAATTAATAATGCTGTAGTGTGCAAGGGAAGGAGAGGAAGAATCATA	120
Query	121	TTCCTTCACTAGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTG	180
Sbjct	121	TTCCTTCACTAGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTG	180
Query	181	AAGGATTGGTAAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATT	240
Sbjct	181	AAGGATTGGTAAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATT	240
Query	241	TATTGCATGCTTATCTTGTATCAACATTGNGATGAAAGCNCAAGAATGAAAGAGGAGGGA	300
Sbjct	241	TATTGCATGCTTATCTTGTATCAACATTGNGATGAAAGCNCAAGAATGAAAGAGGAGGGA	300
Query	301	GAATGTTTANAGAATAAGGCTGAAACACAGATTTTGTAGGGAGCGTAGGGGAGACTGANA	360
Sbjct	301	GAATGTTTANAGAATAAGGCTGAAACACAGATTTTGTAGGGAGCGTAGGGGAGACTGANA	360
Query	361	AAACAG 366	
Sbjct	361	AAACAG 366	

Sequence 403 matched with Sequence 66

Query= Sequence ID 403
Length=202

SEQ ID NO: 66

ALIGNMENTS

Identities = 200/200 (100%), Gaps = 0/200 (0%)

Query	1	AAGACACCTGATAGATTGTCTTGTATTATTTTCCTTTGCCTTCTTACAATCTCAGTGAT	60
Sbjct	1	AAGACACCTGATAGATTGTCTTGTATTATTTTCCTTTGCCTTCTTACAATCTCAGTGAT	60
Query	61	TAGAATTGGGCTGAAAACAATACATCAAATTCTCAGCAAAATCCTTATGGGTTGCTGGAT	120
Sbjct	61	TAGAATTGGGCTGAAAACAATACATCAAATTCTCAGCAAAATCCTTATGGGTTGCTGGAT	120
Query	121	ACCGAGGGTTTTTAAGATCTTTAGACTTCACTATATAGAACAAATGTTGAATGGGAATTT	180
Sbjct	121	ACCGAGGGTTTTTAAGATCTTTAGACTTCACTATATAGAACAAATGTTGAATGGGAATTT	180
Query	181	TCTTTATTTCTATANCGTTT	200
Sbjct	181	TCTTTATTTCTATANCGTTT	200

Sequence 405 matched with Sequence 67

Query= Sequence ID 405

Length=634

SEQ ID NO: 67

ALIGNMENTS

Identities = 634/634 (100%), Gaps = 0/634 (0%)

Query	1	CCCGBAATCGCGGCCGCTCGACGATGAGCATTTCATGTGTCTTTGGCTGCATAAA	60
Sbjct	1	CCCGBAATCGCGGCCGCTCGACGATGAGCATTTCATGTGTCTTTGGCTGCATAAA	60
Query	61	TGTCTTCTTTGAGAAGTGTGCGTTCATATCCTTTGCCCACTTTTGATGGGGTTGtttt	120
Sbjct	61	TGTCTTCTTTGAGAAGTGTGCGTTCATATCCTTTGCCCACTTTTGATGGGGTTGTTTT	120
Query	121	tttCTTGTAATTTGTTTGAGTTCATTGTAGATTCTGGATATTAGCCCTTTGTCAGATGA	180
Sbjct	121	TTTCTTGTAATTTGTTTGAGTTCATTGTAGATTCTGGATATTAGCCCTTTGTCAGATGA	180
Query	181	GTAGGTTGCGAAAATTTCTCCCATTTTGTAGGTTGCCTGTTCACTCTGATGGTAGTTTC	240
Sbjct	181	GTAGGTTGCGAAAATTTCTCCCATTTTGTAGGTTGCCTGTTCACTCTGATGGTAGTTTC	240
Query	241	ATTTGCTGTGCAGAAGCTCTTTAGTTTAATTAGATCCCATTTGTCAATTTTGGCTTTTGT	300
Sbjct	241	ATTTGCTGTGCAGAAGCTCTTTAGTTTAATTAGATCCCATTTGTCAATTTTGGCTTTTGT	300
Query	301	TGCCATTGCTTTTGGTGTTTTAGACTTGAAGTCCTTGCCCATGCCTATGTCCTGAATGGT	360
Sbjct	301	TGCCATTGCTTTTGGTGTTTTAGACTTGAAGTCCTTGCCCATGCCTATGTCCTGAATGGT	360
Query	361	AATGCCTAGGTTTCTTCTAGGGTTTGTATGGTTTTAGGTCTAACGTTTCAGTCTTTAAT	420
Sbjct	361	AATGCCTAGGTTTCTTCTAGGGTTTGTATGGTTTTAGGTCTAACGTTTCAGTCTTTAAT	420
Query	421	CCATCTTTTAAAAGTCTCTTCACAGTACATGAGTAGTAGTGACACCAATAATGTCAGAGC	480
Sbjct	421	CCATCTTTTAAAAGTCTCTTCACAGTACATGAGTAGTAGTGACACCAATAATGTCAGAGC	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGGGAAC	CCCAGG	TCTGCC	CATCCAC	AAAAACA	ACAAATA	AAGCTGG	CAAAAA	CTTTAA	540
Sbjct	481	AGGGAAC	CCCAGG	TCTGCC	CATCCAC	AAAAACA	ACAAATA	AAGCTGG	CAAAAA	CTTTAA	540
Query	541	GAATCA	ACTTTT	GCAGAT	CTCTGA	AATCTAG	TCAAACT	TAAACAG	AGGAA	AGATTA	ATA 600
Sbjct	541	GAATCA	ACTTTT	GCAGAT	CTCTGA	AATCTAG	TCAAACT	TAAACAG	AGGAA	AGATTA	ATA 600
Query	601	AAGACN	GGCTGC	CTGAG	ATAACA	CTAAC	CACAC	CAC 634			
Sbjct	601	AAGACN	GGCTGC	CTGAG	ATAACA	CTAAC	CACAC	CAC 634			

Sequence 406 matched with Sequence 68

Query= Sequence ID 406
Length=644

SEQ ID NO: 68

ALIGNMENTS

Identities = 641/641 (100%), Gaps = 0/641 (0%)

Query	1	CATCAAATAAAATAAAATAAAATTTTAAAAGTCACAGCATTGAATTTTAAATGTTTGG	60
Sbjct	1	CATCAAATAAAATAAAATAAAATTTTAAAAGTCACAGCATTGAATTTTAAATGTTTGG	60
Query	61	GATGATAAAGCACCTGCTTATCATGAAGCTANAGAAATTCAATGACACGTTTGCCAGGGT	120
Sbjct	61	GATGATAAAGCACCTGCTTATCATGAAGCTANAGAAATTCAATGACACGTTTGCCAGGGT	120
Query	121	CTTTGCTAGTGATGTTGGAACAAGTCTGTAATGCTGATGAAACATCACTGTTCGGGCATT	180
Sbjct	121	CTTTGCTAGTGATGTTGGAACAAGTCTGTAATGCTGATGAAACATCACTGTTCGGGCATT	180
Query	181	ATTGCCCCAGAAAGACACTGACTGCAGCTGATGAAACAGCCCTTCCAAGAATTAAGGATG	240
Sbjct	181	ATTGCCCCAGAAAGACACTGACTGCAGCTGATGAAACAGCCCTTCCAAGAATTAAGGATG	240
Query	241	CCAAAGACCAAATAACTGTGCTGAGATATACTTACGCAGCAGGCATGCATAAGTGTA AAC	300
Sbjct	241	CCAAAGACCAAATAACTGTGCTGAGATATACTTACGCAGCAGGCATGCATAAGTGTA AAC	300
Query	301	TTGCTGTTATAAGCAAAAGCTTGCGTTCTCACTGTTTTCAAGGAGTGAATTTCATACCAA	360
Sbjct	301	TTGCTGTTATAAGCAAAAGCTTGCGTTCTCACTGTTTTCAAGGAGTGAATTTCATACCAA	360
Query	361	TCCATTATTATGCTAATAAAAAGGCATGGATCACCAGGGACATCTTTTCAGATTGGTTTC	420
Sbjct	361	TCCATTATTATGCTAATAAAAAGGCATGGATCACCAGGGACATCTTTTCAGATTGGTTTC	420
Query	421	ACAAACATTTTGTACCAGCAGCTTGTGCTTACTGCAGGGAAGCTGACTGGATGATGACTG	480
Sbjct	421	ACAAACATTTTGTACCAGCAGCTTGTGCTTACTGCAGGGAAGCTGACTGGATGATGACTG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CAAGATTTTGTTATATCTTAACAACCTGTTGTGCTCATCCTCCAGCTGAAATTCTCATCAA	540
Sbjct	481	CAAGATTTTGTTATATCTTAACAACCTGTTGTGCTCATCCTCCAGCTGAAATTCTCATCAA	540
Query	541	AAATAATGTTTATGGCTCACACCTGTAATCTCAACACTTTGGGAGGATTGCCTGACCCAG	600
Sbjct	541	AAATAATGTTTATGGCTCACACCTGTAATCTCAACACTTTGGGAGGATTGCCTGACCCAG	600
Query	601	GAGTTCAAGCCCACCCTGGGCAACACAGCAAGACCCAACCT	641
Sbjct	601	GAGTTCAAGCCCACCCTGGGCAACACAGCAAGACCCAACCT	641

Sequence 407 matched with Sequence 69

Query= Sequence ID 407
Length=639

SEQ ID NO: 69

ALIGNMENTS

Identities = 639/639 (100%), Gaps = 0/639 (0%)

Query	1	TTTTAAAAATCATAAAACGTTTCTTACAAAAGAGCATTACATTNTGCACACTGCTCTGAA	60
Sbjct	1	TTTTAAAAATCATAAAACGTTTCTTACAAAAGAGCATTACATTNTGCACACTGCTCTGAA	60
Query	61	CAGATGCCAGGGACATGTGGACTATTGTTACTTTTCCTCCCTGTCCCACCCCCCAAATGT	120
Sbjct	61	CAGATGCCAGGGACATGTGGACTATTGTTACTTTTCCTCCCTGTCCCACCCCCCAAATGT	120
Query	121	TACAGTGACCACAAAGCAAGGTGTTTACAATAATTACATGGGGGGAATTTTTTAAACCAC	180
Sbjct	121	TACAGTGACCACAAAGCAAGGTGTTTACAATAATTACATGGGGGGAATTTTTTAAACCAC	180
Query	181	CAACAATAACGAAAAATAAAATCCACTCACTCTGCTGCTGTTTCAAAATTTCAATGTTAG	240
Sbjct	181	CAACAATAACGAAAAATAAAATCCACTCACTCTGCTGCTGTTTCAAAATTTCAATGTTAG	240
Query	241	TTTTTGCACGCCCTTcccccccccAACCCCTGTTTGTAAAGGAACATAAACATTACATCTGG	300
Sbjct	241	TTTTTGCACGCCCTTCCCCCCCCCAACCCTGTTTGTAAAGGAACATAAACATTACATCTGG	300
Query	301	TGAACAGCAAAGATTTCACTACACCTCAAATGCAGAACACCTATGAAGCAGAGGAATGTT	360
Sbjct	301	TGAACAGCAAAGATTTCACTACACCTCAAATGCAGAACACCTATGAAGCAGAGGAATGTT	360
Query	361	GGCTTTTTTAAACAGAAGCAGATAaaaaaaaaaGATGCAGGACTCCTTCAGTTCTTCACTA	420
Sbjct	361	GGCTTTTTTAAACAGAAGCAGATAAAAAAAAAAAGATGCAGGACTCCTTCAGTTCTTCACTA	420
Query	421	GTCTTAGAAAAAAGTTTCCAGAATACTGCTTCACACTATAaaaaaagaaaaaTATCTTGCA	480
Sbjct	421	GTCTTAGAAAAAAGTTTCCAGAATACTGCTTCACACTATAAAAAAGAAAAAATATCTTGCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTAGAATCCTTCAACATCTGCATACTGCTTCACACTGTTTCGTTTCTAGGAGCACTTTGTC	540
Sbjct	481	TTAGAATCCTTCAACATCTGCATACTGCTTCACACTGTTTCGTTTCTAGGAGCACTTTGTC	540
Query	541	ACAGGACACTTCTGCTTATATTTCTTTAATCAGAACTTAGTTGGATGGGCCGGGCATGGT	600
Sbjct	541	ACAGGACACTTCTGCTTATATTTCTTTAATCAGAACTTAGTTGGATGGGCCGGGCATGGT	600
Query	601	GGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGG	639
Sbjct	601	GGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGG	639

Sequence 408 matched with Sequence 70

Query= Sequence ID 408

Length=752

SEQ ID NO: 70

ALIGNMENTS

Identities = 752/752 (100%), Gaps = 0/752 (0%)

Query	1	CCATCTCCAAATTTAGTATTCATTCTGTTTAGCATATTATCAGTTGCCATCTATTTGTTT	60
Sbjct	1	CCATCTCCAAATTTAGTATTCATTCTGTTTAGCATATTATCAGTTGCCATCTATTTGTTT	60
Query	61	TAACTGATTACTTGAATCTGATTAAACATCACAGAAATGGGCTTTGATAAGAACAATATT	120
Sbjct	61	TAACTGATTACTTGAATCTGATTAAACATCACAGAAATGGGCTTTGATAAGAACAATATT	120
Query	121	GAATAAGAAATTTTAAATAACAAAACAGCTTATAGAAAATTCAGCATAACTTTTCCATC	180
Sbjct	121	GAATAAGAAATTTTAAATAACAAAACAGCTTATAGAAAATTCAGCATAACTTTTCCATC	180
Query	181	ACCTTCACCACCCTTGCCTTTTATTATCCTGTCCTGTATCACTGCTTTCTGTTAGCAGTG	240
Sbjct	181	ACCTTCACCACCCTTGCCTTTTATTATCCTGTCCTGTATCACTGCTTTCTGTTAGCAGTG	240
Query	241	TTGTGTGAGTTAGGATTTGGGCAGGAAAGCAAAAGCAACCACCCGTCATTTTCCCAGAAT	300
Sbjct	241	TTGTGTGAGTTAGGATTTGGGCAGGAAAGCAAAAGCAACCACCCGTCATTTTCCCAGAAT	300
Query	301	GAAGGGTTTGACGTAGGATGTAGACTTTGTATAGTAGTTGGGAGAGCTGTGGGAGTGAAG	360
Sbjct	301	GAAGGGTTTGACGTAGGATGTAGACTTTGTATAGTAGTTGGGAGAGCTGTGGGAGTGAAG	360
Query	361	GTCAGGGATGTCACCTACAGAAGTCAGGGAATCTGCCACCAGAGATCCTGCATCAGAAAC	420
Sbjct	361	GTCAGGGATGTCACCTACAGAAGTCAGGGAATCTGCCACCAGAGATCCTGCATCAGAAAC	420
Query	421	AGCCAACAGCGTGCTTCTGAAGAACTAGTGGGGAAGTGGCTATAATTCTTAGGAATCCCA	480
Sbjct	421	AGCCAACAGCGTGCTTCTGAAGAACTAGTGGGGAAGTGGCTATAATTCTTAGGAATCCCA	480

Query	481	GCAAGTCCGCACCACTGTCTCAGTCTACAGCAGTGGAGAAAGGGGTTTCCAGGAGCTCTC	540
Sbjct	481	GCAAGTCCGCACCACTGTCTCAGTCTACAGCAGTGGAGAAAGGGGTTTCCAGGAGCTCTC	540
Query	541	TGGAAAGTTCTGCCCACACTTTGCAACAATCTTCAGAGGATAATGGGCTTCTCTTCCAG	600
Sbjct	541	TGGAAAGTTCTGCCCACACTTTGCAACAATCTTCAGAGGATAATGGGCTTCTCTTCCAG	600
Query	601	CTTCCACACCCAACAAGAGTGCCTTTCATCGGCCAACTCTAACCTGGAACCCTATGGCAG	660
Sbjct	601	CTTCCACACCCAACAAGAGTGCCTTTCATCGGCCAACTCTAACCTGGAACCCTATGGCAG	660
Query	661	AGGGGATTTAGGAGACAGTTTGTNATGTCTGTGGAATGCAAATGAANANGTANCAATGCT	720
Sbjct	661	AGGGGATTTAGGAGACAGTTTGTNATGTCTGTGGAATGCAAATGAANANGTANCAATGCT	720
Query	721	TANTTGACAGCGGNCATACACAAATNTNGAAA	752
Sbjct	721	TANTTGACAGCGGNCATACACAAATNTNGAAA	752

Sequence 409 matched with Sequence 71

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 409
Length=12

SEQ ID NO: 71	18.3	2e-04
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ALIGNMENTS

Identities = 12/12 (100%), Gaps = 0/12 (0%)

Query	1	GATCCGTNGACT	12
Sbjct	1	GATCCGTNGACT	12

Sequence 410 matched with Sequence 72

Query= Sequence ID 410
Length=505

SEQ ID NO: 72

ALIGNMENTS

Identities = 505/505 (100%), Gaps = 0/505 (0%)

Query	1	CTCTTCCCAGCCCCTGAGCCCAGCCCCTCCCAAGTGGTGCCAGACAAAAAACTACATGG	60
Sbjct	1	CTCTTCCCAGCCCCTGAGCCCAGCCCCTCCCAAGTGGTGCCAGACAAAAAACTACATGG	60
Query	61	CCCTTTCGTGTCTTGGGGGTGGAAGGGAGGGATGAATTGGGGTGATAGAACCCTGGTGA	120
Sbjct	61	CCCTTTCGTGTCTTGGGGGTGGAAGGGAGGGATGAATTGGGGTGATAGAACCCTGGTGA	120
Query	121	ATTCAGAGTAATCTTTCTTTAGAAAACTGGTGTTTTCTAAAGAAACAGGATAGGAGTTTA	180
Sbjct	121	ATTCAGAGTAATCTTTCTTTAGAAAACTGGTGTTTTCTAAAGAAACAGGATAGGAGTTTA	180
Query	181	GAGAAGGCACCAAAGCTTTCACTTTGGTTTGGCACCAGTTTCTAACCATCTGTTTTTTCT	240
Sbjct	181	GAGAAGGCACCAAAGCTTTCACTTTGGTTTGGCACCAGTTTCTAACCATCTGTTTTTTCT	240
Query	241	ACCCTAGCTATCTTTTATTGGTAAATATAAATGTATAATTATGTTTGTAGAGCTTTACC	300
Sbjct	241	ACCCTAGCTATCTTTTATTGGTAAATATAAATGTATAATTATGTTTGTAGAGCTTTACC	300
Query	301	AAGGAGTTTCCCTCCTTTTTTGTGTTGATTAGCAAATTTTGAATCTCCATTTTCCAA	360
Sbjct	301	AAGGAGTTTCCCTCCTTTTTTGTGTTGATTAGCAAATTTTGAATCTCCATTTTCCAA	360
Query	361	AAGTAAGAGACTCCAGCATGGCCTTCTGTTTGCCCCGCAGTAAAGTAACTTCCATATAAA	420
Sbjct	361	AAGTAAGAGACTCCAGCATGGCCTTCTGTTTGCCCCGCAGTAAAGTAACTTCCATATAAA	420
Query	421	ATGGTATTTGAAAGTGAGAGTTCATGACAACAGACCGTTTTCCATTTTCATCTGTATTTTA	480
Sbjct	421	ATGGTATTTGAAAGTGAGAGTTCATGACAACAGACCGTTTTCCATTTTCATCTGTATTTTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCTCCGTGACTCCACTTGTGGGTTT	505
Sbjct	481	TCTCCGTGACTCCACTTGTGGGTTT	505

Sequence 411 matched with Sequence 73

Query= Sequence ID - 411
Length=505

nt: 505

SEQ ID NO: 73

nt: 505

ALIGNMENTS

Identities = 505/505 (100%), Gaps = 0/505 (0%)

Query	1	TGGAGCTGAAAAATTCCTATTACCTAGGGGCATCACAACGCATTGCATTTCGCCCCGTGTT	60
Sbjct	1	TGGAGCTGAAAAATTCCTATTACCTAGGGGCATCACAACGCATTGCATTTCGCCCCGTGTT	60
Query	61	TGGGATGATGCTGGTGTAAACCTACTATGCTGCCAGTCATGTAAAAGTATAGCACACACA	120
Sbjct	61	TGGGATGATGCTGGTGTAAACCTACTATGCTGCCAGTCATGTAAAAGTATAGCACACACA	120
Query	121	ATTAGTAGGTAATGCTTGCAAATAATAATGAAAGACTCTGCTACTGGTTTATGTATTTAC	180
Sbjct	121	ATTAGTAGGTAATGCTTGCAAATAATAATGAAAGACTCTGCTACTGGTTTATGTATTTAC	180
Query	181	TATGCTATACTTTTTGTCATTACTTTAGAGTGTACTCCTACTtttttttttttttttttttt	240
Sbjct	181	TATGCTATACTTTTTGTCATTACTTTAGAGTGTACTCCTACTTTTTTTTTTTTTTTTTTTT	240
Query	241	GAGATGGAGTTTCACTCTTGTCTGTAGGCTGGAGCGAANTGGCGGATCTCGGCTTACT	300
Sbjct	241	GAGATGGAGTTTCACTCTTGTCTGTAGGCTGGAGCGAANTGGCGGATCTCGGCTTACT	300
Query	301	GCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCANCTTCCCAGAGTAGCTGAG	360
Sbjct	301	GCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCANCTTCCCAGAGTAGCTGAG	360
Query	361	ATTACAGGCATGCACCGCCACGCACGGGTAATTTTGTATTTTGGTAGAGACAGGGTTTC	420
Sbjct	361	ATTACAGGCATGCACCGCCACGCACGGGTAATTTTGTATTTTGGTAGAGACAGGGTTTC	420
Query	421	ACCATGTTGGCCAGGCTGGTCACCAACTCCTGACCTCAGGTGACCCGCCTCCTCACCTCC	480
Sbjct	421	ACCATGTTGGCCAGGCTGGTCACCAACTCCTGACCTCAGGTGACCCGCCTCCTCACCTCC	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGAGTGTGGGATTACAGGNGTGAG	505
Sbjct	481	AGAGTGTGGGATTACAGGNGTGAG	505

Sequence 412 matched with Sequence 74

Query= Sequence ID 412
Length=580

SEQ ID NO: 74

ALIGNMENTS

Identities = 580/580 (100%), Gaps = 0/580 (0%)

Query	1	ATAAAAATTAGCTGGGGGTGATGGGCCCTGTACCCAGCTACTCGGGAGGTGAGGTAGGA	60
Sbjct	1	ATAAAAATTAGCTGGGGGTGATGGGCCCTGTACCCAGCTACTCGGGAGGTGAGGTAGGA	60
Query	61	GAATCACTTGAACCCGGGAGATGGAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTCC	120
Sbjct	61	GAATCACTTGAACCCGGGAGATGGAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTCC	120
Query	121	AGCCTGTGTGACAGAACAAGACTCTGTCTCaaaaaaaaataataataataataataa	180
Sbjct	121	AGCCTGTGTGACAGAACAAGACTCTGTCTCAAAAAAAAAATAATAATAATAATAATAA	180
Query	181	aaaggaataacatagctaggaataaatTTAATCAAAGAGGTGAAAGACTTATACACTTAA	240
Sbjct	181	AAAGGAATAACATAGCTAGGAATAAATTTAATCAAAGAGGTGAAAGACTTATACACTTAA	240
Query	241	AACTACaaaaaaaaaTCACTGAAGGAATTATAGACCCaaataaaaaataaaaaaGAC	300
Sbjct	241	AACTACAAAAAAAAAATCACTGAAGGAATTATAGACCCAAATAAAAAATAATAAAGAC	300
Query	301	ATTCTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAGTG	360
Sbjct	301	ATTCTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAGTG	360
Query	361	ATCTACAGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAATGGAA	420
Sbjct	361	ATCTACAGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAATGGAA	420
Query	421	AAGCCAATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAACACAATCTT	480
Sbjct	421	AAGCCAATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAACACAATCTT	480

PATENT SEQUENCE ALIGNMENT

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Query  481  GGGGaaaaaaaacaaaaacaaaGTCAAAGAACTCACACTTCTCTATTTATAATTTACTA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGGGAAAAAAAAACAAAAACAAAGTCAAAGAACTCACACTTCTCTATTTATAATTTACTA  540

Query  541  CAAAGTTATAGNATCAAAGTCGACGCGCCGCGATCCGGGC  580
          |||||||||||||||||||||||||||||||||||
Sbjct  541  CAAAGTTATAGNATCAAAGTCGACGCGCCGCGATCCGGGC  580
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Sequence 413 matched with Sequence 75

Query= Sequence ID 413
Length=535

SEQ ID NO: 75

ALIGNMENTS

Identities = 535/535 (100%), Gaps = 0/535 (0%)

Query	1	CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAAATAATAAATGCTTACACGAA	60
Sbjct	1	CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAAATAATAAATGCTTACACGAA	60
Query	61	AATTATTTATTGAGAATATTCATATAAAAAATTACCTAAAGCAAAGTaaaaaaGTAAAT	120
Sbjct	61	AATTATTTATTGAGAATATTCATATAAAAAATTACCTAAAGCAAAGTAAAAAAGTAAAT	120
Query	121	CAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTGTAGCTGTAACAAAAAGAAAG	180
Sbjct	121	CAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTGTAGCTGTAACAAAAAGAAAG	180
Query	181	AAAACAACtttttttAAAGCCTCATTCTCTTTTCTTTCAAAATGTACCTTATTCCCACAC	240
Sbjct	181	AAAACAACCTTTTTTAAAGCCTCATTCTCTTTTCTTTCAAAATGTACCTTATTCCCACAC	240
Query	241	ACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATATTACTTTGTTTAAATAAGAT	300
Sbjct	241	ACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATATTACTTTGTTTAAATAAGAT	300
Query	301	GCTTCAGCAAAAGTCATTCTCTCTTTAACCATATAATTTAAAAACTCCTCTTCACGATTG	360
Sbjct	301	GCTTCAGCAAAAGTCATTCTCTCTTTAACCATATAATTTAAAAACTCCTCTTCACGATTG	360
Query	361	ATAGCAAAATCAGAAACGTTAGGGCACCAGTGAGTTGAAAAAACTGGTCTTAAGTTGGAA	420
Sbjct	361	ATAGCAAAATCAGAAACGTTAGGGCACCAGTGAGTTGAAAAAACTGGTCTTAAGTTGGAA	420
Query	421	AAACTATTATTAATAATATTATCCTATCCATCCATATCTATTGAAATTGTCAGGTCCATA	480
Sbjct	421	AAACTATTATTAATAATATTATCCTATCCATCCATATCTATTGAAATTGTCAGGTCCATA	480

PATENT SEQUENCE ALIGNMENT

Query	481	ATTTCATTTTAATTAATTATAGGAAAGAAGAAAAGATAATACCCATTGTTCTAT	535
Sbjct	481	ATTTCATTTTAATTAATTATAGGAAAGAAGAAAAGATAATACCCATTGTTCTAT	535

Sequence 414 matched with Sequence 76

Query= Sequence ID 414

Length=505

SEQ ID NO: 76

ALIGNMENTS

Identities = 505/505 (100%), Gaps = 0/505 (0%)

Query	1	CTCAGACTCTTTCTGCCCTAATGGCCATTACTATCCAGTCTGTATTGCTACAAGGGACCC	60
Sbjct	1	CTCAGACTCTTTCTGCCCTAATGGCCATTACTATCCAGTCTGTATTGCTACAAGGGACCC	60
Query	61	ACTGGTACCCCTTTTAGATTCTATCAAAAGGAACAGGGTTTTCTAGAGGCAGGCAGCCT	120
Sbjct	61	ACTGGTACCCCTTTTAGATTCTATCAAAAGGAACAGGGTTTTCTAGAGGCAGGCAGCCT	120
Query	121	GGTGGTATGGCACAGCAGAAGCTTACTGCTAATGAAATGGGAACCTCCCCCTCCCTTGTG	180
Sbjct	121	GGTGGTATGGCACAGCAGAAGCTTACTGCTAATGAAATGGGAACCTCCCCCTCCCTTGTG	180
Query	181	GTTTCAGCACAGAACCTGAATGCCAGGAAAAATTCCTGGGCCAAGAAGCTAAAGCTAAAG	240
Sbjct	181	GTTTCAGCACAGAACCTGAATGCCAGGAAAAATTCCTGGGCCAAGAAGCTAAAGCTAAAG	240
Query	241	AAACCTTCCTTTTTTCAACGtttttttttCTTTCAAACGTAGGGTCACTTTTGATTGAG	300
Sbjct	241	AAACCTTCCTTTTTTCAACGTTTTTTTTCTTTCAAACGTAGGGTCACTTTTGATTGAG	300
Query	301	GCAAAGGGGTCCTACTGTAAGTGGAAGAAAGACTCACTCCCCTAACATAAGTTTTCACTGTG	360
Sbjct	301	GCAAAGGGGTCCTACTGTAAGTGGAAGAAAGACTCACTCCCCTAACATAAGTTTTCACTGTG	360
Query	361	GTGGGATGGTGCCGCCGATATGCTTGATATGCTTTTCCTTCCACATGTTAAGCTAGGAA	420
Sbjct	361	GTGGGATGGTGCCGCCGATATGCTTGATATGCTTTTCCTTCCACATGTTAAGCTAGGAA	420
Query	421	ACCTAACAGGATGTCAGCAGGGCAGTTAACTCTGGACTCANAGCCCTCAAGGGCATGTGG	480
Sbjct	421	ACCTAACAGGATGTCAGCAGGGCAGTTAACTCTGGACTCANAGCCCTCAAGGGCATGTGG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CANAACCTCATGGCATNCAAGACCA	505
Sbjct	481	CANAACCTCATGGCATNCAAGACCA	505

Sequence 415 matched with Sequence 77

Query= Sequence ID - 415
Length=596

nt: 596

SEQ ID NO: 77

nt: 596

ALIGNMENTS

Identities = 596/596 (100%), Gaps = 0/596 (0%)

Query	1	GTATAATTGATTCTTTTGAACCTAAAGTATAAGACTTCACGATTAGaaaaaaTTATCCA	60
Sbjct	1	GTATAATTGATTCTTTTGAACCTAAAGTATAAGACTTCACGATTAGAAAAAAATTATCCA	60
Query	61	AAGACTAATGTAATTAAGTGAGGAAAAGGTGCTGGAGGAACTGGATAACCACATGGAAAT	120
Sbjct	61	AAGACTAATGTAATTAAGTGAGGAAAAGGTGCTGGAGGAACTGGATAACCACATGGAAAT	120
Query	121	GTATGAACCATGACCTCTATGTCACATACTATATATAAACTTAATTTGAGGTGTATCAC	180
Sbjct	121	GTATGAACCATGACCTCTATGTCACATACTATATATAAACTTAATTTGAGGTGTATCAC	180
Query	181	AGAGCTAACTGTGGGGGCTAAAACGTTGAAGCCTTTGGATGGCCGCACAAGAGATGTCTG	240
Sbjct	181	AGAGCTAACTGTGGGGGCTAAAACGTTGAAGCCTTTGGATGGCCGCACAAGAGATGTCTG	240
Query	241	CATTCATAACCTTGGGGAGGGTATGAACATTTCTTGGTAACATGCAAAAAGCACTAACTG	300
Sbjct	241	CATTCATAACCTTGGGGAGGGTATGAACATTTCTTGGTAACATGCAAAAAGCACTAACTG	300
Query	301	TAAAAGAGAACAGTTGGTCAGTTGAATTTTCATGAAACATTGTAACTTCTGCTAAACAAC	360
Sbjct	301	TAAAAGAGAACAGTTGGTCAGTTGAATTTTCATGAAACATTGTAACTTCTGCTAAACAAC	360
Query	361	TGACACCATTAAGAATGTGGAAAAAGGCTGGGCACAGTGGCTCATGCCTATAATCCCAGC	420
Sbjct	361	TGACACCATTAAGAATGTGGAAAAAGGCTGGGCACAGTGGCTCATGCCTATAATCCCAGC	420
Query	421	ATTTTGGGAGGCCGGGGCGGGAGAATCACTTGAGGCCAGGAGTTTGAAACCAGCCTGGGC	480
Sbjct	421	ATTTTGGGAGGCCGGGGCGGGAGAATCACTTGAGGCCAGGAGTTTGAAACCAGCCTGGGC	480

PATENT SEQUENCE ALIGNMENT

Query	481	AACATGGCAAGACCCCGACTCTACAAAAATATTTTAAAAATTAGTTGGGTGTGGTGATG	540
Sbjct	481	AACATGGCAAGACCCCGACTCTACAAAAATATTTTAAAAATTAGTTGGGTGTGGTGATG	540
Query	541	CACTCCTGTAGTCCTAGCTGCCAGGANGCTAAGNGGAAGGATCACTTAACCCTGG	596
Sbjct	541	CACTCCTGTAGTCCTAGCTGCCAGGANGCTAAGNGGAAGGATCACTTAACCCTGG	596

Sequence 416 matched with Sequence 78

Query= Sequence ID 416

Length=504

SEQ ID NO: 78

ALIGNMENTS

Identities = 504/504 (100%), Gaps = 0/504 (0%)

Query	1	CTGGTGGCGGCGGTCTGTGCGGACGCAAACATGCAGATCTTTGTGAAGACCCTCACTGGCA	60
Sbjct	1	CTGGTGGCGGCGGTCTGTGCGGACGCAAACATGCAGATCTTTGTGAAGACCCTCACTGGCA	60
Query	61	AAACCATCACCTTGAGGTCGAGCCCAGTGACACCATTGAGAATGTCAAAGCCAAAATTC	120
Sbjct	61	AAACCATCACCTTGAGGTCGAGCCCAGTGACACCATTGAGAATGTCAAAGCCAAAATTC	120
Query	121	AAGACAAGGAGGGTATCCACCTGACCAGCAGCGTCTGATATTTGCCGGCAAACAGCTGG	180
Sbjct	121	AAGACAAGGAGGGTATCCACCTGACCAGCAGCGTCTGATATTTGCCGGCAAACAGCTGG	180
Query	181	AGGATGGCCGCACTCTCTCAGACTACAACATCCAGAAAGAGTCCACCCTGCACCTGGTGT	240
Sbjct	181	AGGATGGCCGCACTCTCTCAGACTACAACATCCAGAAAGAGTCCACCCTGCACCTGGTGT	240
Query	241	TGCGCCTGCGAGGTGGCATTATTGAGCCTTCTCTCCGCCAGCTTGCCAGAAATACAAC	300
Sbjct	241	TGCGCCTGCGAGGTGGCATTATTGAGCCTTCTCTCCGCCAGCTTGCCAGAAATACAAC	300
Query	301	GCGACAAGATGATCTGCCGCAAGTGCTATGCTCGCCTTACCCTCGTGCTGTCAACTGCC	360
Sbjct	301	GCGACAAGATGATCTGCCGCAAGTGCTATGCTCGCCTTACCCTCGTGCTGTCAACTGCC	360
Query	361	GCAAGAAGAAGTGTGGTCACACCAACAACCTGCGTCCCAAGAAGAAGGTCAAATAAGGTT	420
Sbjct	361	GCAAGAAGAAGTGTGGTCACACCAACAACCTGCGTCCCAAGAAGAAGGTCAAATAAGGTT	420
Query	421	GTTCTTTCCTTGAAGGGCAGCCTCCTGCCCAGGCCCGTGGCCCTGGAGCCTCAATAAAG	480
Sbjct	421	GTTCTTTCCTTGAAGGGCAGCCTCCTGCCCAGGCCCGTGGCCCTGGAGCCTCAATAAAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	TGTCCCTTTCATTGACTGGAGCAG	504
Sbjct	481	TGTCCCTTTCATTGACTGGAGCAG	504

Sequence 417 matched with Sequence 79

Query= Sequence ID 417
Length=564

SEQ ID NO: 79

ALIGNMENTS

Identities = 564/564 (100%), Gaps = 0/564 (0%)

Query	1	GCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCCGCAGATAAGttttttt	60
Sbjct	1	GCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCCGCAGATAAGTTTTTTT	60
Query	61	CTCTTTGAAAGATAGAGATTAATACAACACTTTAAAAATATAGTCAATAGGTTACTAAG	120
Sbjct	61	CTCTTTGAAAGATAGAGATTAATACAACACTTTAAAAATATAGTCAATAGGTTACTAAG	120
Query	121	ATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAAT	180
Sbjct	121	ATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAAT	180
Query	181	ATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAAGGTTTCTAAAACATGACG	240
Sbjct	181	ATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAAGGTTTCTAAAACATGACG	240
Query	241	GAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGAGAA	300
Sbjct	241	GAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGAGAA	300
Query	301	AGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAA	360
Sbjct	301	AGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAA	360
Query	361	GGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTGAAG	420
Sbjct	361	GGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTGAAG	420
Query	421	GCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGACGC	480
Sbjct	421	GCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGACGC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACCAAATGG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACCAAATGG  540

Query  541  AAAGATTAATTGGGAGTGGTAGGA  564
          ||||||||||||||||
Sbjct  541  AAAGATTAATTGGGAGTGGTAGGA  564
```

Sequence 418 matched with Sequence 80

Query= Sequence ID 418
Length=270

SEQ ID NO: 80

ALIGNMENTS

Identities = 270/270 (100%), Gaps = 0/270 (0%)

Query	1	CCCGGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTATGTAA	60
Sbjct	1	CCCGGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTATGTAA	60
Query	61	TGCAAAAtttttttaatcttcgccttaataacttttttattttgttttattttGAATGATG	120
Sbjct	61	TGCAAAATTTTTTAATCTTCGCCTTAATACTTTTTTATTTTGTTTTATTTTGAATGATG	120
Query	121	AGCCTTCGTGcccccccttcccccttttttgtccccAACTTGAGATGTATGAAGGCTTT	180
Sbjct	121	AGCCTTCGTGCCCCCCTTCCCCCTTTTTTGTCCCCAACTTGAGATGTATGAAGGCTTT	180
Query	181	TGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCA	240
Sbjct	181	TGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCA	240
Query	241	GTTGAATAAAAAGTGCACACCTTATAAAAAA	270
Sbjct	241	GTTGAATAAAAAGTGCACACCTTATAAAAAA	270

Sequence 419 matched with Sequence 81

Query= Sequence ID 419
Length=268

SEQ ID NO: 81

ALIGNMENTS

Identities = 268/268 (100%), Gaps = 0/268 (0%)

Query	1	CCC	GGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTATGTAA	60
Sbjct	1	CCC	GGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTATGTAA	60
Query	61	TGCAAAA	AtttttttaatcttcgccttaataacttttttattttgttttattttGAATGATG	120
Sbjct	61	TGCAAAA	ATTTTAAATCTTCGCCTTAATACTTTTTTATTTTGTTTATTTTGAATGATG	120
Query	121	AGCCTTCGTG	cccccccttcccccttttttgtccccAACTTGAGATGTATGAAGGCTTT	180
Sbjct	121	AGCCTTCGTG	CCCCCCCCTTCCCCCTTTTTGTCCCCAACTTGAGATGTATGAAGGCTTT	180
Query	181	TGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCA	240	
Sbjct	181	TGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCA	240	
Query	241	GTTGAATAAAAAGTGCACACCTTATAAAA	268	
Sbjct	241	GTTGAATAAAAAGTGCACACCTTATAAAA	268	

Sequence 420 matched with Sequence 82

Query= Sequence ID 420
Length=334

SEQ ID NO: 82

ALIGNMENTS

Identities = 334/334 (100%), Gaps = 0/334 (0%)

Query	1	CTTCATTTGAAATGGTTGAATCTGCTGTGTAATAAAGTGGTTCAACCATGATTAGGAACT	60
Sbjct	1	CTTCATTTGAAATGGTTGAATCTGCTGTGTAATAAAGTGGTTCAACCATGATTAGGAACT	60
Query	61	GAAATTTAGTAGAAGAGGGAAAAGGAGTTAATGTAACAAATTATTTTAGCTACAAACCCC	120
Sbjct	61	GAAATTTAGTAGAAGAGGGAAAAGGAGTTAATGTAACAAATTATTTTAGCTACAAACCCC	120
Query	121	GGTAATAGAGCACTTGGGGGATGGGATGGGGTGGGTGGTGAGACAATCAGAATGGTAAA	180
Sbjct	121	GGTAATAGAGCACTTGGGGGATGGGATGGGGTGGGTGGTGAGACAATCAGAATGGTAAA	180
Query	181	TTGATTAAATGCTCCTAACCCCTGTAATTTTGTGCATAGAGCACCCCTATGCTGTGGAAATA	240
Sbjct	181	TTGATTAAATGCTCCTAACCCCTGTAATTTTGTGCATAGAGCACCCCTATGCTGTGGAAATA	240
Query	241	ACTGTTCTTAGATTTTCATTGTAACCTGGACTGTTCAGGTTGCCAGAGGGAAAGAACATTC	300
Sbjct	241	ACTGTTCTTAGATTTTCATTGTAACCTGGACTGTTCAGGTTGCCAGAGGGAAAGAACATTC	300
Query	301	CTAATTCTAATAAAATAAACTTTTATTTTGTTTA	334
Sbjct	301	CTAATTCTAATAAAATAAACTTTTATTTTGTTTA	334

Sequence 421 matched with Sequence 83

Query= Sequence ID 421

Length=675

SEQ ID NO: 83

ALIGNMENTS

Identities = 675/675 (100%), Gaps = 0/675 (0%)

Query	1	TGTCATTGAATCTGCTTGTTACTTAAATGCTAAACTCAATTCTGTAATTCAATAGGTGCA	60
Sbjct	1	TGTCATTGAATCTGCTTGTTACTTAAATGCTAAACTCAATTCTGTAATTCAATAGGTGCA	60
Query	61	CCTCTCTGAGAAACATAAGAGACAATGAGGAAAAGGATTGAGCATTCCGTGGAATTTGTA	120
Sbjct	61	CCTCTCTGAGAAACATAAGAGACAATGAGGAAAAGGATTGAGCATTCCGTGGAATTTGTA	120
Query	121	CCATGATCAGTGTGAATCCCAGTGGCGTAATCCAAGTAAGATGTTACAAAAGATTTGTTT	180
Sbjct	121	CCATGATCAGTGTGAATCCCAGTGGCGTAATCCAAGTAAGATGTTACAAAAGATTTGTTT	180
Query	181	TTAATGTCTAATTAATAAAATTTTAAAGGAAGAAACATTCTAATACTTTAATTATAAAAA	240
Sbjct	181	TTAATGTCTAATTAATAAAATTTTAAAGGAAGAAACATTCTAATACTTTAATTATAAAAA	240
Query	241	GTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCTTTAAATGTATATTTCTTAAT	300
Sbjct	241	GTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCTTTAAATGTATATTTCTTAAT	300
Query	301	ATCTTGAAATTGTAATGCCttttttttttcctaaattttttttGTCATGAAATGAGATAG	360
Sbjct	301	ATCTTGAAATTGTAATGCCTTTTTTTTTTCCTAAATTTTTTTTGTGTCATGAAATGAGATAG	360
Query	361	TAACAGCAGATTGGGACAACAAGGTTATATTCTTGTCTTGAATCAGGCCATGGCTTCTTT	420
Sbjct	361	TAACAGCAGATTGGGACAACAAGGTTATATTCTTGTCTTGAATCAGGCCATGGCTTCTTT	420
Query	421	CATCCAAATTTTCAGACCTCATTTATTTACTTTGTCCCTGCCTCCCATCCCTGGATATCAG	480
Sbjct	421	CATCCAAATTTTCAGACCTCATTTATTTACTTTGTCCCTGCCTCCCATCCCTGGATATCAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTTGTGGATATCTACAGTTAATAGAGTGACCAAATAGTAGGAATACTGTCTCTCTATTCT	540
Sbjct	481	TTTGTGGATATCTACAGTTAATAGAGTGACCAAATAGTAGGAATACTGTCTCTCTATTCT	540
Query	541	GAATAAAATCTTTGAATCAGATTTAGAAATAATGAATAAAATACAAATCAGCCATTGAAA	600
Sbjct	541	GAATAAAATCTTTGAATCAGATTTAGAAATAATGAATAAAATACAAATCAGCCATTGAAA	600
Query	601	TTGCTCTAATTTTGAGAGCTTATGATTTATTCATCTTTGGTTTCCAAGTTCAAGTTATAT	660
Sbjct	601	TTGCTCTAATTTTGAGAGCTTATGATTTATTCATCTTTGGTTTCCAAGTTCAAGTTATAT	660
Query	661	GTAGACATTTTAATT	675
Sbjct	661	GTAGACATTTTAATT	675

Sequence 422 matched with Sequence 84

Query= Sequence ID 422
Length=485

SEQ ID NO: 84

ALIGNMENTS

Identities = 485/485 (100%), Gaps = 0/485 (0%)

Query	1	GCTTCCTAGGTGAGGTCACGAGGAAACCTGCTGGCCAAGTGACCTGGCAGGGTGTGGCCA	60
Sbjct	1	GCTTCCTAGGTGAGGTCACGAGGAAACCTGCTGGCCAAGTGACCTGGCAGGGTGTGGCCA	60
Query	61	GTGTGGCCAGGGCCGCCGAGCCTGCTTTCCTTCCCTGCAGCAGGAACCCTTCTGGGGCTG	120
Sbjct	61	GTGTGGCCAGGGCCGCCGAGCCTGCTTTCCTTCCCTGCAGCAGGAACCCTTCTGGGGCTG	120
Query	121	TGATCCTGCGATGGTGCCTGGGTGGGAGTgggggtggggggCGGGATGGTCTCCCTACCT	180
Sbjct	121	TGATCCTGCGATGGTGCCTGGGTGGGAGTGGGGGTGGGGGGCGGGATGGTCTCCCTACCT	180
Query	181	GCCAGCTTCTTGGTTTGAGGTGAGGACAGCCCCGGAAGCTCANACTTGGCTCCTGTCCAT	240
Sbjct	181	GCCAGCTTCTTGGTTTGAGGTGAGGACAGCCCCGGAAGCTCANACTTGGCTCCTGTCCAT	240
Query	241	GTA CTTGGGGCCATGAGCTCTGCAGGGACCTTGAAAGANAGAGACGGGTGGTGTANGGC	300
Sbjct	241	GTA CTTGGGGCCATGAGCTCTGCAGGGACCTTGAAAGANAGAGACGGGTGGTGTANGGC	300
Query	301	ANGGGAAGGCATTGTCTTCAAACAGGAAAAAGCTGANAATGGAAACAGGCGAAACTTACC	360
Sbjct	301	ANGGGAAGGCATTGTCTTCAAACAGGAAAAAGCTGANAATGGAAACAGGCGAAACTTACC	360
Query	361	AAGTGTAACATCACCTGGAAGTGAAGGAGGGTGGGAAGGTTTAAATTATTTTAAAAATAG	420
Sbjct	361	AAGTGTAACATCACCTGGAAGTGAAGGAGGGTGGGAAGGTTTAAATTATTTTAAAAATAG	420
Query	421	AGATGGGGTCTCACTATGTTGCCAGGCTGGTCTCAAACACTGGGGCTCAAGTGAACCTC	480
Sbjct	421	AGATGGGGTCTCACTATGTTGCCAGGCTGGTCTCAAACACTGGGGCTCAAGTGAACCTC	480

PATENT SEQUENCE ALIGNMENT

Query	481	CTTCT	485
Sbjct	481	CTTCT	485

Sequence 423 matched with Sequence 85

Query= Sequence ID - 423
Length=387

nt: 387

SEQ ID NO: 85

nt: 387

ALIGNMENTS

Identities = 387/387 (100%), Gaps = 0/387 (0%)

Query	1	TGTTTCTCNAGGGCGAGAGGCTGTCTTANAGCACCATTCTCTGGCCCTNGTCCCATGAGA	60
Sbjct	1	TGTTTCTCNAGGGCGAGAGGCTGTCTTANAGCACCATTCTCTGGCCCTNGTCCCATGAGA	60
Query	61	AGGAACCGCACTCAGGAGCCACACTCTCCCACTNCCCTTGCCCANAAAGACTCACAGAGGG	120
Sbjct	61	AGGAACCGCACTCAGGAGCCACACTCTCCCACTNCCCTTGCCCANAAAGACTCACAGAGGG	120
Query	121	CACGGAGCTGGCTGTGGTGAGAGGAGGTCCANCAAATTCCTGTCTGCANAAGGGTTCTGA	180
Sbjct	121	CACGGAGCTGGCTGTGGTGAGAGGAGGTCCANCAAATTCCTGTCTGCANAAGGGTTCTGA	180
Query	181	ACACCACCGCCTGGCAGCGTGCTGGAGGAGGGATTCTCTTTTCCTCACAGCAATTCTGA	240
Sbjct	181	ACACCACCGCCTGGCAGCGTGCTGGAGGAGGGATTCTCTTTTCCTCACAGCAATTCTGA	240
Query	241	CCAGAAACCTGTCAAATCAGGAATGGCTAAAATAAGACCAGGGTATGAATGACCATCAGC	300
Sbjct	241	CCAGAAACCTGTCAAATCAGGAATGGCTAAAATAAGACCAGGGTATGAATGACCATCAGC	300
Query	301	CACAGTAAAACCAAGGCACAGCTCTCCTGAGCCCACCCAAGCTGCTGTGGCCCAGACTGG	360
Sbjct	301	CACAGTAAAACCAAGGCACAGCTCTCCTGAGCCCACCCAAGCTGCTGTGGCCCAGACTGG	360
Query	361	TGACATCACCTCAGGGCaaaaaaaaa	387
Sbjct	361	TGACATCACCTCAGGGCAAAAAAAAAA	387

Sequence 424 matched with Sequence 86

Query= Sequence ID - 424
Length=420

nt: 420

SEQ ID NO: 86

nt: 420

ALIGNMENTS

Identities = 420/420 (100%), Gaps = 0/420 (0%)

Query	1	CGCAGAATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCATCAAC	60
Sbjct	1	CGCAGAATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCATCAAC	60
Query	61	GAAGTGGTAACCCGAGAATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTC	120
Sbjct	61	GAAGTGGTAACCCGAGAATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTC	120
Query	121	AAGAAGCGTGACCTCGGGCACTCAAAGAGATTCGGAATTTGCCATGAAGGAGATGGGA	180
Sbjct	121	AAGAAGCGTGACCTCGGGCACTCAAAGAGATTCGGAATTTGCCATGAAGGAGATGGGA	180
Query	181	ACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCTGGGCCAAAGGAATAAGG	240
Sbjct	181	ACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCTGGGCCAAAGGAATAAGG	240
Query	241	AATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAACGTAATGAGGATGAAGATTCA	300
Sbjct	241	AATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAACGTAATGAGGATGAAGATTCA	300
Query	301	CCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAG	360
Sbjct	301	CCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAG	360
Query	361	ACAGTCAATGTGGATGAGAACTAATCGCTGATCGTCAGATCAAATAAAGTTATAAAATTG	420
Sbjct	361	ACAGTCAATGTGGATGAGAACTAATCGCTGATCGTCAGATCAAATAAAGTTATAAAATTG	420

Sequence 425 matched with Sequence 87

Query= Sequence ID 425
Length=675

SEQ ID NO: 87

ALIGNMENTS

Identities = 675/675 (100%), Gaps = 0/675 (0%)

Query	1	GGAAACTGATGCCAGTCAGAACTCAGATCAAATGAAGGGGTGAAGAGAACCAGAATTGA	60
Sbjct	1	GGAAACTGATGCCAGTCAGAACTCAGATCAAATGAAGGGGTGAAGAGAACCAGAATTGA	60
Query	61	TCTCTCTGTAGGAGAATATAAATGACTTTTTTAAAGTACATATTTTCTGTGAAAGACAGT	120
Sbjct	61	TCTCTCTGTAGGAGAATATAAATGACTTTTTTAAAGTACATATTTTCTGTGAAAGACAGT	120
Query	121	TTTTTGTTTAATGCAAAAATGTTAACAATGTTTATATCATGTAGAAGTAAAAGATCGTGA	180
Sbjct	121	TTTTTGTTTAATGCAAAAATGTTAACAATGTTTATATCATGTAGAAGTAAAAGATCGTGA	180
Query	181	AACAGCACAGAGAACAGTAGTAAGACAGATTGAATTGCACTGTTGTAAGATGATGAACTT	240
Sbjct	181	AACAGCACAGAGAACAGTAGTAAGACAGATTGAATTGCACTGTTGTAAGATGATGAACTT	240
Query	241	ACAATATTAAGTGAAGGTAGACTGTGATAGATTAAGGATATATATTGTAATCCCTAGAGC	300
Sbjct	241	ACAATATTAAGTGAAGGTAGACTGTGATAGATTAAGGATATATATTGTAATCCCTAGAGC	300
Query	301	AATTGTCAAAGTGGTACAGGTAAAAAGCCAATAGAGGTGATAAAATGGAATACTAAAAAA	360
Sbjct	301	AATTGTCAAAGTGGTACAGGTAAAAAGCCAATAGAGGTGATAAAATGGAATACTAAAAAA	360
Query	361	TATCAGATGAATAATAAAGAAGACAGGAAATGAGGAACAGTGGAACAGAATGAATAAAAA	420
Sbjct	361	TATCAGATGAATAATAAAGAAGACAGGAAATGAGGAACAGTGGAACAGAATGAATAAAAA	420
Query	421	ACAAGACCATTAACCTTAATCATTAATAATTACTTTAAATGGGTAAACATTATGGTTATA	480
Sbjct	421	ACAAGACCATTAACCTTAATCATTAATAATTACTTTAAATGGGTAAACATTATGGTTATA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGGCAGAGATTTTCAGACTAGATAAAAAGAGCAAGCTCCACTATATACTGTCTACAAGAGA  540
          |||
Sbjct  481  AGGCAGAGATTTTCAGACTAGATAAAAAGAGCAAGCTCCACTATATACTGTCTACAAGAGA  540

Query  541  TATACTTTAAAGTGTATATTATATTTAAATATAAAAGATTTGGAATAAAATAAACCTAAGAA  600
          |||
Sbjct  541  TATACTTTAAAGTGTATATTATATTTAAATATAAAAGATTTGGAATAAAATAAACCTAAGAA  600

Query  601  TAAGCTTACTAGGGAAGTGAAAGATCTGTACAACAAGAATTACAAAACACTGCTGAACGA  660
          |||
Sbjct  601  TAAGCTTACTAGGGAAGTGAAAGATCTGTACAACAAGAATTACAAAACACTGCTGAACGA  660

Query  661  AATCATAGGTGACCA  675
          |||
Sbjct  661  AATCATAGGTGACCA  675
```


Sequence 426 matched with Sequence 88

Query= Sequence ID 426
Length=594

SEQ ID NO: 88

ALIGNMENTS

Identities = 594/594 (100%), Gaps = 0/594 (0%)

Query	1	GTCCCGGAATCGCGGCCGCGTCGACGTTTCCTCAAAATTTATCTTCCTGTTAATGTCAGG	60
Sbjct	1	GTCCCGGAATCGCGGCCGCGTCGACGTTTCCTCAAAATTTATCTTCCTGTTAATGTCAGG	60
Query	61	CATGTATCTCCTTAGCTTGCCACAAATAACTATATATACACAGACCTTCCTTTGTAGGG	120
Sbjct	61	CATGTATCTCCTTAGCTTGCCACAAATAACTATATATACACAGACCTTCCTTTGTAGGG	120
Query	121	CTAACAGTGTTCATTGTAAGTGGAGGCCTCATAGATACCTGGCCTTTTCCTACCTTATT	180
Sbjct	121	CTAACAGTGTTCATTGTAAGTGGAGGCCTCATAGATACCTGGCCTTTTCCTACCTTATT	180
Query	181	CCAAAGATGGTTGCATCTTATAAATAATGTCATTCTTCAGCAAATGGTATGGAAATGAGA	240
Sbjct	181	CCAAAGATGGTTGCATCTTATAAATAATGTCATTCTTCAGCAAATGGTATGGAAATGAGA	240
Query	241	TTGTAATGTCATTATTTCTCTTTAAATAATCAGGACAACCTCATGATACAAAGAGCTCTT	300
Sbjct	241	TTGTAATGTCATTATTTCTCTTTAAATAATCAGGACAACCTCATGATACAAAGAGCTCTT	300
Query	301	CTCTATAAAAGGTGGGACTtttttttttAGTAATAGCAAAAATAAAATTGTACCTCCTTA	360
Sbjct	301	CTCTATAAAAGGTGGGACTTTTTTTTTTAGTAATAGCAAAAATAAAATTGTACCTCCTTA	360
Query	361	ATCTTCTACAGAAAGATGGATTTCAATTTCAACATTAAGAGGTAGTTTAAAGAAGCAGTA	420
Sbjct	361	ATCTTCTACAGAAAGATGGATTTCAATTTCAACATTAAGAGGTAGTTTAAAGAAGCAGTA	420
Query	421	GAAGTCAGCCTGGGCAGCATGGTGAAACCCCGTCTCTACAAAAAAGTTAGCTGGGCTTAG	480
Sbjct	421	GAAGTCAGCCTGGGCAGCATGGTGAAACCCCGTCTCTACAAAAAAGTTAGCTGGGCTTAG	480

Sequence 427 matched with Sequence 89

Query= Sequence ID 427
Length=530

SEQ ID NO: 89

ALIGNMENTS

Identities = 530/530 (100%), Gaps = 0/530 (0%)

Query	1	TTCCAATCTTCGTGTTCACTTTAAGAACACTCGTGAAACTGCTCAGGCCATCAAGGGTAT	60
Sbjct	1	TTCCAATCTTCGTGTTCACTTTAAGAACACTCGTGAAACTGCTCAGGCCATCAAGGGTAT	60
Query	61	GCATATACGAAAAGCCACGAAGTATCTGAAAGATGTCACTTTACAGAAACAGTGTGTACC	120
Sbjct	61	GCATATACGAAAAGCCACGAAGTATCTGAAAGATGTCACTTTACAGAAACAGTGTGTACC	120
Query	121	ATTCCGACGTTACAATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCAATGGGGCTGGAC	180
Sbjct	121	ATTCCGACGTTACAATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCAATGGGGCTGGAC	180
Query	181	ACAAGGTCGGTGGCCCCAAAAAGAGTGCTGAATTTTTGCTGCACATGCTTAAAAACGCAGA	240
Sbjct	181	ACAAGGTCGGTGGCCCCAAAAAGAGTGCTGAATTTTTGCTGCACATGCTTAAAAACGCAGA	240
Query	241	GAGTAATGCTGAACTTAAGGGTTTAGATGTAGATTCTCTGGTCATTGAGCATATCCAAGT	300
Sbjct	241	GAGTAATGCTGAACTTAAGGGTTTAGATGTAGATTCTCTGGTCATTGAGCATATCCAAGT	300
Query	301	GAACAAAGCACCTAAGATGCGCCGCCGACCTACAGAGCTCATGGTCGGATTAACCCATA	360
Sbjct	301	GAACAAAGCACCTAAGATGCGCCGCCGACCTACAGAGCTCATGGTCGGATTAACCCATA	360
Query	361	CATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGAAAAGGAACAGATTGTTTCCTAA	420
Sbjct	361	CATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGAAAAGGAACAGATTGTTTCCTAA	420
Query	421	ACCAGAAGAGGAGGTTGCCCAGAAGAAAAAGATATCCCAGAAGAACTGAAGAAACAAAA	480
Sbjct	421	ACCAGAAGAGGAGGTTGCCCAGAAGAAAAAGATATCCCAGAAGAACTGAAGAAACAAAA	480

Sequence 428 matched with Sequence 90

Query= Sequence ID 428
Length=381

SEQ ID NO: 90

ALIGNMENTS

Identities = 381/381 (100%), Gaps = 0/381 (0%)

Query	1	TGCAGGATCCGTCGACTCTAGATAACATGGCTAGAAAAGAGAATGAAAAAGTTGGAATTT	60
Sbjct	1	TGCAGGATCCGTCGACTCTAGATAACATGGCTAGAAAAGAGAATGAAAAAGTTGGAATTT	60
Query	61	TTAATTGCCATGGTATGGGGGGTAATCAGGTTTTCTCTTATACTGCCAACAAAGAAATTA	120
Sbjct	61	TTAATTGCCATGGTATGGGGGGTAATCAGGTTTTCTCTTATACTGCCAACAAAGAAATTA	120
Query	121	GAACAGATGACCTTTGCTTGGATGTTTCCAAACTTAATGGCCCAGTTACAATGCTCAAAT	180
Sbjct	121	GAACAGATGACCTTTGCTTGGATGTTTCCAAACTTAATGGCCCAGTTACAATGCTCAAAT	180
Query	181	GCCACCACCTAAAAGGCAACCAACTCTGGGAGTATGACCCAGTGAAATTAACCCTGCAGC	240
Sbjct	181	GCCACCACCTAAAAGGCAACCAACTCTGGGAGTATGACCCAGTGAAATTAACCCTGCAGC	240
Query	241	ATGTGAACAGTAATCAGTGCCTGGATAAAGCCACAGAAGAGGATAGCCAGGTGCCCAGCA	300
Sbjct	241	ATGTGAACAGTAATCAGTGCCTGGATAAAGCCACAGAAGAGGATAGCCAGGTGCCCAGCA	300
Query	301	TTAGAGACTGCAATGGAAGTCGGTCCCAGCAGTGGCTTCTTCGAAACGTCACCCTGCCAG	360
Sbjct	301	TTAGAGACTGCAATGGAAGTCGGTCCCAGCAGTGGCTTCTTCGAAACGTCACCCTGCCAG	360
Query	361	AAATATTCTGAGACCAAATTT	381
Sbjct	361	AAATATTCTGAGACCAAATTT	381

Sequence 429 matched with Sequence 91

Query= Sequence ID - 429
Length=535

nt: 535

SEQ ID NO: 91

nt: 535

ALIGNMENTS

Identities = 535/535 (100%), Gaps = 0/535 (0%)

Query	1	CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAAATAATAAATGCTTACACGAA	60
Sbjct	1	CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAAATAATAAATGCTTACACGAA	60
Query	61	AATTATTTATTGAGAATATTCATATAAAAAATTACCTAAAGCAAAGTaaaaaaGTAAAT	120
Sbjct	61	AATTATTTATTGAGAATATTCATATAAAAAATTACCTAAAGCAAAGTAAAAAAGTAAAT	120
Query	121	CAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTGTAGCTGTAACAAAAAGAAAG	180
Sbjct	121	CAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTGTAGCTGTAACAAAAAGAAAG	180
Query	181	AAAACAACtttttttAAAGCCTCATTCTCTTTTCTTTCAAAATGTACCTTATTCCCACAC	240
Sbjct	181	AAAACAACCTTTTTTAAAGCCTCATTCTCTTTTCTTTCAAAATGTACCTTATTCCCACAC	240
Query	241	ACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATATTACTTTGTTTAAATAAGAT	300
Sbjct	241	ACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATATTACTTTGTTTAAATAAGAT	300
Query	301	GCTTCAGCAAAAGTCATTCTCTCTTTAACCATATAATTTAAAAACTCCTCTTCACGATTG	360
Sbjct	301	GCTTCAGCAAAAGTCATTCTCTCTTTAACCATATAATTTAAAAACTCCTCTTCACGATTG	360
Query	361	ATAGCAAAATCAGAAACGTTAGGGCACCAGTGAGTTGAAAAAACTGGTCTTAAGTTGGAA	420
Sbjct	361	ATAGCAAAATCAGAAACGTTAGGGCACCAGTGAGTTGAAAAAACTGGTCTTAAGTTGGAA	420
Query	421	AAACTATTATTAATAATATTATCCTATCCATCCATATCTATTGAAATTGTCAGGTCCATA	480
Sbjct	421	AAACTATTATTAATAATATTATCCTATCCATCCATATCTATTGAAATTGTCAGGTCCATA	480

PATENT SEQUENCE ALIGNMENT

Query	481	ATTTCATTTTAATTAATTATAGGAAAGAAGAAAAGATAATACCCATTGTTCTAT	535
Sbjct	481	ATTTCATTTTAATTAATTATAGGAAAGAAGAAAAGATAATACCCATTGTTCTAT	535

Sequence 430 matched with Sequence 92

Query= Sequence ID 430
Length=619

SEQ ID NO: 92

ALIGNMENTS

Identities = 619/619 (100%), Gaps = 0/619 (0%)

Query	1	CAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGtttttttCT	60
Sbjct	1	CAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTTTTTCT	60
Query	61	CTTTGAAAGATAGAGATTAATACAACACTTAAAAAATATAGTCAATAGGTTACTAAGAT	120
Sbjct	61	CTTTGAAAGATAGAGATTAATACAACACTTAAAAAATATAGTCAATAGGTTACTAAGAT	120
Query	121	ATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAATAT	180
Sbjct	121	ATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAATAT	180
Query	181	GAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATGACGGA	240
Sbjct	181	GAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATGACGGA	240
Query	241	GGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGAGAAAG	300
Sbjct	241	GGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGAGAAAG	300
Query	301	GACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAAGG	360
Sbjct	301	GACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAAGG	360
Query	361	TGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTGAAGGC	420
Sbjct	361	TGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTGAAGGC	420
Query	421	GATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGACGCAG	480
Sbjct	421	GATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGACGCAG	480

Sequence 431 matched with Sequence 93

Query= Sequence ID 431
Length=131

SEQ ID NO: 93

ALIGNMENTS

Identities = 126/126 (100%), Gaps = 0/126 (0%)

Query	1	CGCTGGGTGCCTGCAGCGCCTCCCTTGTCTCATATGGTGTGTCCAGCACTCTATTGTTGT	60
Sbjct	1	CGCTGGGTGCCTGCAGCGCCTCCCTTGTCTCATATGGTGTGTCCAGCACTCTATTGTTGT	60
Query	61	AAACTGTTGNTTTGNCTGACCTAAATTNTCTTTACTAAACANATTTAATAGTTnaaaaaa	120
Sbjct	61	AAACTGTTGNTTTGNCTGACCTAAATTNTCTTTACTAAACANATTTAATAGTTNAAAAAA	120
Query	121	aaaaaa 126	
Sbjct	121	AAAAAA 126	

Sequence 432 matched with Sequence 94

Query= Sequence ID 432
Length=607

SEQ ID NO: 94

ALIGNMENTS

Identities = 607/607 (100%), Gaps = 0/607 (0%)

Query	1	TTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAAGAAAGGGTCCA	60
Sbjct	1	TTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAAGAAAGGGTCCA	60
Query	61	AGACTCCATTAAGTCCCTGGATGAAGGGCACTGCTACAGCAGCTAGTACCAGAGACTCT	120
Sbjct	61	AGACTCCATTAAGTCCCTGGATGAAGGGCACTGCTACAGCAGCTAGTACCAGAGACTCT	120
Query	121	CCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGAATGCTTATAGG	180
Sbjct	121	CCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGAATGCTTATAGG	180
Query	181	AAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCCAGTGCAACCCT	240
Sbjct	181	AAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCCAGTGCAACCCT	240
Query	241	TGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCTGGAAACACACC	300
Sbjct	241	TGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCTGGAAACACACC	300
Query	301	AGCTTCTGCTACCTTCATGCTCATTGTTaaaaaaaGATTAACCAGTGTGAACATTCTGAT	360
Sbjct	301	AGCTTCTGCTACCTTCATGCTCATTGTTAAAAAAGATTAACCAGTGTGAACATTCTGAT	360
Query	361	CTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGGTTAGATAACCCCCA	420
Sbjct	361	CTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGGTTAGATAACCCCCA	420
Query	421	AAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAAGAATGGACTGG	480
Sbjct	421	AAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAAGAATGGACTGG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CGGCGTGGTTGAGCTGATATGGAAAAGCTGCACCTTCCTGCAGAAGATCAACTGACCTGC	540
Sbjct	481	CGGCGTGGTTGAGCTGATATGGAAAAGCTGCACCTTCCTGCAGAAGATCAACTGACCTGC	540
Query	541	TATCCACCCCAAATTTCAACCTGAGGTATATTTCAATGAAGGCAGGTAGCTGTGCTTCT	600
Sbjct	541	TATCCACCCCAAATTTCAACCTGAGGTATATTTCAATGAAGGCAGGTAGCTGTGCTTCT	600
Query	601	CAGAGCA	607
Sbjct	601	CAGAGCA	607

Sequence 433 matched with Sequence 95

Query= Sequence ID 433

Length=687

SEQ ID NO: 95

ALIGNMENTS

Identities = 684/684 (100%), Gaps = 0/684 (0%)

Query	1	TCCCGGAATCGCGCCGCGTCGACCCGCCGCCGAGGATTCAGCAgcctcccccttgagcc	60
Sbjct	1	TCCCGGAATCGCGCCGCGTCGACCCGCCGCCGAGGATTCAGCAGCCTCCCCCTTGAGCC	60
Query	61	ccctcgcttcccgacgttcggttccccctgcccgccttctcccgccaccgcccgcgcg	120
Sbjct	61	CCCTCGCTTCCCGACGTTCCGTTCCCCCTGCCCGCCTTCTCCCGCCACCGCCGCCGCCG	120
Query	121	ccttccgcaggccgTTTCCACCGAGGAAAAGGAATCGTATCGTATGTCCGCTATCCAGAA	180
Sbjct	121	CCTTCCGCAGGCCGTTTCCACCGAGGAAAAGGAATCGTATCGTATGTCCGCTATCCAGAA	180
Query	181	CCTCCACTCTTTCGACCCCTTTGCTGATGCAAGTAAGGGTGATGACCTGCTTCCTGCTGG	240
Sbjct	181	CCTCCACTCTTTCGACCCCTTTGCTGATGCAAGTAAGGGTGATGACCTGCTTCCTGCTGG	240
Query	241	CACTGAGGATTATATCCATATAAGAATTCAACAGAGAAACGGCAGGAAGACCCTTACTAC	300
Sbjct	241	CACTGAGGATTATATCCATATAAGAATTCAACAGAGAAACGGCAGGAAGACCCTTACTAC	300
Query	301	TGTCCAAGGGATCGCTGATGATTACGATAAAAAGAACTAGTGAAGGCGTTTAAGAAAAA	360
Sbjct	301	TGTCCAAGGGATCGCTGATGATTACGATAAAAAGAACTAGTGAAGGCGTTTAAGAAAAA	360
Query	361	GTTTGCCTGCAATGGTACTGTAATTGAGCATCCGGAATATGGAGAAGTAATTCAGCTACA	420
Sbjct	361	GTTTGCCTGCAATGGTACTGTAATTGAGCATCCGGAATATGGAGAAGTAATTCAGCTACA	420
Query	421	GGGTGACCAACGCAAGAACATATGCCAGTTCCTCGTAGAGATTGGACTGGCTAAGGACGA	480
Sbjct	421	GGGTGACCAACGCAAGAACATATGCCAGTTCCTCGTAGAGATTGGACTGGCTAAGGACGA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCAGCTGAAGGTTTCATGGGTTTTAAGTGCTTGTGGCTCACTGAAGCTTAAGTGAGGATTT	540
Sbjct	481	TCAGCTGAAGGTTTCATGGGTTTTAAGTGCTTGTGGCTCACTGAAGCTTAAGTGAGGATTT	540
Query	541	CCTTGCAATGAGTAGAATTTCCCTTCCTCCCTTGTCACAGGTTTAAAAACCTCACAGCTT	600
Sbjct	541	CCTTGCAATGAGTAGAATTTCCCTTCCTCCCTTGTCACAGGTTTAAAAACCTCACAGCTT	600
Query	601	GTATAATGTAACCATTTGGGGTCCGCTTTTAACTTGGACTAGTGTAACNTTCATGCAA	660
Sbjct	601	GTATAATGTAACCATTTGGGGTCCGCTTTTAACTTGGACTAGTGTAACNTTCATGCAA	660
Query	661	TAAACTGAAAAGACCATGCTGCTA	684
Sbjct	661	TAAACTGAAAAGACCATGCTGCTA	684

Sequence 434 matched with Sequence 96

Query= Sequence ID 434

Length=462

SEQ ID NO: 96

ALIGNMENTS

Identities = 462/462 (100%), Gaps = 0/462 (0%)

Query	1	TTCGGACGCAAGAAGACAGCGACAGCTGTGGCGCACTGCAAACGCGGCAATGGTCTCATC	60
Sbjct	1	TTCGGACGCAAGAAGACAGCGACAGCTGTGGCGCACTGCAAACGCGGCAATGGTCTCATC	60
Query	61	AAGGTGAACGGGCGGCCCTGGAGATGATTGAGCCGCGCACGCTACAGTACAAGCTGCTG	120
Sbjct	61	AAGGTGAACGGGCGGCCCTGGAGATGATTGAGCCGCGCACGCTACAGTACAAGCTGCTG	120
Query	121	GAGCCAGTTCTGCTTCTCGGCAAGGAGCGATTTGCTGGTGTAGACATCCGTGTCCGTGTA	180
Sbjct	121	GAGCCAGTTCTGCTTCTCGGCAAGGAGCGATTTGCTGGTGTAGACATCCGTGTCCGTGTA	180
Query	181	AAGGGTGGTGGTCACGTGGCCCANATTTATGCTATCCGTCAGTCCATCTCCAAAGCCCTG	240
Sbjct	181	AAGGGTGGTGGTCACGTGGCCCANATTTATGCTATCCGTCAGTCCATCTCCAAAGCCCTG	240
Query	241	GTGGCCTATTACCANAATATGTGGATGAGGCTTCCAAGAAGGAGATCAAAGACATCCTC	300
Sbjct	241	GTGGCCTATTACCANAATATGTGGATGAGGCTTCCAAGAAGGAGATCAAAGACATCCTC	300
Query	301	ATCCAGTATGACCGGACCCTGCTGGTAGCTGACCCTCGTCGCTGCGAGTCCAAAAAGTTT	360
Sbjct	301	ATCCAGTATGACCGGACCCTGCTGGTAGCTGACCCTCGTCGCTGCGAGTCCAAAAAGTTT	360
Query	361	GGAGGCCCTGGTGCCCGCGCTCGCTACCAGAAATCCTACCGATAAGCCCATCGTGACTCA	420
Sbjct	361	GGAGGCCCTGGTGCCCGCGCTCGCTACCAGAAATCCTACCGATAAGCCCATCGTGACTCA	420
Query	421	AAACTCACTTGTATAATAAACAGTTTTTTGAGGGATTTTAAAA	462
Sbjct	421	AAACTCACTTGTATAATAAACAGTTTTTTGAGGGATTTTAAAA	462

Length=535

SEQ ID NO: 97

Identities = 535/535 (100%), Gaps = 0/535 (0%)

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Query	481	AACCAGATCTTTTAGTGCAGAAGCTTTCCACTGTATTANAAGTGAGGAAGTTGGT	535
Sbjct	481	AACCAGATCTTTTAGTGCAGAAGCTTTCCACTGTATTANAAGTGAGGAAGTTGGT	535

Sequence 436 matched with Sequence 98

Query= Sequence ID 436
Length=512

SEQ ID NO: 98

ALIGNMENTS

Identities = 512/512 (100%), Gaps = 0/512 (0%)

Query	1	aaaaaaaCTCCAGAGAAGTTTATAGAAAGAGATGACATGTAAACCCTGCTGAAAAATAGT	60
Sbjct	1	AAAAAACTCCAGAGAAGTTTATAGAAAGAGATGACATGTAAACCCTGCTGAAAAATAGT	60
Query	61	TTCATTTGTTAGAATATAATTGTCTTCCACTaaaaaaagaaaaaaaaaGCATTTAAGGC	120
Sbjct	61	TTCATTTGTTAGAATATAATTGTCTTCCACTAAAAAAGAAAAAAAAAAGCATTTAAGGC	120
Query	121	TCTAAGATCTCTTGAAGTACCACTTTTCCTGAATCCCAGAGTTTTTATGTGCATTATTTT	180
Sbjct	121	TCTAAGATCTCTTGAAGTACCACTTTTCCTGAATCCCAGAGTTTTTATGTGCATTATTTT	180
Query	181	TATGCGTTTGTAGTTTGATATGTTGTATTTATAAGTAGTTTTAGCTTTCCATTATGAATT	240
Sbjct	181	TATGCGTTTGTAGTTTGATATGTTGTATTTATAAGTAGTTTTAGCTTTCCATTATGAATT	240
Query	241	CTTCTTTGACCCATGAGTTATTTAGGTAAGTGTTTAAAAATTTACAATAGTTTATATATG	300
Sbjct	241	CTTCTTTGACCCATGAGTTATTTAGGTAAGTGTTTAAAAATTTACAATAGTTTATATATG	300
Query	301	CAAATATTATGTTGTTAGAGTTGGTTTTTCATGTCATTTTTACATATACAGGGGCAGTTTC	360
Sbjct	301	CAAATATTATGTTGTTAGAGTTGGTTTTTCATGTCATTTTTACATATACAGGGGCAGTTTC	360
Query	361	CCCAACTAAATTGTATATTCCTTAAAGCAGCACTCTTAAATTTTATTCTGTGTCAATTT	420
Sbjct	361	CCCAACTAAATTGTATATTCCTTAAAGCAGCACTCTTAAATTTTATTCTGTGTCAATTT	420
Query	421	CTTGNCTGTGTTTCCTGGCATGGAATACATGGCATAAAATTTGTTATGTAATTAAATGAA	480
Sbjct	421	CTTGNCTGTGTTTCCTGGCATGGAATACATGGCATAAAATTTGTTATGTAATTAAATGAA	480

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Query    481  ATATTATTATACTTTCTATTTTTTAGAAAAAA  512
        |||
Sbjct    481  ATATTATTATACTTTCTATTTTTTAGAAAAAA  512
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nt: 577

nt: 577

Identities = 577/577 (100%), Gaps = 0/577 (0%)

Query	1	GTTCGACAGGGATGACATAACTATTAGTGGCAGGTTAGTTGTTGGTCACTTTCAACTCTGG	60
Sbjct	1	GTTCGACAGGGATGACATAACTATTAGTGGCAGGTTAGTTGTTGGTCACTTTCAACTCTGG	60
Query	61	GTTCAAGCGATTCTCCTACCTCAGCCTCCCGAGTAGCTGGGATTACAGGCATGCACCGCC	120
Sbjct	61	GTTCAAGCGATTCTCCTACCTCAGCCTCCCGAGTAGCTGGGATTACAGGCATGCACCGCC	120
Query	121	ACACCTAATTTTCTATTCTTAGTAGAGACGGGGTTTCTCCCTGTTGGTCAGGCTGGTCTC	180
Sbjct	121	ACACCTAATTTTCTATTCTTAGTAGAGACGGGGTTTCTCCCTGTTGGTCAGGCTGGTCTC	180
Query	181	GAACTCCCGACCTCAGGTGATCTGCCTGCCTCAGTCTCCCAAAGTCCTGGAACACAGAC	240
Sbjct	181	GAACTCCCGACCTCAGGTGATCTGCCTGCCTCAGTCTCCCAAAGTCCTGGAACACAGAC	240
Query	241	ATGAGCCACCACGCCTGGCCCCCTTTTAAAATATTTCTGCTCATTGATGATGCACCCAGTC	300
Sbjct	241	ATGAGCCACCACGCCTGGCCCCCTTTTAAAATATTTCTGCTCATTGATGATGCACCCAGTC	300
Query	301	ACCCAAGTGCTCTGATGGAGATGTATAAGGAGATGAATGCTGTTTTCATGGCTGCTAATA	360
Sbjct	301	ACCCAAGTGCTCTGATGGAGATGTATAAGGAGATGAATGCTGTTTTCATGGCTGCTAATA	360
Query	361	CAACATTCAATTCTGCAACCCCCAAATCAAGAAGTAATTTTGACTTTCAAGTCTTATTATT	420
Sbjct	361	CAACATTCAATTCTGCAACCCCCAAATCAAGAAGTAATTTTGACTTTCAAGTCTTATTATT	420
Query	421	TAAGAAATATATTTTGAAGACTATAGCTGCCATAGACCGTGATTCCCTCTGATGGATCAG	480
Sbjct	421	TAAGAAATATATTTTGAAGACTATAGCTGCCATAGACCGTGATTCCCTCTGATGGATCAG	480

PATENT SEQUENCE ALIGNMENT

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Query  481  ACAAACATAAAATGAAAACCTCCTGCAACGTATTCATCATTCTAGATCCCTGAGGAATCGC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ACAAACATAAAATGAAAACCTCCTGCAACGTATTCATCATTCTAGATCCCTGAGGAATCGC  540

Query  541  CAACTGACTTNCACAATGGGTGAACTGGGTACAGT  577
          |||||||||||||||||||||||||||||
Sbjct  541  CAACTGACTTNCACAATGGGTGAACTGGGTACAGT  577
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nt: 552

nt: 552

Identities = 552/552 (100%), Gaps = 0/552 (0%)

Query	1	AAACAAAATTATTCTCTGAGAGGGAAAGGACATTTGAGGGAAACATCAAATTTCCCCATA 	60
Sbjct	1	AAACAAAATTATTCTCTGAGAGGGAAAGGACATTTGAGGGAAACATCAAATTTCCCCATA 	60
Query	61	AATAAATGAATGGAGTTTGCAGGAAGGTGAGGGTGAGCAGAGATGTGTGTGGACATCTCT 	120
Sbjct	61	AATAAATGAATGGAGTTTGCAGGAAGGTGAGGGTGAGCAGAGATGTGTGTGGACATCTCT 	120
Query	121	GACCATCCATCGCTGTATTCAAATGGATTGTTTTATTCCATTCTGGTCTCAGGCATGACC 	180
Sbjct	121	GACCATCCATCGCTGTATTCAAATGGATTGTTTTATTCCATTCTGGTCTCAGGCATGACC 	180
Query	181	ACGTCCAGTGAAGACATTTGAGGCAGCACATCTCAGGACCCAGGCAATAGACTGGCCCCA 	240
Sbjct	181	ACGTCCAGTGAAGACATTTGAGGCAGCACATCTCAGGACCCAGGCAATAGACTGGCCCCA 	240
Query	241	ACTCAGGCTGGACTAAGGTGTGATTAATTCTTTGTTTTTTGTGTGGAACAGCTCACCTTG 	300
Sbjct	241	ACTCAGGCTGGACTAAGGTGTGATTAATTCTTTGTTTTTTGTGTGGAACAGCTCACCTTG 	300
Query	301	TCAGACAGCCTCAGGGCATCTCTGAGACACAGGGGCAGAAAATGACATTCATCTTTTGAG 	360
Sbjct	301	TCAGACAGCCTCAGGGCATCTCTGAGACACAGGGGCAGAAAATGACATTCATCTTTTGAG 	360
Query	361	TCCTCATCCATGGAGTGCTGTGTTTGGGGGGCTGCATCTGCTGAAGCGAGAACCCCATTC 	420
Sbjct	361	TCCTCATCCATGGAGTGCTGTGTTTGGGGGGCTGCATCTGCTGAAGCGAGAACCCCATTC 	420
Query	421	TGCCACCCACCAGGATGCCCATTTCTCCAGGACTTCTCCAACTTACTATTAGACTAAACC 	480
Sbjct	421	TGCCACCCACCAGGATGCCCATTTCTCCAGGACTTCTCCAACTTACTATTAGACTAAACC 	480

PATENT SEQUENCE ALIGNMENT

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Query  481  AGAACAAGCAACAAACTGTATTTATGCAAGCAAAATTGATGAGAAAATTATATTCAAATA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGAACAAGCAACAAACTGTATTTATGCAAGCAAAATTGATGAGAAAATTATATTCAAATA  540

Query  541  AAGCAAAAATTA  552
          |||||||||
Sbjct  541  AAGCAAAAATTA  552
```


Sequence 442 matched with Sequence 101

Query= Sequence ID - 442
Length=606

nt: 606

SEQ ID NO: 101

nt: 606

ALIGNMENTS

Identities = 606/606 (100%), Gaps = 0/606 (0%)

Query	1	TCGTGCCACTGCACTCCAGCCTGGACGACAGAGTGAGACTCCATCTCaaaataaataaat	60
Sbjct	1	TCGTGCCACTGCACTCCAGCCTGGACGACAGAGTGAGACTCCATCTCAAAATAAATAAAT	60
Query	61	aaataaataaataaataaataaataaaaaataaaaaataCTTCTGCTATGAAAAACCTA	120
Sbjct	61	AAATAAATAAATAAATAAATAAATAAAAAATAAAAAATACTTCTGCTATGAAAAACCTA	120
Query	121	GTTGGTATTTTGGCTTATTTAATACTATAGAAATATGGTGATCTCATCTTTAATAGAGTG	180
Sbjct	121	GTTGGTATTTTGGCTTATTTAATACTATAGAAATATGGTGATCTCATCTTTAATAGAGTG	180
Query	181	CTTTTAAGGTCCCCAGTGATAATCTCCTAAAATCATGAACCTTAAGAATTTATAATGTTA	240
Sbjct	181	CTTTTAAGGTCCCCAGTGATAATCTCCTAAAATCATGAACCTTAAGAATTTATAATGTTA	240
Query	241	ATATGAGGAAATGAAATCTGGATTATCTCACCACATATTATATAATTCATTAGTGACAGA	300
Sbjct	241	ATATGAGGAAATGAAATCTGGATTATCTCACCACATATTATATAATTCATTAGTGACAGA	300
Query	301	GCAAGAACTCCAGGTCACCTGTCTATTCCATGTTTTTCCTATCTGCCTTTAAATGTTGAG	360
Sbjct	301	GCAAGAACTCCAGGTCACCTGTCTATTCCATGTTTTTCCTATCTGCCTTTAAATGTTGAG	360
Query	361	ATACTACCTTATCTCATGTGAATGGAGAACTGCCTAAAATGCTAAAACTGACTCAGAG	420
Sbjct	361	ATACTACCTTATCTCATGTGAATGGAGAACTGCCTAAAATGCTAAAACTGACTCAGAG	420
Query	421	GCACCCAGACATAAGTGAAGTGTGATTAGAAAATCCTGGTCAGTTGAGTCTTAGCCAAAT	480
Sbjct	421	GCACCCAGACATAAGTGAAGTGTGATTAGAAAATCCTGGTCAGTTGAGTCTTAGCCAAAT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GTGTACCTACTGTGTCTGCCTCTATCAAGTCAATGAAAACATGATCTGAGAACTGTAAGT	540
Sbjct	481	GTGTACCTACTGTGTCTGCCTCTATCAAGTCAATGAAAACATGATCTGAGAACTGTAAGT	540
Query	541	CCATTTATGGAAAGGGTTGATTTANAGATATTTTGAAGTTNCAGTGATGAGCCCCTTCTC	600
Sbjct	541	CCATTTATGGAAAGGGTTGATTTANAGATATTTTGAAGTTNCAGTGATGAGCCCCTTCTC	600
Query	601	AAATAG	606
Sbjct	601	AAATAG	606

Sequence 446 matched with Sequence 102

Query= Sequence ID 446
Length=341

SEQ ID NO: 102

ALIGNMENTS

Identities = 336/336 (100%), Gaps = 0/336 (0%)

Query	1	CGGACTCCTGTGCTAATTGTCAGCTTACATATCATTGTATAGAGACTGTTTATTCTGTAC	60
Sbjct	1	CGGACTCCTGTGCTAATTGTCAGCTTACATATCATTGTATAGAGACTGTTTATTCTGTAC	60
Query	61	CAAAC TGATTTC AAAAGTACTACATNGAAAAATAAACCGGTGACTGTTTTCTTCATAAAG	120
Sbjct	61	CAAAC TGATTTC AAAAGTACTACATNGAAAAATAAACCGGTGACTGTTTTCTTCATAAAG	120
Query	121	TTCTGCGTTTGGCATCTTCACTCTTTCCAAAATGTATCTGTACATCANAAATGTCACTAT	180
Sbjct	121	TTCTGCGTTTGGCATCTTCACTCTTTCCAAAATGTATCTGTACATCANAAATGTCACTAT	180
Query	181	TCCAAGTGTCTTTTTAGTGTGGCTTTAGTATGGCTTCCTTTTAATATTGNACATACATTG	240
Sbjct	181	TCCAAGTGTCTTTTTAGTGTGGCTTTAGTATGGCTTCCTTTTAATATTGNACATACATTG	240
Query	241	NATCTTTGTTTTATGGNAATAAGTAATAAAAAATGTAGACTTCATATTTGTACAAAATGT	300
Sbjct	241	NATCTTTGTTTTATGGNAATAAGTAATAAAAAATGTAGACTTCATATTTGTACAAAATGT	300
Query	301	CCTATGTACAGAATAAAAAAGTTCATAGAAACAGCC	336
Sbjct	301	CCTATGTACAGAATAAAAAAGTTCATAGAAACAGCC	336

Sequence 447 matched with Sequence 103

Query= Sequence ID 447
Length=85

SEQ ID NO: 103

ALIGNMENTS

Identities = 85/85 (100%), Gaps = 0/85 (0%)

```
Query   1   AGGCCGAGGCAGGCAGATCNCNTGAGGTCAAGAGTTTGAGACCAGCNTAGCTAACATGGT   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1   AGGCCGAGGCAGGCAGATCNCNTGAGGTCAAGAGTTTGAGACCAGCNTAGCTAACATGGT   60

Query   61   GAAACCCCATCTCTACAAAAATATA   85
          ||||||||||||||||||||
Sbjct   61   GAAACCCCATCTCTACAAAAATATA   85
```

Sequence 448 matched with Sequence 104

Query= Sequence ID - 448
Length=329

nt: 329

SEQ ID NO: 104

nt: 329

ALIGNMENTS

Identities = 329/329 (100%), Gaps = 0/329 (0%)

Query	1	TACGCACACGAGAACATGCCTCTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGAGGAG	60
Sbjct	1	TACGCACACGAGAACATGCCTCTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGAGGAG	60
Query	61	AAGAGGAAACACAAGAAGAAACGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTG	120
Sbjct	61	AAGAGGAAACACAAGAAGAAACGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTG	120
Query	121	AAATGCCCAGGATGCTATAAAATCACCACGGTCTTTAGCCATGCACAAACGGTAGTTTTG	180
Sbjct	121	AAATGCCCAGGATGCTATAAAATCACCACGGTCTTTAGCCATGCACAAACGGTAGTTTTG	180
Query	181	TGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGAGGAAAAGCAAGGCTTACAGAA	240
Sbjct	181	TGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGAGGAAAAGCAAGGCTTACAGAA	240
Query	241	GGATGTTCCCTTCAGGAGGAAGCAGCACTAAAAGCACTCTGAGTCAAGATGAGTGGGAAAC	300
Sbjct	241	GGATGTTCCCTTCAGGAGGAAGCAGCACTAAAAGCACTCTGAGTCAAGATGAGTGGGAAAC	300
Query	301	CATCTCAATAAACACATTTTGGGTAAAA	329
Sbjct	301	CATCTCAATAAACACATTTTGGGTAAAA	329

Sequence 450 matched with Sequence 105

Query= Sequence ID 450

Length=504

SEQ ID NO: 105

ALIGNMENTS

Identities = 504/504 (100%), Gaps = 0/504 (0%)

Query	1	GAGCAGTGGCATGATCACACCTTACTGCGGCCTCCAACCCCTGAGCTTAAGTGATTCTCC	60
Sbjct	1	GAGCAGTGGCATGATCACACCTTACTGCGGCCTCCAACCCCTGAGCTTAAGTGATTCTCC	60
Query	61	CGCATTATCCTCCTGAGTAGCTGAGACTACAGGTGCATGCCACCATACACTACTAAATTT	120
Sbjct	61	CGCATTATCCTCCTGAGTAGCTGAGACTACAGGTGCATGCCACCATACACTACTAAATTT	120
Query	121	GGGTCGGGTGGTGGTGGTGATTTTTTAATATTTTTGTAGAGACAGGGTCTCACTGTGATG	180
Sbjct	121	GGGTCGGGTGGTGGTGGTGATTTTTTAATATTTTTGTAGAGACAGGGTCTCACTGTGATG	180
Query	181	CCCAGGCTGGTCTTGAACCTCCTGGGCTCAAGCAGTCACCCACCTCAGCCTCCCAAAGCAC	240
Sbjct	181	CCCAGGCTGGTCTTGAACCTCCTGGGCTCAAGCAGTCACCCACCTCAGCCTCCCAAAGCAC	240
Query	241	TGGGATTACAGGTGTGAGCCACCACACTGGCCAGCTTTGTTTTGTTTTGATGACTAAGCT	300
Sbjct	241	TGGGATTACAGGTGTGAGCCACCACACTGGCCAGCTTTGTTTTGTTTTGATGACTAAGCT	300
Query	301	GCTCTTGCTAAAAGGGCTTCTCTCTGAACTTCCCTACCTTTCTTCTGTTTCCCTGGGCTA	360
Sbjct	301	GCTCTTGCTAAAAGGGCTTCTCTCTGAACTTCCCTACCTTTCTTCTGTTTCCCTGGGCTA	360
Query	361	GGGCTCCATGTTGGCAGTCCTACTCCCAATTAACCTGGGGCTGTCTGGTTAACCTTTATA	420
Sbjct	361	GGGCTCCATGTTGGCAGTCCTACTCCCAATTAACCTGGGGCTGTCTGGTTAACCTTTATA	420
Query	421	AGATCTGCAGTCATTGGGAGACCCGGGGACCAGGAATATTGTTGTTGAGGGAGCTACCCT	480
Sbjct	421	AGATCTGCAGTCATTGGGAGACCCGGGGACCAGGAATATTGTTGTTGAGGGAGCTACCCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GGAAAGTGGATGGGTGGCCAAAGG	504
Sbjct	481	GGAAAGTGGATGGGTGGCCAAAGG	504

Sequence 452 matched with Sequence 106

Query= Sequence ID 452
Length=582

SEQ ID NO: 106

ALIGNMENTS

Identities = 582/582 (100%), Gaps = 0/582 (0%)

Query	1	TTTGGCTTTGCCTCTAGGCATTAGATGTTATCTTTGGAGGCATCCTTCTATGAGCATTCA	60
Sbjct	1	TTTGGCTTTGCCTCTAGGCATTAGATGTTATCTTTGGAGGCATCCTTCTATGAGCATTCA	60
Query	61	TTTTTGGACCAAGCCTGGATTTACAATTCTATTACTGGCCCAGACTTCATTTCTATCCAA	120
Sbjct	61	TTTTTGGACCAAGCCTGGATTTACAATTCTATTACTGGCCCAGACTTCATTTCTATCCAA	120
Query	121	TTTCATTCCACTGTGCTATAGTTTACAACATATAATTTGACTTATAAATAATTCCTGACT	180
Sbjct	121	TTTCATTCCACTGTGCTATAGTTTACAACATATAATTTGACTTATAAATAATTCCTGACT	180
Query	181	ATGGGTTTAAAGACTGAAAATGGATCAATAGAACTTTGAAAATGTAAACATCTTGATTG	240
Sbjct	181	ATGGGTTTAAAGACTGAAAATGGATCAATAGAACTTTGAAAATGTAAACATCTTGATTG	240
Query	241	CTTTTCTCAGTGTAGAAATGGACAATGTTTAGCTTAAAAACTGCATGTTTTTAATGAGAT	300
Sbjct	241	CTTTTCTCAGTGTAGAAATGGACAATGTTTAGCTTAAAAACTGCATGTTTTTAATGAGAT	300
Query	301	ACGGGGTTGAAAGACTTATTCCTGGAATTTATTGTTCTGGAGAAAGCCTGTTGCTATCTG	360
Sbjct	301	ACGGGGTTGAAAGACTTATTCCTGGAATTTATTGTTCTGGAGAAAGCCTGTTGCTATCTG	360
Query	361	CCATACCTTGTTTACTTTGTGCAAAATGAGCTTCTTTTTAAGTAATGAGCTCTTCCAT	420
Sbjct	361	CCATACCTTGTTTACTTTGTGCAAAATGAGCTTCTTTTTAAGTAATGAGCTCTTCCAT	420
Query	421	G TTCAGCTTAAATTGCTGTCTTAGACACTTCATCAGGGTTCCCTGCTCTGCCTCATTCCC	480
Sbjct	421	G TTCAGCTTAAATTGCTGTCTTAGACACTTCATCAGGGTTCCCTGCTCTGCCTCATTCCC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CCTTTTGCTCACTTGCAGCCTTTGACATAATCCTGGGAGGCAATTGGCATCATACATATT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CCTTTTGCTCACTTGCAGCCTTTGACATAATCCTGGGAGGCAATTGGCATCATACATATT  540

Query  541  TTGCTTTGTAATCTCCTGCTTTGATTCTGACTGGGACCCAGC  582
          ||||||||||||||||||||||||||||||||
Sbjct  541  TTGCTTTGTAATCTCCTGCTTTGATTCTGACTGGGACCCAGC  582
```

Sequence 453 matched with Sequence 107

Query= Sequence ID - 453
Length=747

nt: 747

SEQ ID NO: 107

nt: 747

ALIGNMENTS

Identities = 747/747 (100%), Gaps = 0/747 (0%)

Query	1	GGATCTAAGACCAGCCTGGCAGCCACCAGATGGTGATTCTAGTCCTGGCTCAGTCAGTAA	60
Sbjct	1	GGATCTAAGACCAGCCTGGCAGCCACCAGATGGTGATTCTAGTCCTGGCTCAGTCAGTAA	60
Query	61	TAGGTCACTGACCCAGAGAAATCAATTCAGCCTCCCAGGTCCTTGGATTTCTTTCTGT	120
Sbjct	61	TAGGTCACTGACCCAGAGAAATCAATTCAGCCTCCCAGGTCCTTGGATTTCTTTCTGT	120
Query	121	GAAAATGAAAGCATAGGTAGGAATTTCCCATGGAACAGCTAGCAGAGGAGAAATATTTAA	180
Sbjct	121	GAAAATGAAAGCATAGGTAGGAATTTCCCATGGAACAGCTAGCAGAGGAGAAATATTTAA	180
Query	181	AGTCAGGAGACTCATGCTATAGTTTTCATACTTCATTACAACAATGTTGTTTAGGACAAG	240
Sbjct	181	AGTCAGGAGACTCATGCTATAGTTTTCATACTTCATTACAACAATGTTGTTTAGGACAAG	240
Query	241	TGAGTTAACCTGTTAGCTTCCTCTATATAAAATGGAAAGTCATTAACCTACATAGCA	300
Sbjct	241	TGAGTTAACCTGTTAGCTTCCTCTATATAAAATGGAAAGTCATTAACCTACATAGCA	300
Query	301	GGGTTCTTGTGAAGATCAAGTGATAATGTAGGAAGCATGTACAAATGTCACATTCTGCCG	360
Sbjct	301	GGGTTCTTGTGAAGATCAAGTGATAATGTAGGAAGCATGTACAAATGTCACATTCTGCCG	360
Query	361	TCACGTAATGGTCCTCACAGCTTGAGGTAGCATTTAGCATGTGTCATGATTTAGTACAAG	420
Sbjct	361	TCACGTAATGGTCCTCACAGCTTGAGGTAGCATTTAGCATGTGTCATGATTTAGTACAAG	420
Query	421	GGTTGGCAAACCTGTTGCTCTTGGATTAAGTCTGGCTCATTGCCTGTTTTTCAAAGGaaaaa	480
Sbjct	421	GGTTGGCAAACCTGTTGCTCTTGGATTAAGTCTGGCTCATTGCCTGTTTTTCAAAGAAAAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	aaTtgtatatgtgtgtatatatggtatatataggtacacacacatatgtgctatatatag	540
Sbjct	481	AATTGTATATGTGTGTATATATGTTATATATAGGTACACACACATATGTGCTATATATAG	540
Query	541	catatatacacacataatatataaacatgtacatatatagcattatatatataccgtgta	600
Sbjct	541	CATATATACACACATAATATATAAACATGTACATATATAGCATTATATATATACCGTGTA	600
Query	601	taatatCTCCAGTCCTCATGACCAGCCATGCTTGTTTCATTTACATTTGCATACTCTATGA	660
Sbjct	601	TAATATCTCCAGTCCTCATGACCAGCCATGCTTGTTTCATTTACATTTGCATACTCTATGA	660
Query	661	TTGCTTTCATGCAACAATGGCAGAGTTGAGTGATTGTTTTGCACAGANACTGTATGGCCC	720
Sbjct	661	TTGCTTTCATGCAACAATGGCAGAGTTGAGTGATTGTTTTGCACAGANACTGTATGGCCC	720
Query	721	ACTAAACCTAAAAATATTAATCTCTGCC	747
Sbjct	721	ACTAAACCTAAAAATATTAATCTCTGCC	747

Sequence 454 matched with Sequence 108

Query= Sequence ID 454
Length=522

SEQ ID NO: 108

ALIGNMENTS

Identities = 522/522 (100%), Gaps = 0/522 (0%)

Query	1	CTCCTGCCGGGCTCGTGGCGGCTTCTGTCCGCTCCGCGGAGGGAAGCGCCTTCCCCACAG	60
Sbjct	1	CTCCTGCCGGGCTCGTGGCGGCTTCTGTCCGCTCCGCGGAGGGAAGCGCCTTCCCCACAG	60
Query	61	GACATCAATGCAAGCTTGAATAAGAAAAACAAATTCTTCCTCCTAAGCCATGGCATATCA	120
Sbjct	61	GACATCAATGCAAGCTTGAATAAGAAAAACAAATTCTTCCTCCTAAGCCATGGCATATCA	120
Query	121	GTTATACAGAAATACTACTTTGGGAAACAGTCTTCAGGAGAGCCTAGATGAGCTCATACA	180
Sbjct	121	GTTATACAGAAATACTACTTTGGGAAACAGTCTTCAGGAGAGCCTAGATGAGCTCATACA	180
Query	181	GTCTCAACAGATCACCCCCCAACTTGCCCTTCAAGTTCTACTTCAGTTTGATAAGGCTAT	240
Sbjct	181	GTCTCAACAGATCACCCCCCAACTTGCCCTTCAAGTTCTACTTCAGTTTGATAAGGCTAT	240
Query	241	AAATGCAGCACTGGCTCAGAGGGTCAGGAACAGAGTCAATTTAGGGGCTCTCTAAATAC	300
Sbjct	241	AAATGCAGCACTGGCTCAGAGGGTCAGGAACAGAGTCAATTTAGGGGCTCTCTAAATAC	300
Query	301	GTACAGATTCTGCGATAATGTGTGGACTTTTGTACTGAATGATGTTGAATTCAGAGAGGT	360
Sbjct	301	GTACAGATTCTGCGATAATGTGTGGACTTTTGTACTGAATGATGTTGAATTCAGAGAGGT	360
Query	361	GACAGAACTTATTAAAGTGGATAAAGTGAAAATTGTAGCCTGTGATGGTAAAAATACTGG	420
Sbjct	361	GACAGAACTTATTAAAGTGGATAAAGTGAAAATTGTAGCCTGTGATGGTAAAAATACTGG	420
Query	421	CTCCAATACTACAGAATGAATAGAAAAAATATGACTTTTTTACACCATCTTCTGTTATTC	480
Sbjct	421	CTCCAATACTACAGAATGAATAGAAAAAATATGACTTTTTTACACCATCTTCTGTTATTC	480

```

Query    481  ATTGCTTTTGAAGAGAAGCATAGAAGAGACTTTTTATTTATT  522
        |||||||||||||||||||||||||||||||||||||||
Sbjct    481  ATTGCTTTTGAAGAGAAGCATAGAAGAGACTTTTTATTTATT  522

```

Sequence 458 matched with Sequence 109

Query= Sequence ID - 458
Length=682

nt: 682

SEQ ID NO: 109

nt: 682

ALIGNMENTS

Identities = 682/682 (100%), Gaps = 0/682 (0%)

Query	1	TGCCACTGAAGATCCTGGTGTGCGCCATGGGCCGCCGCCCGCCCGTTGTTACCGGTATTG	60
Sbjct	1	TGCCACTGAAGATCCTGGTGTGCGCCATGGGCCGCCGCCCGCCCGTTGTTACCGGTATTG	60
Query	61	TAAGAACAAGCCGTACCCAAAGTCTCGCTTCTGCCGAGGTGTCCCTGATGCCAAGATTCTG	120
Sbjct	61	TAAGAACAAGCCGTACCCAAAGTCTCGCTTCTGCCGAGGTGTCCCTGATGCCAAGATTCTG	120
Query	121	CATTTTTGACCTGGGGCGGAAAAAGGCCAAAAGTGGATGAGTTTCCGCTTTGTGGCCACAT	180
Sbjct	121	CATTTTTGACCTGGGGCGGAAAAAGGCCAAAAGTGGATGAGTTTCCGCTTTGTGGCCACAT	180
Query	181	GGTGTGACAGATGAATATGAGCAGCTGTCCTCTGAAGCCCTGGAGGCTGCCCGAATTTGTGC	240
Sbjct	181	GGTGTGACAGATGAATATGAGCAGCTGTCCTCTGAAGCCCTGGAGGCTGCCCGAATTTGTGC	240
Query	241	CAATAAGTACATGGTAAAAAGTTGTGGCAAAGATGGCTTCCATATCCGGGTGCGGCTCCA	300
Sbjct	241	CAATAAGTACATGGTAAAAAGTTGTGGCAAAGATGGCTTCCATATCCGGGTGCGGCTCCA	300
Query	301	CCCCTTCCACGTCATCCGCATCAACAAGATGTTGTCTGTGCTGGGGCTGACAGGCTCCA	360
Sbjct	301	CCCCTTCCACGTCATCCGCATCAACAAGATGTTGTCTGTGCTGGGGCTGACAGGCTCCA	360
Query	361	AACAGGCATGCGAGGTGCCTTTGGAAAGCCCCAGGGCACTGTGGCCAGGGTTCACATTGG	420
Sbjct	361	AACAGGCATGCGAGGTGCCTTTGGAAAGCCCCAGGGCACTGTGGCCAGGGTTCACATTGG	420
Query	421	CCAAGTTATCATGTCCATCCGCACCAAGCTGCAGAACAAGGAGCATGTGATTGAGGCCCT	480
Sbjct	421	CCAAGTTATCATGTCCATCCGCACCAAGCTGCAGAACAAGGAGCATGTGATTGAGGCCCT	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 GCGCAGGGCCAAGTTCAAGTTTCTGGCCGCAGAAGATCCACATCTCAAAGAAGTGGGGCT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 GCGCAGGGCCAAGTTCAAGTTTCTGGCCGCAGAAGATCCACATCTCAAAGAAGTGGGGCT 540

Query 541 TCACCAAGTTCAATGCTGATGAATTTGAAGACATGGTGGCTGAAAAGCGGCTCATCCCAN 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 TCACCAAGTTCAATGCTGATGAATTTGAAGACATGGTGGCTGAAAAGCGGCTCATCCCAN 600

Query 601 ATGGCTGTGGGGTCAAGTACATCCCCAATCGTGGCCCTCTGGACAAGTGGCGGCCCTGCA 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 ATGGCTGTGGGGTCAAGTACATCCCCAATCGTGGCCCTCTGGACAAGTGGCGGCCCTGCA 660

Query 661 CTCATGAAGGCTTTCAATGTGC 682
          |||||||||||||||
Sbjct 661 CTCATGAAGGCTTTCAATGTGC 682
```

Sequence 459 matched with Sequence 110

Query= Sequence ID 459

Length=668

SEQ ID NO: 110

ALIGNMENTS

Identities = 668/668 (100%), Gaps = 0/668 (0%)

Query	1	TCCCGGAATCGCGCCGCGTCGACCTTGTCCTTGAGCGTCAACCTTCTTCCCTGAAGTG	60
Sbjct	1	TCCCGGAATCGCGCCGCGTCGACCTTGTCCTTGAGCGTCAACCTTCTTCCCTGAAGTG	60
Query	61	GCTGGGGTTCCTGTTTCCTTCTTTGATTGACAACTTGTGTTAACCCCTCGCACATCTCTGG	120
Sbjct	61	GCTGGGGTTCCTGTTTCCTTCTTTGATTGACAACTTGTGTTAACCCCTCGCACATCTCTGG	120
Query	121	GCCAATTTTGTCTTGTAAGTCTTCCGGAGACCCCTGGAATTTAAATCATTAGCACCGCG	180
Sbjct	121	GCCAATTTTGTCTTGTAAGTCTTCCGGAGACCCCTGGAATTTAAATCATTAGCACCGCG	180
Query	181	CCCTTCCCCGAAGAGTCTTCGAAGGGTTGCCGCTTTTCGGTGGCGCAGTTCTCGCGAGAA	240
Sbjct	181	CCCTTCCCCGAAGAGTCTTCGAAGGGTTGCCGCTTTTCGGTGGCGCAGTTCTCGCGAGAA	240
Query	241	GGTGACTTTCTTCTCGGTATTTCTGGTTTCCAGAATCCTTAGCGCGAGGCGGAAAAAA	300
Sbjct	241	GGTGACTTTCTTCTCGGTATTTCTGGTTTCCAGAATCCTTAGCGCGAGGCGGAAAAAA	300
Query	301	TATTTCTCCCAGCTTGTTGATGCCGCGATTTTGAAGTCTTCTTCCACGATTTCT	360
Sbjct	301	TATTTCTCCCAGCTTGTTGATGCCGCGATTTTGAAGTCTTCTTCCACGATTTCT	360
Query	361	GTTTTTGCTTCTCCAAGGAAAATGGCAGCTCCCGAGCAGCCGCTTGCGATATCAAGGGGA	420
Sbjct	361	GTTTTTGCTTCTCCAAGGAAAATGGCAGCTCCCGAGCAGCCGCTTGCGATATCAAGGGGA	420
Query	421	TGCACGAGCTCCTCCTCGCTTTCCCGCCTCGGGGCGACCGAACCCCTTCTGGTCAGGCAC	480
Sbjct	421	TGCACGAGCTCCTCCTCGCTTTCCCGCCTCGGGGCGACCGAACCCCTTCTGGTCAGGCAC	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 CTGCCGGCTGAGCTTACTGCTGAGGAGAAAGAGGACTTGCTGAAGTACTTCGGGGCTCAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 CTGCCGGCTGAGCTTACTGCTGAGGAGAAAGAGGACTTGCTGAAGTACTTCGGGGCTCAG 540

Query 541 TCTGTGCGGGTCCTGTCAGATAAGGGGCGACTGAAACATACAGCTTTTGCCACATTCCCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 TCTGTGCGGGTCCTGTCAGATAAGGGGCGACTGAAACATACAGCTTTTGCCACATTCCCT 600

Query 601 AATGAAAAAGCAGCTNTAAAGGCATTGACAACTNCATCAACTGAAACTTTTAGTCATAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 AATGAAAAAGCAGCTNTAAAGGCATTGACAACTNCATCAACTGAAACTTTTAGTCATAC 660

Query 661 TTTAATCG 668
          |||||||
Sbjct 661 TTTAATCG 668
```

Sequence 460 matched with Sequence 111

Query= Sequence ID - 460
Length=536

nt: 536

SEQ ID NO: 111

nt: 536

ALIGNMENTS

Identities = 536/536 (100%), Gaps = 0/536 (0%)

Query	1	CAGAGATCAAAATAGGCCTTACACAGTGCGACGCGAATTTAAAAGATTACCCCATTCAGG	60
Sbjct	1	CAGAGATCAAAATAGGCCTTACACAGTGCGACGCGAATTTAAAAGATTACCCCATTCAGG	60
Query	61	TGTATGGATTTTGCAGTATTAAAGATGCTGCCTGGAATAGGTCATTATCTTCTCCAAGTA	120
Sbjct	61	TGTATGGATTTTGCAGTATTAAAGATGCTGCCTGGAATAGGTCATTATCTTCTCCAAGTA	120
Query	121	CTCTGTAAAGTCAATGAGTCACATAGAGTATAAGGTTTATTATCTGCTTTTCTTTCATTA	180
Sbjct	121	CTCTGTAAAGTCAATGAGTCACATAGAGTATAAGGTTTATTATCTGCTTTTCTTTCATTA	180
Query	181	AATAAATCTTTATTGAATTTCTACTACATTaaaaaaccaaaccaaaccaaaccaaaa	240
Sbjct	181	AATAAATCTTTATTGAATTTCTACTACATTAAAAAACCAACCAAAACAAACAAACAAA	240
Query	241	aaaaacaCTTCCCTGAGCCATAAAGGAGAAGGTAGTTTTGACTGGAACCTTGAAGGATGG	300
Sbjct	241	AAAAACACTTCCCTGAGCCATAAAGGAGAAGGTAGTTTTGACTGGAACCTTGAAGGATGG	300
Query	301	GTAAACTTTTCAGCAGATAAAGATTGAGAGAAGACCTTCCAGGTAGAGAAAGCAGTGTGGG	360
Sbjct	301	GTAAACTTTTCAGCAGATAAAGATTGAGAGAAGACCTTCCAGGTAGAGAAAGCAGTGTGGG	360
Query	361	CACAGGCAAAGATGGAAGAACACACGTGGCTGTGGGAAACACAGCTAGAAGCCAGTGCGG	420
Sbjct	361	CACAGGCAAAGATGGAAGAACACACGTGGCTGTGGGAAACACAGCTAGAAGCCAGTGCGG	420
Query	421	ATAGAGAGTAGGCTATGATGTGCAAAGGTTANACACTGGGAGAGACAGGTCCATGAGAGT	480
Sbjct	421	ATAGAGAGTAGGCTATGATGTGCAAAGGTTANACACTGGGAGAGACAGGTCCATGAGAGT	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGCTTGGA	CTAACACAGGGAGGGTTT	GGAATCCCAACTGGGGAACCTANAAATCAA	536
Sbjct	481	AGCTTGGA	CTAACACAGGGAGGGTTT	GGAATCCCAACTGGGGAACCTANAAATCAA	536

Sequence 461 matched with Sequence 112

Query= Sequence ID 461
Length=368

SEQ ID NO: 112

ALIGNMENTS

Identities = 368/368 (100%), Gaps = 0/368 (0%)

Query	1	TAGGAGGCTTATTCACTGATTTCCCCTATTCTCAGGCTACACCCTAGACCAAACCTACGC	60
Sbjct	1	TAGGAGGCTTATTCACTGATTTCCCCTATTCTCAGGCTACACCCTAGACCAAACCTACGC	60
Query	61	CAAAATCCATTTCACTATCATATTCATCGGCGTAAATCTAACTTTCTTCCCACAACACTT	120
Sbjct	61	CAAAATCCATTTCACTATCATATTCATCGGCGTAAATCTAACTTTCTTCCCACAACACTT	120
Query	121	TCTCGGCCTATCCGGAATGCCCCGACGTTACTCGGACTACCCCGATGCATACACCACATG	180
Sbjct	121	TCTCGGCCTATCCGGAATGCCCCGACGTTACTCGGACTACCCCGATGCATACACCACATG	180
Query	181	AAACATCCTATCATCTGTAGGCTCATTCAATTTCTCTAACAGCAGTAATATTAATAATTTT	240
Sbjct	181	AAACATCCTATCATCTGTAGGCTCATTCAATTTCTCTAACAGCAGTAATATTAATAATTTT	240
Query	241	CATGATTTGAGAAGCCTTCGCTTCGAAGCGAAAAGTCCTAATAGTAGAAGAACCCTCCAT	300
Sbjct	241	CATGATTTGAGAAGCCTTCGCTTCGAAGCGAAAAGTCCTAATAGTAGAAGAACCCTCCAT	300
Query	301	AAACCTGGAGTGACTATATGGATGCCCCCACCCTACCACACATTCTGAAGAACCCGTATA	360
Sbjct	301	AAACCTGGAGTGACTATATGGATGCCCCCACCCTACCACACATTCTGAAGAACCCGTATA	360
Query	361	CATAAAAT	368
Sbjct	361	CATAAAAT	368

Sequence 462 matched with Sequence 113

Query= Sequence ID 462
Length=338

SEQ ID NO: 113

ALIGNMENTS

Identities = 338/338 (100%), Gaps = 0/338 (0%)

Query	1	TCTTTATCAAGTTGAGAAAGTTCCTCCCCTCTATTCCTAGTTTGCTAAGAGTCCTTCTAT	60
Sbjct	1	TCTTTATCAAGTTGAGAAAGTTCCTCCCCTCTATTCCTAGTTTGCTAAGAGTCCTTCTAT	60
Query	61	CCTATTTCTTAATGGTTTAGTAGATGACTCTGTGGTACTTTGAAGGTTGTTTGCAGAATT	120
Sbjct	61	CCTATTTCTTAATGGTTTAGTAGATGACTCTGTGGTACTTTGAAGGTTGTTTGCAGAATT	120
Query	121	TCCATGCCATAGGCAATTTACCTTTCCTTGACATTTGAAGGATTGATGTTGGTGCCAAGT	180
Sbjct	121	TCCATGCCATAGGCAATTTACCTTTCCTTGACATTTGAAGGATTGATGTTGGTGCCAAGT	180
Query	181	ATAGAATCTTCACAGAGTCCTCCTGTAGCTTCTAAAGGTTTAGCTTGAAAATGTTAATTG	240
Sbjct	181	ATAGAATCTTCACAGAGTCCTCCTGTAGCTTCTAAAGGTTTAGCTTGAAAATGTTAATTG	240
Query	241	CTTAACGCTAGTAAGTGAGTGAAAAAGCTGGGGATAAATTTGTATCTTGCTTATATTTTC	300
Sbjct	241	CTTAACGCTAGTAAGTGAGTGAAAAAGCTGGGGATAAATTTGTATCTTGCTTATATTTTC	300
Query	301	AGTTCCACCTCTGTCCNGACNAAACCCCATATATAA	338
Sbjct	301	AGTTCCACCTCTGTCCNGACNAAACCCCATATATAA	338

Sequence 463 matched with Sequence 114

Query= Sequence ID 463

Length=383

SEQ ID NO: 114

ALIGNMENTS

Identities = 383/383 (100%), Gaps = 0/383 (0%)

Query	1	TAGTTTACATATCCCAACCTTTAAAAATATTCCTCTTATTAGCTTTATATTCACCTTTATA	60
Sbjct	1	TAGTTTACATATCCCAACCTTTAAAAATATTCCTCTTATTAGCTTTATATTCACCTTTATA	60
Query	61	GAAGTTGAGTTTAAATTAATAATTCCTGGCATCCTGAAGTATGTCACATAGCATGTGCTCC	120
Sbjct	61	GAAGTTGAGTTTAAATTAATAATTCCTGGCATCCTGAAGTATGTCACATAGCATGTGCTCC	120
Query	121	TTATAAATATGTTGATATCTCAGAAGACAGCATCCCGGTTTTTCATTTTATAAAGTACCAT	180
Sbjct	121	TTATAAATATGTTGATATCTCAGAAGACAGCATCCCGGTTTTTCATTTTATAAAGTACCAT	180
Query	181	ACTTAAGAATGCTGTAATACTTATCTTTTATAACATGTTTCCTTCGCTTTGCTTGNCTTT	240
Sbjct	181	ACTTAAGAATGCTGTAATACTTATCTTTTATAACATGTTTCCTTCGCTTTGCTTGNCTTT	240
Query	241	TATGNCATCAGTTTTAACTGTTTACTTCATTTAACAGNTTACATCATNCAACAGTTTACT	300
Sbjct	241	TATGNCATCAGTTTTAACTGTTTACTTCATTTAACAGNTTACATCATNCAACAGTTTACT	300
Query	301	TCATTAAACAGTAGGTGGAAAAATAGATGCCAGTCTATGAAAATCTTCCCATCTATATCA	360
Sbjct	301	TCATTAAACAGTAGGTGGAAAAATAGATGCCAGTCTATGAAAATCTTCCCATCTATATCA	360
Query	361	AAATACTTTCAAGGATATACTTT	383
Sbjct	361	AAATACTTTCAAGGATATACTTT	383

Sequence 464 matched with Sequence 115

Query= Sequence ID - 464
Length=615

nt: 615

SEQ ID NO: 115

nt: 615

ALIGNMENTS

Identities = 615/615 (100%), Gaps = 0/615 (0%)

Query	1	CGACTTTCAACCATCAAGTGAGGAATACCTTCACATAACTGAGCCTCCCTCTTTATCTCC	60
Sbjct	1	CGACTTTCAACCATCAAGTGAGGAATACCTTCACATAACTGAGCCTCCCTCTTTATCTCC	60
Query	61	TGACACAAAATTAGAACCTTCAGAAGATGATGGTAAACCTGAGTTATTAGAAGAAATGGA	120
Sbjct	61	TGACACAAAATTAGAACCTTCAGAAGATGATGGTAAACCTGAGTTATTAGAAGAAATGGA	120
Query	121	AGCTTCTCCACAGAACTTATTGCTGTGGAAGGAACTGAGATTCTCCAAGATTTCCAAAA	180
Sbjct	121	AGCTTCTCCACAGAACTTATTGCTGTGGAAGGAACTGAGATTCTCCAAGATTTCCAAAA	180
Query	181	CAAAACCTATGGTCAAGTTTCTGGAGAAGCAATCAAGATGTTTCCCACCATTAAACACC	240
Sbjct	181	CAAAACCTATGGTCAAGTTTCTGGAGAAGCAATCAAGATGTTTCCCACCATTAAACACC	240
Query	241	TGAGGCTGGAAGCTGTTATTACAACTGCCGATGAAATTGAATTAGAAGGTGCTACACAGTG	300
Sbjct	241	TGAGGCTGGAAGCTGTTATTACAACTGCCGATGAAATTGAATTAGAAGGTGCTACACAGTG	300
Query	301	GCCACACTCTACTTCTGCTTCTGCCACCTATGGGGTCGAGGCAGGTGTGGTGCCTTGGCT	360
Sbjct	301	GCCACACTCTACTTCTGCTTCTGCCACCTATGGGGTCGAGGCAGGTGTGGTGCCTTGGCT	360
Query	361	AAGTCCACAGACTTCTGAGAGGCCACGCTTTCTTCTTCTCCAGAAATAAACCTGAAAC	420
Sbjct	361	AAGTCCACAGACTTCTGAGAGGCCACGCTTTCTTCTTCTCCAGAAATAAACCTGAAAC	420
Query	421	TCAAGCAGCTTTAATCAGAGGGCAGGATTCCACGATAGCAGCATCAGAACAGCAAGTGGC	480
Sbjct	421	TCAAGCAGCTTTAATCAGAGGGCAGGATTCCACGATAGCAGCATCAGAACAGCAAGTGGC	480

Query	481	AGCGAGAATTCTTGATTCCAATGATCAGGCAACAGTAAACCCTGTGGAATTTAATACTGA	540
Sbjct	481	AGCGAGAATTCTTGATTCCAATGATCAGGCAACAGTAAACCCTGTGGAATTTAATACTGA	540
Query	541	GGGTGCAACACCCCATTTTCCCTTCTGGAGACTTCTAATGAAACANATTTCCCTGATTGGC	600
Sbjct	541	GGGTGCAACACCCCATTTTCCCTTCTGGAGACTTCTAATGAAACANATTTCCCTGATTGGC	600
Query	601	ATTAATGAANAGTCA	615
Sbjct	601	ATTAATGAANAGTCA	615

Sequence 469 matched with Sequence 116

Query= Sequence ID 469
Length=161

SEQ ID NO: 116

ALIGNMENTS

Identities = 159/159 (100%), Gaps = 0/159 (0%)

Query	1	GATTTTTTAAAAATACATATAGCAAAAATATTACAGGGTCAGGGGAGACAATTAGAATGAT	60
Sbjct	1	GATTTTTTAAAAATACATATAGCAAAAATATTACAGGGTCAGGGGAGACAATTAGAATGAT	60
Query	61	ATAATTCAAAGTGGATTaaaaaaaaaCTGTCACCCAGAATACAATACCCAGCAAAGTTG	120
Sbjct	61	ATAATTCAAAGTGGATTAAAAAAAAAACTGTCACCCAGAATACAATACCCAGCAAAGTTG	120
Query	121	TCCTTCATAAATGAAAGAAAAATNAAATCTTTNCCNAAC	159
Sbjct	121	TCCTTCATAAATGAAAGAAAAATNAAATCTTTNCCNAAC	159

Sequence 471 matched with Sequence 117

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 471
Length=28

SEQ ID NO: 117 56.0 8e-15

ALIGNMENTS

Identities = 8/8 (100%), Gaps = 0/8 (0%)

```
Query 1 TCCCGGGA 8
      |||||
Sbjct 8 TCCCGGGA 1
```

Sequence 472 matched with Sequence 118

Query= Sequence ID 472
Length=258

SEQ ID NO: 118

ALIGNMENTS

Identities = 258/258 (100%), Gaps = 0/258 (0%)

Query	1	GACAGTGCCCGAGGGCTCTGATATGTCTNTCACANCTTGNAAGTGTGAGACAGCTGCCTT	60
Sbjct	1	GACAGTGCCCGAGGGCTCTGATATGTCTNTCACANCTTGNAAGTGTGAGACAGCTGCCTT	60
Query	61	GTGTGGGACTGAAAGGCAAGATTTGTTCCCTGCCCTTCCCTTTGTGACTTGAAGAACCCTG	120
Sbjct	61	GTGTGGGACTGAAAGGCAAGATTTGTTCCCTGCCCTTCCCTTTGTGACTTGAAGAACCCTG	120
Query	121	ACTTTGTTTCTGCAAAGGCACCTGCATGTGTCTGTGTTCTTGTAGGCATAATGTGAGGAG	180
Sbjct	121	ACTTTGTTTCTGCAAAGGCACCTGCATGTGTCTGTGTTCTTGTAGGCATAATGTGAGGAG	180
Query	181	GTGGGGANACCACCCACCCCATGTCCACCATGACCCTCTTNCCACNCTNACCTGTGCT	240
Sbjct	181	GTGGGGANACCACCCACCCCATGTCCACCATGACCCTCTTNCCACNCTNACCTGTGCT	240
Query	241	CCCTCCCCAATCATNTTT	258
Sbjct	241	CCCTCCCCAATCATNTTT	258

Sequence 473 matched with Sequence 119

Query= Sequence ID - 473
Length=694

nt: 694

SEQ ID NO: 119

nt: 694

ALIGNMENTS

Identities = 694/694 (100%), Gaps = 0/694 (0%)

Query	1	TGGGCTTTGGGCTGGCTGCAGTCTGTCTGAGGGCGGCCGAAGTGGCTGGCTCATTTAAGA	60
Sbjct	1	TGGGCTTTGGGCTGGCTGCAGTCTGTCTGAGGGCGGCCGAAGTGGCTGGCTCATTTAAGA	60
Query	61	TGAGGCTTCTGCTGCTTCTCCTAGNGGCGGCGTCTGCGATGGTCCGGAGCGAGGCCTCGG	120
Sbjct	61	TGAGGCTTCTGCTGCTTCTCCTAGNGGCGGCGTCTGCGATGGTCCGGAGCGAGGCCTCGG	120
Query	121	CCAATCTGGGCGGCGTGCCAGCAAGAGATTAAAGATGCAGTACGCCACGGGGCCGCTGC	180
Sbjct	121	CCAATCTGGGCGGCGTGCCAGCAAGAGATTAAAGATGCAGTACGCCACGGGGCCGCTGC	180
Query	181	TCAAGTTCCAGATTTGTGTTTCCTGAGGTTATAGGCGGGTGTTTGAGGAGTACATGCGGG	240
Sbjct	181	TCAAGTTCCAGATTTGTGTTTCCTGAGGTTATAGGCGGGTGTTTGAGGAGTACATGCGGG	240
Query	241	TTATTAGCCAGCGGTACCCAGACATCCGCATTGAAGGAGAGAATTACCTCCCTCAACCAA	300
Sbjct	241	TTATTAGCCAGCGGTACCCAGACATCCGCATTGAAGGAGAGAATTACCTCCCTCAACCAA	300
Query	301	TATATAGACACATAGCATCTTTCCTGTCAGTCTTCAAACCTAGTATTAATAGGCTTAATAA	360
Sbjct	301	TATATAGACACATAGCATCTTTCCTGTCAGTCTTCAAACCTAGTATTAATAGGCTTAATAA	360
Query	361	TTGTTGGCAAGGATCCTTTTGCTTTCTTTGGCATGCAAGCTCCTAGCATCTGGCAGTGGG	420
Sbjct	361	TTGTTGGCAAGGATCCTTTTGCTTTCTTTGGCATGCAAGCTCCTAGCATCTGGCAGTGGG	420
Query	421	GCCAAGAAAATAAGGTTTATGCATGTATGATGGTTTTCTTCTTGAGCAACATGATTGAGA	480
Sbjct	421	GCCAAGAAAATAAGGTTTATGCATGTATGATGGTTTTCTTCTTGAGCAACATGATTGAGA	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 ACCAGTGTATGTCAACAGGTGCATTTGAGATAACTTTAAATGATGTACCTGTGTGGTCTA 540
          |||
Sbjct 481 ACCAGTGTATGTCAACAGGTGCATTTGAGATAACTTTAAATGATGTACCTGTGTGGTCTA 540

Query 541 AGCTGGAATCTGGTCACCTTCCATCCATGCAACAACCTTGTTCAAATTCTTGACAATGAAA 600
          |||
Sbjct 541 AGCTGGAATCTGGTCACCTTCCATCCATGCAACAACCTTGTTCAAATTCTTGACAATGAAA 600

Query 601 TGAAACTCAATGTGCATATGGGATTCAATCCCCACCATCGATCATAGCACCCCCTATCAG 660
          |||
Sbjct 601 TGAAACTCAATGTGCATATGGGATTCAATCCCCACCATCGATCATAGCACCCCCTATCAG 660

Query 661 CACTGNAAACTCTTTTGCATTAAGGGATCATTGC 694
          |||
Sbjct 661 CACTGNAAACTCTTTTGCATTAAGGGATCATTGC 694
```

Sequence 474 matched with Sequence 120

Query= Sequence ID 474
Length=337

SEQ ID NO: 120

ALIGNMENTS

Identities = 337/337 (100%), Gaps = 0/337 (0%)

Query	1	GGCAGCGCGGGGAGCCCGTCGGCGCCGGCGGGCGGGCCGGTTTCGAAGTTGATGCAATCG	60
Sbjct	1	GGCAGCGCGGGGAGCCCGTCGGCGCCGGCGGGCGGGCCGGTTTCGAAGTTGATGCAATCG	60
Query	61	GTTTAAACATGGCTGAACGCGTGTGTACACGGGACTGACGCAACCCACGTGTAAGTGTCA	120
Sbjct	61	GTTTAAACATGGCTGAACGCGTGTGTACACGGGACTGACGCAACCCACGTGTAAGTGTCA	120
Query	121	GCCGGGCCCTGAGTAATCGCTTAAAGATGTTCCCTACGGGCTtggtgctggtgatgtttg	180
Sbjct	121	GCCGGGCCCTGAGTAATCGCTTAAAGATGTTCCCTACGGGCTTGTGCTGTTGATGTTTTG	180
Query	181	ttttgttttggtttttggtccttttttTATTATAAAAAATAATCTATTTCTATGAGAAA	240
Sbjct	181	TTTTGTTTTGTTTTTGGTCTTTTTTTGTATTATAAAAAATAATCTATTTCTATGAGAAA	240
Query	241	AGAGGCGTCTGTATATTTTGGGAATCTTTTCCGTTTCAAGCATTAAGAACACTTTTAATA	300
Sbjct	241	AGAGGCGTCTGTATATTTTGGGAATCTTTTCCGTTTCAAGCATTAAGAACACTTTTAATA	300
Query	301	AACttttttttGATAATGGTTaaaaaaaaaaaaaaaaa	337
Sbjct	301	AACTTTTTTTTGATAATGGTTAAAAAAAAAAAAAAAAA	337

Sequence 475 matched with Sequence 121

Query= Sequence ID 475
Length=210

SEQ ID NO: 121

ALIGNMENTS

Identities = 210/210 (100%), Gaps = 0/210 (0%)

Query	1	CATAATAAAAAACAATCAACAAACAGGGAATGGAAAGAACTTCCTCAGCATGGTGAAGG	60
Sbjct	1	CATAATAAAAAACAATCAACAAACAGGGAATGGAAAGAACTTCCTCAGCATGGTGAAGG	60
Query	61	CCACATATGAAAATCCCACAGCTAACATCATACTCAATGATGAAAGACTGAAAGCTTTTC	120
Sbjct	61	CCACATATGAAAATCCCACAGCTAACATCATACTCAATGATGAAAGACTGAAAGCTTTTC	120
Query	121	TCCTGAGATCAGGAACAAGACAAAGATGTCACCTTTTGTCACTTCTATTCAACTCATTAT	180
Sbjct	121	TCCTGAGATCAGGAACAAGACAAAGATGTCACCTTTTGTCACTTCTATTCAACTCATTAT	180
Query	181	TGGAAGTTTTTGCCAGAGCAATTAGGTAAG	210
Sbjct	181	TGGAAGTTTTTGCCAGAGCAATTAGGTAAG	210

nt: 476

nt: 476

Identities = 476/476 (100%), Gaps = 0/476 (0%)

Query	1	CAGAATCTTTTCATAGGCTGAATGTTGCTCCACAATGTGTCCTTTGACTATCTCTGGCTA 	60
Sbjct	1	CAGAATCTTTTCATAGGCTGAATGTTGCTCCACAATGTGTCCTTTGACTATCTCTGGCTA	60
Query	61	ATTATTATTTTAATCTCTTCTCAGCTTTTCCAAGAACATAACGTTAACCAAAGATCTTAG 	120
Sbjct	61	ATTATTATTTTAATCTCTTCTCAGCTTTTCCAAGAACATAACGTTAACCAAAGATCTTAG	120
Query	121	GCCATTCACAACTCTTTTGTA AAAAATTAATGTGGATGTGAAACGAGGCAACAAATCCTGA 	180
Sbjct	121	GCCATTCACAACTCTTTTGTA AAAAATTAATGTGGATGTGAAACGAGGCAACAAATCCTGA	180
Query	181	AGTAGAAAGTTATTCTGGCCAGGCACGGTGGCTCACGCCTGTAATCCTGGCACTTTGGG 	240
Sbjct	181	AGTAGAAAGTTATTCTGGCCAGGCACGGTGGCTCACGCCTGTAATCCTGGCACTTTGGG	240
Query	241	AGGCCGAGGTGGGTGGATCATGAGGACAGGAGATCGAGACCATCCTGGCCAACATGATGA 	300
Sbjct	241	AGGCCGAGGTGGGTGGATCATGAGGACAGGAGATCGAGACCATCCTGGCCAACATGATGA	300
Query	301	AACCCCATCTCTACTAAAATACAAAAAATTAGCTGGGCATGGTGACGCGTGCCTGTAGTC 	360
Sbjct	301	AACCCCATCTCTACTAAAATACAAAAAATTAGCTGGGCATGGTGACGCGTGCCTGTAGTC	360
Query	361	CCAGTTACTCGGGAGGCTGAGGCAGGGGAATTGCTTGAACCTCGGAGGTGGGAGGTTGCA 	420
Sbjct	361	CCAGTTACTCGGGAGGCTGAGGCAGGGGAATTGCTTGAACCTCGGAGGTGGGAGGTTGCA	420
Query	421	GTGTGCCGAGATCACGCTACTGCACTCCAGCCTGGCAACAGAGCAAGACTCCATCT 	476
Sbjct	421	GTGTGCCGAGATCACGCTACTGCACTCCAGCCTGGCAACAGAGCAAGACTCCATCT	476

Sequence 477 matched with Sequence 123

Query= Sequence ID 477
Length=250

SEQ ID NO: 123

ALIGNMENTS

Identities = 250/250 (100%), Gaps = 0/250 (0%)

Query	1	AAACAGAAAGTTTCTTCTAAAGGCATGATTCAGTTAAGTCATTCTTAAGTGTTAAAAAAT	60
Sbjct	1	AAACAGAAAGTTTCTTCTAAAGGCATGATTCAGTTAAGTCATTCTTAAGTGTTAAAAAAT	60
Query	61	TGTGAAAAATGTGCCTGTAATCCCAACACTTTGGGAGGCCGAGGCAGGCAGATCACGAGG	120
Sbjct	61	TGTGAAAAATGTGCCTGTAATCCCAACACTTTGGGAGGCCGAGGCAGGCAGATCACGAGG	120
Query	121	TCAGGAGATCAAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACGAAAAATACCA	180
Sbjct	121	TCAGGAGATCAAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACGAAAAATACCA	180
Query	181	AAAACATTAGCCGGGCGTGTTGTGGGCGCCTGTAGTCCCAGCTACTTGAGAGGCTGAGG	240
Sbjct	181	AAAACATTAGCCGGGCGTGTTGTGGGCGCCTGTAGTCCCAGCTACTTGAGAGGCTGAGG	240
Query	241	CAGGAGAATG	250
Sbjct	241	CAGGAGAATG	250

Sequence 478 matched with Sequence 124

Query= Sequence ID 478

Length=523

SEQ ID NO: 124

ALIGNMENTS

Identities = 523/523 (100%), Gaps = 0/523 (0%)

Query	1	TTCTTGGGATATTGATGACTACTGTCTGAGAGGTGCTGTGGGGAGATTTTCAGGATTGTG	60
Sbjct	1	TTCTTGGGATATTGATGACTACTGTCTGAGAGGTGCTGTGGGGAGATTTTCAGGATTGTG	60
Query	61	TGGTCTTTGAGGGGGGTGtttttttAAGACAACATTGACCACTGTCCACTGTCCACATGA	120
Sbjct	61	TGGTCTTTGAGGGGGGTGTTTTTTTAAGACAACATTGACCACTGTCCACTGTCCACATGA	120
Query	121	TCATTGTAAAAATTGCAATGCCGCATGCTAGTTGGTTACATAAGACATAATTCCAGTGATT	180
Sbjct	121	TCATTGTAAAAATTGCAATGCCGCATGCTAGTTGGTTACATAAGACATAATTCCAGTGATT	180
Query	181	GAAGGTGGTTACACTGTATGGTGGTGTGTTCAAGATGGCACTGGCATCTTTGAGCAGAGC	240
Sbjct	181	GAAGGTGGTTACACTGTATGGTGGTGTGTTCAAGATGGCACTGGCATCTTTGAGCAGAGC	240
Query	241	CTGGCTATGCAGCATCATTGAGTTTTTTTAAACACCCTANAGGTCTGGTTGTTGTTGCTG	300
Sbjct	241	CTGGCTATGCAGCATCATTGAGTTTTTTTAAACACCCTANAGGTCTGGTTGTTGTTGCTG	300
Query	301	TTGTCCTTTCCTGTGAAAGTCACaananaaGTTACAGTCCAGGTGAACCTGGAGTTTATA	360
Sbjct	301	TTGTCCTTTCCTGTGAAAGTCACAAANANAAGTTACAGTCCAGGTGAACCTGGAGTTTATA	360
Query	361	GGTTGGTTTTGTTTCTGntatatatatatatatatatatttttttttttttAACATTT	420
Sbjct	361	GGTTGGTTTTGTTTCTGNTATATATATATATATATATATATTTTTTTTTTTTTTAACATTT	420
Query	421	ACCTGTAGTGCTGTAGCTGTTGATACTATCACCTGCATGCTATTTCTAGTGAGTGCTAAA	480
Sbjct	421	ACCTGTAGTGCTGTAGCTGTTGATACTATCACCTGCATGCTATTTCTAGTGAGTGCTAAA	480

```
Query 481 TACAGTATGGTCCAATGACAATAACAGCCCATGGTACTGCCAG 523
          |||
Sbjct 481 TACAGTATGGTCCAATGACAATAACAGCCCATGGTACTGCCAG 523
```

Sequence 479 matched with Sequence 125

Query= Sequence ID 479

Length=487

SEQ ID NO: 125

ALIGNMENTS

Identities = 487/487 (100%), Gaps = 0/487 (0%)

Query	1	CATCAGTCTGTTATCCATGCTGACTTTCCGAAGACTTGCAGCTACTGCATTGATATCTTT	60
Sbjct	1	CATCAGTCTGTTATCCATGCTGACTTTCCGAAGACTTGCAGCTACTGCATTGATATCTTT	60
Query	61	CCTGCCAATAAGCAAAGTGTTGAACACTTCACAAAATATTTTACTGAGGCAGGCTTGAAA	120
Sbjct	61	CCTGCCAATAAGCAAAGTGTTGAACACTTCACAAAATATTTTACTGAGGCAGGCTTGAAA	120
Query	121	GAGCTTTCAGAATATGTTTCGGAATCAGCAAACCATCGGAGCTCGTAAGGAGCTCCAGAAA	180
Sbjct	121	GAGCTTTCAGAATATGTTTCGGAATCAGCAAACCATCGGAGCTCGTAAGGAGCTCCAGAAA	180
Query	181	GAACTTCAAGAACAGATGTCCCGTGGTGATCCATTTAAGGATATAATTTTATATGTCAAG	240
Sbjct	181	GAACTTCAAGAACAGATGTCCCGTGGTGATCCATTTAAGGATATAATTTTATATGTCAAG	240
Query	241	GAGGAGATGaaaaaaaaCAACATCCCAGAGCCAGTTGTCATCGGAATAGTCTGGTCAAGT	300
Sbjct	241	GAGGAGATGAAAAAAAAACAACATCCCAGAGCCAGTTGTCATCGGAATAGTCTGGTCAAGT	300
Query	301	GTAATGAGCACTGTGGAATGGAACAAAAAAGAGGAGCTTGTAGCAGAGCAAGCCATCAAG	360
Sbjct	301	GTAATGAGCACTGTGGAATGGAACAAAAAAGAGGAGCTTGTAGCAGAGCAAGCCATCAAG	360
Query	361	CACTTGAAGCAATACAGCCCTCTACTTGCTGCCTTTACTACTCAAGGTCAGTCTGAGCTG	420
Sbjct	361	CACTTGAAGCAATACAGCCCTCTACTTGCTGCCTTTACTACTCAAGGTCAGTCTGAGCTG	420
Query	421	ACTCTGTTACTGAAGATTAGGGAGTATTGCTATGACAACATTCATTTTCATGAAAGCCTTC	480
Sbjct	421	ACTCTGTTACTGAAGATTAGGGAGTATTGCTATGACAACATTCATTTTCATGAAAGCCTTC	480

PATENT SEQUENCE ALIGNMENT

Query	481	CANAAAA	487
Sbjct	481	CANAAAA	487

Sequence 481 matched with Sequence 126

Query= Sequence ID 481
Length=274

SEQ ID NO: 126

ALIGNMENTS

Identities = 274/274 (100%), Gaps = 0/274 (0%)

Query	1	CACACTTTCATGATAAAAAACAGAACCTAGGAATGAAAAGAAATTATAGCAACATAATAAA	60
Sbjct	1	CACACTTTCATGATAAAAAACAGAACCTAGGAATGAAAAGAAATTATAGCAACATAATAAA	60
Query	61	GACCATATATGAGAAGCCACAGCTAACATACTGTATGGTGAAAAACTGAAAGCTCTTCC	120
Sbjct	61	GACCATATATGAGAAGCCACAGCTAACATACTGTATGGTGAAAAACTGAAAGCTCTTCC	120
Query	121	TCTAAGATCAGGAACAAGGCAAGGATGCCCATTCCTTGCCACTTCTATCGAACGTAGTACT	180
Sbjct	121	TCTAAGATCAGGAACAAGGCAAGGATGCCCATTCCTTGCCACTTCTATCGAACGTAGTACT	180
Query	181	GGAAGCCCTAGCCAGAACAACCTAGGCAATAGAAAGAAATTAAAGGCATCCATNTCAGAAA	240
Sbjct	181	GGAAGCCCTAGCCAGAACAACCTAGGCAATAGAAAGAAATTAAAGGCATCCATNTCAGAAA	240
Query	241	GGAAGAANCAAAAATGCTGTCTGTTTAANATGACA	274
Sbjct	241	GGAAGAANCAAAAATGCTGTCTGTTTAANATGACA	274

Sequence 482 matched with Sequence 127

Length=130

Identities = 130/130 (100%), Gaps = 0/130 (0%)

```
Query   1      TTTCTATanaaaaaaatttttttaaataattgtaaagttagattttaaattgtaaaatat   60
          |||
Sbjct   1      TTTCTATANAAAAAATTTTTTAAATAATTGTAAAGTTAGATTTAAAATTGTAAAATAT   60

Query   61     aaaatcacaaaggaatgtacccaataaaatgtaaatgcnccataaaaaaaaaaaaaaaaaa  120
          |||
Sbjct   61     AAAATCACAAAGGAATGTACCCAATAAAATGTAAATGCNCCATAAAAAAAAAAAAAAAAAA  120

Query   121    aaaaaaaaaa   130
          |||
Sbjct   121    AAAAAAAAAA   130
```


Sequence 483 matched with Sequence 128

Query= Sequence ID 483

Length=519

SEQ ID NO: 128

ALIGNMENTS

Identities = 516/516 (100%), Gaps = 0/516 (0%)

Query	4	TAACGTGCAATCCGCCGCACGCCAGCAAAC	TGGACAACTCCGGGATCTCATCGAAGCGA	63
Sbjct	4	TAACGTGCAATCCGCCGCACGCCAGCAAAC	TGGACAACTCCGGGATCTCATCGAAGCGA	63
Query	64	TTGAGCACCACTACCAGAGTAATACCGGACTGATGTAACGAGGCGAGTCGCTCATCCAGC		123
Sbjct	64	TTGAGCACCACTACCAGAGTAATACCGGACTGATGTAACGAGGCGAGTCGCTCATCCAGC		123
Query	124	TTGCTGACGTGAGGCAACATCCAGGCCATCGAACGGNTCATCAAGAATCAACAAGTCAGG		183
Sbjct	124	TTGCTGACGTGAGGCAACATCCAGGCCATCGAACGGNTCATCAAGAATCAACAAGTCAGG		183
Query	184	CTCCGACATCAGCGCCTGACACAGCAGGGTTTTTCGCGTCTCGCCAGTGGAAGGTATTT		243
Sbjct	184	CTCCGACATCAGCGCCTGACACAGCAGGGTTTTTCGCGTCTCGCCAGTGGAAGGTATTT		243
Query	244	AAAGCGTCNGTCGAGGAGGGCGGTAATACCGAACTGCTGCGCCAGTTGCATGCAACGCGG		303
Sbjct	244	AAAGCGTCNGTCGAGGAGGGCGGTAATACCGAACTGCTGCGCCAGTTGCATGCAACGCGG		303
Query	304	TGCATCCTTTACTTCATCCTGAATGATCTCAGCCGTAGTGCGTCCGGTGCCATCTTCGCC		363
Sbjct	304	TGCATCCTTTACTTCATCCTGAATGATCTCAGCCGTAGTGCGTCCGGTGCCATCTTCGCC		363
Query	364	AGGGCCGAGCATATCGGTGTTATTCCGCTGCCATTCGTCGCTGACGAGTTTTTGCAATTG		423
Sbjct	364	AGGGCCGAGCATATCGGTGTTATTCCGCTGCCATTCGTCGCTGACGAGTTTTTGCAATTG		423
Query	424	CTCGAAGGAGAGACGAGTGATGTGGGAAAAC	TGGCTTTGCCGTTACCTTTCAAAGCGG	483
Sbjct	424	CTCGAAGGAGAGACGAGTGATGTGGGAAAAC	TGGCTTTGCCGTTACCTTTCAAAGCGG	483

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Query    484  GAAGTTCCCCGCCAGCGCGCGGGCCAGGGCCCGAT  519
        ||||||||||||||||||||||||||||||||
Sbjct    484  GAAGTTCCCCGCCAGCGCGCGGGCCAGGGCCCGAT  519

```

Sequence 484 matched with Sequence 129

Query= Sequence ID 484
Length=272

SEQ ID NO: 129

ALIGNMENTS

Identities = 272/272 (100%), Gaps = 0/272 (0%)

Query	1	tttttttttttttATTCTatttaaaaaatgttnntgaaaaaagataacttaaatttttaagat	60
Sbjct	1	TTTTTTTTTTTATTCTATTAATAAAATGTTNNTGAAAAAAGATACTTAAATTTTAAAGAT	60
Query	61	aactnaattcctaangattttaaataATCCAAGCAGAGATGAAAGANCAAATGCAAATGC	120
Sbjct	61	AACTNAATTCCTAANGATTATAAATAATCCAAGCAGAGATGAAAGANCAAATGCAAATGC	120
Query	121	NTAAAAAGACCCCANAGCATTGTTtagcaaaaagcaaatatagttagccaagcatatatat	180
Sbjct	121	NTAAAAAGACCCCANAGCATTGTTAGCAAAAAGCAAATATAGTTAGCCAAGCATATATAT	180
Query	181	ntcataaaaagcaataanaaggcntaaagcaagTTTGGGGAGAGCTTATTTAAAACTTGTA	240
Sbjct	181	NTCATAAAAGCAATAANAAGGCNTAAAGCAAGTTTGGGGAGAGCTTATTTAAAACTTGTA	240
Query	241	AAAATCATTTGAATTTTAAAGTTTTCAAAC	272
Sbjct	241	AAAATCATTTGAATTTTAAAGTTTTCAAAC	272

Sequence 485 matched with Sequence 130

Query= Sequence ID - 485
Length=551

nt: 551

SEQ ID NO: 130

nt: 551

ALIGNMENTS

Identities = 551/551 (100%), Gaps = 0/551 (0%)

Query	1	TTTGGAACACAAAGTTCCTTTTTAGAGAATAGGTATTGAGCCCTTGAGCGTGGGTAGA	60
Sbjct	1	TTTGGAACACAAAGTTCCTTTTTAGAGAATAGGTATTGAGCCCTTGAGCGTGGGTAGA	60
Query	61	AAGATAGAGACAGAGTGATTTGCAAAATAATGGAGGATCATATTTATATATGAATTTTCA	120
Sbjct	61	AAGATAGAGACAGAGTGATTTGCAAAATAATGGAGGATCATATTTATATATGAATTTTCA	120
Query	121	CTTATTTGAACTTTCAGATATCANCTTNAANAANCTTTGGTTTAAGTAAAGTNTNTTAATG	180
Sbjct	121	CTTATTTGAACTTTCAGATATCANCTTNAANAANCTTTGGTTTAAGTAAAGTNTNTTAATG	180
Query	181	AGACTCCTTGGATGAAAGTAACCAAAACCAGTAAAAATAAGGTAATAAGGATGTAATAGT	240
Sbjct	181	AGACTCCTTGGATGAAAGTAACCAAAACCAGTAAAAATAAGGTAATAAGGATGTAATAGT	240
Query	241	TTCTTATGGACACTCAACAGCTAGAATGCAGTTAGTCTCAGAAAAGAATTAGAACAAATA	300
Sbjct	241	TTCTTATGGACACTCAACAGCTAGAATGCAGTTAGTCTCAGAAAAGAATTAGAACAAATA	300
Query	301	ACTGGAAGGCCATCAGGAGTCCAAAACCATCACTCttttatatattttatatttttC	360
Sbjct	301	ACTGGAAGGCCATCAGGAGTCCAAAACCATCACTCTTTTATATTTTATATTTTATTTTC	360
Query	361	TCTCTTCANATGAGCATTCTCTTTCTATGTCCATATGGTANAAGGCGGCAGCTCCATAGA	420
Sbjct	361	TCTCTTCANATGAGCATTCTCTTTCTATGTCCATATGGTANAAGGCGGCAGCTCCATAGA	420
Query	421	TTATGGCTTCAGATGTTACAGTTCCGCTNAATGCAGGGACAGACTTGCTATCTTTCAGTC	480
Sbjct	421	TTATGGCTTCAGATGTTACAGTTCCGCTNAATGCAGGGACAGACTTGCTATCTTTCAGTC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CCCTTACATATCCTGGGGAGAGAGCAAATGATTGACTGGCTTGAGTCAGGTGCCC GTTCC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CCCTTACATATCCTGGGGAGAGAGCAAATGATTGACTGGCTTGAGTCAGGTGCCC GTTCC  540

Query  541  CTTTCCAATCT  551
          |||||||||
Sbjct  541  CTTTCCAATCT  551
```

Sequence 487 matched with Sequence 131

Query= Sequence ID - 487 nt:224
Length=224

SEQ ID NO: 131 nt:224

ALIGNMENTS

Identities = 224/224 (100%), Gaps = 0/224 (0%)

Query	1	GTTTGNTTGTGACCATCTGTACTTGTAATTTCTTTACNTTCATTGGTATGAAAAATATGT	60
Sbjct	1	GTTTGNTTGTGACCATCTGTACTTGTAATTTCTTTACNTTCATTGGTATGAAAAATATGT	60
Query	61	TCTTAGAAGCANGAAAAAGAATTCAGNTTGTCTTTGTATACTAAATTAAATGCTGTAATT	120
Sbjct	61	TCTTAGAAGCANGAAAAAGAATTCAGNTTGTCTTTGTATACTAAATTAAATGCTGTAATT	120
Query	121	TTGATAAAATGAAAAATCTGCTTTATTTGCAACAATTGGTTTCTTCCTTGACGTCAGCCT	180
Sbjct	121	TTGATAAAATGAAAAATCTGCTTTATTTGCAACAATTGGTTTCTTCCTTGACGTCAGCCT	180
Query	181	CACTCTTGACTTTGGTATTCAGCCNGNCACCCCTGGGAATTCC	224
Sbjct	181	CACTCTTGACTTTGGTATTCAGCCNGNCACCCCTGGGAATTCC	224

Sequence 488 matched with Sequence 132

Query= Sequence ID - 488
Length=349

nt: 349

SEQ ID NO: 132

nt: 349

ALIGNMENTS

Identities = 349/349 (100%), Gaps = 0/349 (0%)

Query	1	GTGCCTCCCTGTGTGAGTAGCCTAAGGTGCATTGAAAAAGACTGGGATGTGTTTTA	60
Sbjct	1	GTGCCTCCCTGTGTGAGTAGCCTAAGGTGCATTGAAAAAGACTGGGATGTGTTTTATTTT	60
Query	61	tttGTATTAGATAGCATTAACTTACTGTTGAAGTATTTTTGGTGGAGTATTAGTGACAA	120
Sbjct	61	TTTGTATTAGATAGCATTAACTTACTGTTGAAGTATTTTTGGTGGAGTATTAGTGACAA	120
Query	121	GCCATTGAGTCTTAAGCCTTACGGCTTCCTATAAAATCACTAATTCGTGTGTGTTTGTG	180
Sbjct	121	GCCATTGAGTCTTAAGCCTTACGGCTTCCTATAAAATCACTAATTCGTGTGTGTTTGTG	180
Query	181	TGTAGGTTACGTTATATATAGGATTCGTGTTGCGCGTGGTGGCCGAAAAACGCCAGTTCC	240
Sbjct	181	TGTAGGTTACGTTATATATAGGATTCGTGTTGCGCGTGGTGGCCGAAAAACGCCAGTTCC	240
Query	241	TAAGGGTGCAACTTACGGCAAGCCTGTCCATCATGGTGTAAACCAGCTAAAGTTTGCTCG	300
Sbjct	241	TAAGGGTGCAACTTACGGCAAGCCTGTCCATCATGGTGTAAACCAGCTAAAGTTTGCTCG	300
Query	301	AAGCCTTCAGTCCGTTGCAGAGGANCGAGCTGGACNCCCTGGGGGGCTC	349
Sbjct	301	AAGCCTTCAGTCCGTTGCAGAGGANCGAGCTGGACNCCCTGGGGGGCTC	349

Sequence 489 matched with Sequence 133

Query= Sequence ID 489

Length=635

SEQ ID NO: 133

ALIGNMENTS

Identities = 635/635 (100%), Gaps = 0/635 (0%)

Query	1	TTAACAGCTGCATAGAGTTTTAAAAGTACATTATATTTTGTCTCAGACAAGTAAAATATCTG	60
Sbjct	1	TTAACAGCTGCATAGAGTTTTAAAAGTACATTATATTTTGTCTCAGACAAGTAAAATATCTG	60
Query	61	TTTTTCACGCaaaaaaGCCATGAAATACGTAATTTTTTAAAGACAAAAAATCATCTTTT	120
Sbjct	61	TTTTTCACGCAAAAAAGCCATGAAATACGTAATTTTTTAAAGACAAAAAATCATCTTTT	120
Query	121	GAGTTTGCTCTTTGGTTTTTCTTCATTCCTTTTGAGGATTGGGAAAACAGAAAGATTCTT	180
Sbjct	121	GAGTTTGCTCTTTGGTTTTTCTTCATTCCTTTTGAGGATTGGGAAAACAGAAAGATTCTT	180
Query	181	TGATTTGGGTAATGAAGAGGTAATTTGGGACAGTGTGGTGGTACCAGGAAGAAAGAGGAT	240
Sbjct	181	TGATTTGGGTAATGAAGAGGTAATTTGGGACAGTGTGGTGGTACCAGGAAGAAAGAGGAT	240
Query	241	TGGAAAGGCCAGTACTGTTTTAGTTGCTCGGCACTGTTGGTTTTGTTTAAATGTGGTTGC	300
Sbjct	241	TGGAAAGGCCAGTACTGTTTTAGTTGCTCGGCACTGTTGGTTTTGTTTAAATGTGGTTGC	300
Query	301	CCTGTCCACTACATGGTTCTATCAGTAGTGAATCCATTTTCAATGTAAAGCTCTTTTAG	360
Sbjct	301	CCTGTCCACTACATGGTTCTATCAGTAGTGAATCCATTTTCAATGTAAAGCTCTTTTAG	360
Query	361	TTTTTGTCTAGACATAAATTAATATTTTGAGAGGCATCCCTCACCTGTTTCAATTTCTTCT	420
Sbjct	361	TTTTTGTCTAGACATAAATTAATATTTTGAGAGGCATCCCTCACCTGTTTCAATTTCTTCT	420
Query	421	GTGTTGAAATGAAGTACTTAAAATTACCGTTATACATGAACTTTGTGGACTGTAAGATTT	480
Sbjct	421	GTGTTGAAATGAAGTACTTAAAATTACCGTTATACATGAACTTTGTGGACTGTAAGATTT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GTTATATATGTTCAAATGCCTTTTAGCTGGCTTTTAAATTAATATGCCTGTTTTGAGTGC	540
Sbjct	481	GTTATATATGTTCAAATGCCTTTTAGCTGGCTTTTAAATTAATATGCCTGTTTTGAGTGC	540
Query	541	TTAATACAATGTAATGNGGATTGTAAATCATACCTATTTTAAATCATTCCTTCCTGTATA	600
Sbjct	541	TTAATACAATGTAATGNGGATTGTAAATCATACCTATTTTAAATCATTCCTTCCTGTATA	600
Query	601	TTTGNACTCAGAGAGCCTTATTTTATTCTTCCAGC	635
Sbjct	601	TTTGNACTCAGAGAGCCTTATTTTATTCTTCCAGC	635

Sequence 491 matched with Sequence 134

Query= Sequence ID - 491
Length=382

nt: 382

SEQ ID NO: 134

nt: 382

ALIGNMENTS

Identities = 382/382 (100%), Gaps = 0/382 (0%)

Query	1	TTTTCTTAGAACTTTATTTTTTCTGGCCAGGCGCAGTGGCTCACACCTGTAATCCCAGCA	60
Sbjct	1	TTTTCTTAGAACTTTATTTTTTCTGGCCAGGCGCAGTGGCTCACACCTGTAATCCCAGCA	60
Query	61	CTTTGGGAGGCCAAGGCAGGTCGATCACCTGAGGTCAGGAGCTCAAGACCAGCCTGGCCA	120
Sbjct	61	CTTTGGGAGGCCAAGGCAGGTCGATCACCTGAGGTCAGGAGCTCAAGACCAGCCTGGCCA	120
Query	121	ACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGCGCATG	180
Sbjct	121	ACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGCGCATG	180
Query	181	CCTGTAATCCCANCTACTCAGGAGGCTGAGGCAGGAGAATTGTTTGAACCCGGGAGGCGG	240
Sbjct	181	CCTGTAATCCCANCTACTCAGGAGGCTGAGGCAGGAGAATTGTTTGAACCCGGGAGGCGG	240
Query	241	AGGTTGCANTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAGAGCGAAACTC	300
Sbjct	241	AGGTTGCANTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAGAGCGAAACTC	300
Query	301	CATCTCaaaaaaaaaaaaaaaaaaaaCAACCTTTATTTTTTCTGATTTTAAAAGTAATAACT	360
Sbjct	301	CATCTCAAAAAAAAAAAAAAAAAAAAAACACCTTTATTTTTTCTGATTTTAAAAGTAATAACT	360
Query	361	AGTTTGTAGAAACATTTAAAAGT	382
Sbjct	361	AGTTTGTAGAAACATTTAAAAGT	382

Sequence 492 matched with Sequence 135

Query= Sequence ID 492
Length=503

SEQ ID NO: 135

ALIGNMENTS

Identities = 503/503 (100%), Gaps = 0/503 (0%)

Query	1	ACCCTAAACATAACTTAAATTTGTTNGGAATTTGAAAGTACAGAATTTTCCTGTAATTG	60
Sbjct	1	ACCCTAAACATAACTTAAATTTGTTNGGAATTTGAAAGTACAGAATTTTCCTGTAATTG	60
Query	61	AGACTNTTTAAACTTTTGTGGTTGGAGAAGGTATTCTATTTTTTGAAAATATCTGTAAGT	120
Sbjct	61	AGACTNTTTAAACTTTTGTGGTTGGAGAAGGTATTCTATTTTTTGAAAATATCTGTAAGT	120
Query	121	TTTATCTAAATAGTAAACTCTAAGTATTCTTCCCCTTTACTTACAGCCACCCTGGGAATC	180
Sbjct	121	TTTATCTAAATAGTAAACTCTAAGTATTCTTCCCCTTTACTTACAGCCACCCTGGGAATC	180
Query	181	TGAGACTAGAGAAAATAAAGTTTGTCTCTTGTCTAAGGAGGGTCTGGTTTAGAAATCTG	240
Sbjct	181	TGAGACTAGAGAAAATAAAGTTTGTCTCTTGTCTAAGGAGGGTCTGGTTTAGAAATCTG	240
Query	241	ATTTAGACATAGAAAAATTGCAAGAAGCTTGAGGTGATTGGAAGATACGATTTTGTTATC	300
Sbjct	241	ATTTAGACATAGAAAAATTGCAAGAAGCTTGAGGTGATTGGAAGATACGATTTTGTTATC	300
Query	301	AAAGNATGTTTCTGTTTTATAGATTTTATTCATCTACAACCTCCTTATTAATATATTTAAG	360
Sbjct	301	AAAGNATGTTTCTGTTTTATAGATTTTATTCATCTACAACCTCCTTATTAATATATTTAAG	360
Query	361	AAGTCATTAACCCACCATTGATTACTTGATATAAAAGGAGAANCGGTGGTAAAAGGTGAA	420
Sbjct	361	AAGTCATTAACCCACCATTGATTACTTGATATAAAAGGAGAANCGGTGGTAAAAGGTGAA	420
Query	421	ATANAAtttttaattttttttttttaagtttaggatttttttttAAATTCTAAGAGTTT	480
Sbjct	421	ATANAATTTTAAATTTTTTTTTTTTAAAGTTTAGGATTTTTTTTAAATTCTAAGAGTTT	480

PATENT SEQUENCE ALIGNMENT

Query	481	CTGTCATTTGGGGACAATCAGAA	503
Sbjct	481	CTGTCATTTGGGGACAATCAGAA	503

Sequence 493 matched with Sequence 136

Query= Sequence ID 493

Length=576

SEQ ID NO: 136

ALIGNMENTS

Identities = 576/576 (100%), Gaps = 0/576 (0%)

Query	1	TGGGAATCATAATTNGTTAACTGAAGCTNATAAGATGAGAGCATTCANAGAGAAAAGAAC	60
Sbjct	1	TGGGAATCATAATTNGTTAACTGAAGCTNATAAGATGAGAGCATTCANAGAGAAAAGAAC	60
Query	61	GGAAAGATTGAATATCAGTTTCCCTTCTTTaaaaaaATTGTGGATATGTGATCTAGCTTC	120
Sbjct	61	GGAAAGATTGAATATCAGTTTCCCTTCTTTAAAAAAATTGTGGATATGTGATCTAGCTTC	120
Query	121	TTGAGCATCACAGTGAAGTGGCTCGTGGTAATTGATCGCTATGCTGACAATCTTATC	180
Sbjct	121	TTGAGCATCACAGTGAAGTGGCTCGTGGTAATTGATCGCTATGCTGACAATCTTATC	180
Query	181	TCCACCTATGTCATTCAATTTTCTAAGAGGCAAAATCCTTAATCAGGAGGAGAGTTTAGC	240
Sbjct	181	TCCACCTATGTCATTCAATTTTCTAAGAGGCAAAATCCTTAATCAGGAGGAGAGTTTAGC	240
Query	241	TCTAGCTAAATTTCCCTTGTCCAGCATGCTCCTGCTCCCCCAACTTGTGGAAACAGCTAA	300
Sbjct	241	TCTAGCTAAATTTCCCTTGTCCAGCATGCTCCTGCTCCCCCAACTTGTGGAAACAGCTAA	300
Query	301	AGGATTGGACTAGGAGCANAAGTTTGGAATGGTTAAAATGTAGCAACATGTGTTTCCTGA	360
Sbjct	301	AGGATTGGACTAGGAGCANAAGTTTGGAATGGTTAAAATGTAGCAACATGTGTTTCCTGA	360
Query	361	AACAAAATTCCACTATAATAaaaaaaGCATTTGAATGCTCCCTTGTAATTCTGTTGGAGC	420
Sbjct	361	AACAAAATTCCACTATAATAAAAAAAGCATTTGAATGCTCCCTTGTAATTCTGTTGGAGC	420
Query	421	TTGTTGCCTTTTTTATGACACAACCATAATCAGTGATAGACAGTAGCATAAAGAAGCAAG	480
Sbjct	421	TTGTTGCCTTTTTTATGACACAACCATAATCAGTGATAGACAGTAGCATAAAGAAGCAAG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGCAAAGCAATTAAGTAATAATAGCACTACAAAAATGTGTGCTGTACTTACCAAACACGA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGCAAAGCAATTAAGTAATAATAGCACTACAAAAATGTGTGCTGTACTTACCAAACACGA  540

Query  541  CATTTATGAATTATTANATAGGAATAAGGGGATGGT  576
          |||||||||||||||||||||||||||||||
Sbjct  541  CATTTATGAATTATTANATAGGAATAAGGGGATGGT  576
```

Sequence 494 matched with Sequence 137

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 494
Length=22

SEQ ID NO: 137	44.1	2e-11
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ALIGNMENTS

Identities = 22/22 (100%), Gaps = 0/22 (0%)

Query	1	GACCCAGCCATCTAAATAAGTT	22
Sbjct	1	GACCCAGCCATCTAAATAAGTT	22

Sequence 495 matched with Sequence 138

Query	1	TTTC
Sbjct	1	TTTC

Sequence 496 matched with Sequence 139

Query= Sequence ID 496

Length=431

SEQ ID NO: 139

ALIGNMENTS

Identities = 431/431 (100%), Gaps = 0/431 (0%)

Query	1	CTCGCTGGCGGGAGGCCACGGGCTTTCCACAGCGCGGGGGAACGGGAGGCTGCAGGATGG	60
Sbjct	1	CTCGCTGGCGGGAGGCCACGGGCTTTCCACAGCGCGGGGGAACGGGAGGCTGCAGGATGG	60
Query	61	TCAAGCTGACGGCGGAGCTGATCGAGCAGGCGGCGCAGTACACCAACGCGGTGCGCGACC	120
Sbjct	61	TCAAGCTGACGGCGGAGCTGATCGAGCAGGCGGCGCAGTACACCAACGCGGTGCGCGACC	120
Query	121	GGGAGCTGGACCTCCGGGGGTGATCTGGACCCTCTGGCATCTCTCAAATCGCTGACTTAC	180
Sbjct	121	GGGAGCTGGACCTCCGGGGGTGATCTGGACCCTCTGGCATCTCTCAAATCGCTGACTTAC	180
Query	181	CTAAGTATCCTAAGAAATCCGGTAACCAATAAGAAGCATTACAGATTGTATGTGATTTAT	240
Sbjct	181	CTAAGTATCCTAAGAAATCCGGTAACCAATAAGAAGCATTACAGATTGTATGTGATTTAT	240
Query	241	AAAGTTCCGCAAGTCATAGTACTGGATTTCAGAAAGTGAACTAAAATTTTAATCCAGG	300
Sbjct	241	AAAGTTCCGCAAGTCATAGTACTGGATTTCAGAAAGTGAACTAAAATTTTAATCCAGG	300
Query	301	TGCTGGTTTGCCAACTGACAAAAAGAAAGGTGGGCCATCTCCAGGGGATGTAAAAGCAAT	360
Sbjct	301	TGCTGGTTTGCCAACTGACAAAAAGAAAGGTGGGCCATCTCCAGGGGATGTAAAAGCAAT	360
Query	361	CAAGAATGCCATAGCAAATGCTTNAACTCTGGCTGAAGTGGANAGGCTGAANGGGTTGCT	420
Sbjct	361	CAAGAATGCCATAGCAAATGCTTNAACTCTGGCTGAAGTGGANAGGCTGAANGGGTTGCT	420
Query	421	GCAGTCTGGTC	431
Sbjct	421	GCAGTCTGGTC	431

Sequence 497 matched with Sequence 140

Query= Sequence ID 497

Length=606

SEQ ID NO: 140

ALIGNMENTS

Identities = 606/606 (100%), Gaps = 0/606 (0%)

Query	1	GAAGACCTCACATCTGAGAGCTCATCTGCGTTGGCATTCTGGAGAACGCCCTTTTGT	60
Sbjct	1	GAAGACCTCACATCTGAGAGCTCATCTGCGTTGGCATTCTGGAGAACGCCCTTTTGT	60
Query	61	TAACTGGATGTACTGTGGTAAAAGATTTACTCGAAGTGATGAATTACAGAGGCACAGAAG	120
Sbjct	61	TAACTGGATGTACTGTGGTAAAAGATTTACTCGAAGTGATGAATTACAGAGGCACAGAAG	120
Query	121	AACACATACAGGTGAGAAGAAATTTGTTTGTCCAGAATGTTCAAAACGCTTTATGANAAG	180
Sbjct	121	AACACATACAGGTGAGAAGAAATTTGTTTGTCCAGAATGTTCAAAACGCTTTATGANAAG	180
Query	181	TGACCACCTTGCCAAACATATTAACACACCAGAATAAAAAAGGTATTC	240
Sbjct	181	TGACCACCTTGCCAAACATATTAACACACCAGAATAAAAAAGGTATTC	240
Query	241	TACAGTGCTGGCATCTGTGGAAGCTGCGCGAGATGATACTTTGATTACTGCAGGAGGAAC	300
Sbjct	241	TACAGTGCTGGCATCTGTGGAAGCTGCGCGAGATGATACTTTGATTACTGCAGGAGGAAC	300
Query	301	AACGCTTATCCTTGCAAATATTCAACAAGGTTCTGTTTCAGGGATAGGAACTGTTAATAC	360
Sbjct	301	AACGCTTATCCTTGCAAATATTCAACAAGGTTCTGTTTCAGGGATAGGAACTGTTAATAC	360
Query	361	TTCCGCCACCAGCAATCAAGATATCCTTACCAACACTGAAATACCTTTACAGCTTGTCAC	420
Sbjct	361	TTCCGCCACCAGCAATCAAGATATCCTTACCAACACTGAAATACCTTTACAGCTTGTCAC	420
Query	421	AGTTTCTGGAAATGAGACAATGGGAGTAAATATTACACAAATACTTATTCATTGNGGTTA	480
Sbjct	421	AGTTTCTGGAAATGAGACAATGGGAGTAAATATTACACAAATACTTATTCATTGNGGTTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTTTTATACAGTAGTGAGAAGAATATTG TTCCTAAGTTCTTAGATATC	540
Sbjct	481	TTTTTATACAGTAGTGAGAAGAATATTG TTCCTAAGTTCTTAGATATCTTTTTTTGGATG	540
Query	541	TGCAAAAATTTTGGATTGACAGTAACTTGGGTATACATGACACTGAAATGCCTTACTTT	600
Sbjct	541	TGCAAAAATTTTGGATTGACAGTAACTTGGGTATACATGACACTGAAATGCCTTACTTT	600
Query	601	GGATGA	606
Sbjct	601	GGATGA	606

Length=564

Identities = 564/564 (100%), Gaps = 0/564 (0%)

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PATENT SEQUENCE ALIGNMENT

```
Query  481  GGGTGTACGGNATTTCTTGACTCTGGGAACAGCTGCTACCCCCAAGACTTGCCACGTTGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGGTGTACGGNATTTCTTGACTCTGGGAACAGCTGCTACCCCCAAGACTTGCCACGTTGT  540

Query  541  TCTGCCCTCAAATGGAATTAAGTG  564
          ||||||||||||||||
Sbjct  541  TCTGCCCTCAAATGGAATTAAGTG  564
```

Sequence 500 matched with Sequence 142

Query= Sequence ID - 500
Length=390

nt: 390

SEQ ID NO: 142

nt: 390

ALIGNMENTS

Identities = 390/390 (100%), Gaps = 0/390 (0%)

Query	1	GGAATATGGTCAGGATCTTCTCCATACTGTCTTCAAGAATGGCAAGGTGACAAAAAGCTA	60
Sbjct	1	GGAATATGGTCAGGATCTTCTCCATACTGTCTTCAAGAATGGCAAGGTGACAAAAAGCTA	60
Query	61	TTCATTTGATGAAATAAGAAAAAATGCACAGCTGAATATTGAACTGGAAGCAGCACATCA	120
Sbjct	61	TTCATTTGATGAAATAAGAAAAAATGCACAGCTGAATATTGAACTGGAAGCAGCACATCA	120
Query	121	TTAGGCTTTATGACTGGgtgtgtgttgtgtgtatgtaatacataatgtttattgtacana	180
Sbjct	121	TTAGGCTTTATGACTGGGTGTGTGTTGTGTGTATGTAATACATAATGTTTATTGTACANA	180
Query	181	tgtgtgggggtttgtgttttATGATACATTACAGCCAAATTATTTGTTGGTTNATGGACAT	240
Sbjct	181	TGTGTGGGGTTTGTGTTTTATGATACATTACAGCCAAATTATTTGTTGGTTNATGGACAT	240
Query	241	ACTGCCCTTTCAttttttCTTTTCCAGTGTTTAGGTGATCTCAAATTAAGAAATGCATT	300
Sbjct	241	ACTGCCCTTTCATTTTTTTCTTTTCCAGTGTTTAGGTGATCTCAAATTAAGAAATGCATT	300
Query	301	TAACCATGTAAAANATGANTGCTAAAGTCAGCTTTTTAGGGCCCTTTGCCAATAGGTANT	360
Sbjct	301	TAACCATGTAAAANATGANTGCTAAAGTCAGCTTTTTAGGGCCCTTTGCCAATAGGTANT	360
Query	361	CATTCAATCTGGTATTGATCTTTTCACAAA	390
Sbjct	361	CATTCAATCTGGTATTGATCTTTTCACAAA	390

Sequence 502 matched with Sequence 143

Query= Sequence ID 502

Length=546

SEQ ID NO: 143

ALIGNMENTS

Identities = 546/546 (100%), Gaps = 0/546 (0%)

Query	1	ACCCGCCATCTTCCAGTAATTCGCCAAAATGACGAACACAAAGGGAAAGAGGAGAGGCAC	60
Sbjct	1	ACCCGCCATCTTCCAGTAATTCGCCAAAATGACGAACACAAAGGGAAAGAGGAGAGGCAC	60
Query	61	CCGATATATGTTCTCTAGGCCTTTTANAAAACATGGAGTTGTTCTTTGGCCACATATAT	120
Sbjct	61	CCGATATATGTTCTCTAGGCCTTTTANAAAACATGGAGTTGTTCTTTGGCCACATATAT	120
Query	121	GCGAATCTATAAGAAAGGTGATATTGTAGACATCAAGGGAATGGGTACTGTTCAAAAAGG	180
Sbjct	121	GCGAATCTATAAGAAAGGTGATATTGTAGACATCAAGGGAATGGGTACTGTTCAAAAAGG	180
Query	181	AATGCCCCACAAGTGTTACCATGGCAAAACTGGAAGAGTCTACAATGTTACCCAGCATGC	240
Sbjct	181	AATGCCCCACAAGTGTTACCATGGCAAAACTGGAAGAGTCTACAATGTTACCCAGCATGC	240
Query	241	TGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATGT	300
Sbjct	241	TGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATGT	300
Query	301	GCGTATTGAGCACATTAAGCACTCTAAGAGCCGAGATAGCTTCCTGAAACGTGTGAAGGA	360
Sbjct	301	GCGTATTGAGCACATTAAGCACTCTAAGAGCCGAGATAGCTTCCTGAAACGTGTGAAGGA	360
Query	361	AAATGATCAGAAAAAGAAAGAAGCCAAAGAGAAAGGTACCTGGGTTCAACTAAAGCGCCA	420
Sbjct	361	AAATGATCAGAAAAAGAAAGAAGCCAAAGAGAAAGGTACCTGGGTTCAACTAAAGCGCCA	420
Query	421	GCCTGCTCCACCCAGAGAAGCACACTTTGTGAGAACCAATGGGAAGGAGCCTGAGCTGCT	480
Sbjct	421	GCCTGCTCCACCCAGAGAAGCACACTTTGTGAGAACCAATGGGAAGGAGCCTGAGCTGCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGAACCTATTCCCTATGAATTCATGGCATAATAGGTGTTaaaaaaaaaaaaTAAAGGACC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGAACCTATTCCCTATGAATTCATGGCATAATAGGTGTTAAAAAAAAAAAAATAAAGGACC  540

Query  541  TCTGGG  546
          |||||
Sbjct  541  TCTGGG  546
```

Sequence 503 matched with Sequence 144

Query= Sequence ID - 503 nt: 109
Length=109

SEQ ID NO: 144 nt: 109

ALIGNMENTS

Identities = 109/109 (100%), Gaps = 0/109 (0%)

Query	1	ACATTTTCCGGNCCTTTTGCCATACACAGTTACAGAGATCAGTCAAATCCATACCACCAC	60
Sbjct	1	ACATTTTCCGGNCCTTTTGCCATACACAGTTACAGAGATCAGTCAAATCCATACCACCAC	60
Query	61	TGAGATCTCATTTATTGCCACAGATGCACAAAATAAATAACCCAAAATC	109
Sbjct	61	TGAGATCTCATTTATTGCCACAGATGCACAAAATAAATAACCCAAAATC	109

Sequence 504 matched with Sequence 145

Query= Sequence ID - 504
Length=374

nt: 374

SEQ ID NO: 145

nt: 374

ALIGNMENTS

Identities = 374/374 (100%), Gaps = 0/374 (0%)

Query	1	CCAGCAACGACCCATACCTCAGACCCGACGGCCCGAGCGGAGCGCGCCCTGCCCTGGCG	60
Sbjct	1	CCAGCAACGACCCATACCTCAGACCCGACGGCCCGAGCGGAGCGCGCCCTGCCCTGGCG	60
Query	61	CAGCCAGAGCCGCCGGGTGCCCGCTGCAGTTTCTTGGGACATAGGAGCGCAAAGAAGCTA	120
Sbjct	61	CAGCCAGAGCCGCCGGGTGCCCGCTGCAGTTTCTTGGGACATAGGAGCGCAAAGAAGCTA	120
Query	121	CAGCCTGGACTTACCACCACTAAACTGCGAGAGAAGCTAAACGTGTTTATTTCCCTTAA	180
Sbjct	121	CAGCCTGGACTTACCACCACTAAACTGCGAGAGAAGCTAAACGTGTTTATTTCCCTTAA	180
Query	181	ATTATTTTGTAAATGGTAGCTTTTTCTACATCTTACTCCTGTTGATGCAGCTAAGGTACA	240
Sbjct	181	ATTATTTTGTAAATGGTAGCTTTTTCTACATCTTACTCCTGTTGATGCAGCTAAGGTACA	240
Query	241	TTTGTAaaaaagaaaaaaaaaCCAGACTTTTCANACAAACCCTTTGTATTGTANATAAGAGG	300
Sbjct	241	TTTGTAATAAAGAAAAAAACCAGACTTTTCANACAAACCCTTTGTATTGTANATAAGAGG	300
Query	301	AAAAGACTGAGCATGCTCACTTTTTTATATTAATTTTTACAGTATTTGTAAGAATAAAGC	360
Sbjct	301	AAAAGACTGAGCATGCTCACTTTTTTATATTAATTTTTACAGTATTTGTAAGAATAAAGC	360
Query	361	ANCATTTGAAATCG	374
Sbjct	361	ANCATTTGAAATCG	374

Sequence 505 matched with Sequence 146

Query= Sequence ID 505
Length=357

SEQ ID NO: 146

ALIGNMENTS

Identities = 357/357 (100%), Gaps = 0/357 (0%)

Query	1	GTACAGGAGGTAAATTGGATACCCCATCTAAGGGGATCTGTGAGACCAGGTAGTTATTTG	60
Sbjct	1	GTACAGGAGGTAAATTGGATACCCCATCTAAGGGGATCTGTGAGACCAGGTAGTTATTTG	60
Query	61	GAATGAAAGAGTAAGATATTAAACCAGCCAGCATGTCAACAGGTGGGTGATAGTCTTGTT	120
Sbjct	61	GAATGAAAGAGTAAGATATTAAACCAGCCAGCATGTCAACAGGTGGGTGATAGTCTTGTT	120
Query	121	CTCACAGACAACAGATGGCCATCATCTTAAACAACATTTATGTTAACCAGCAGATAAGG	180
Sbjct	121	CTCACAGACAACAGATGGCCATCATCTTAAACAACATTTATGTTAACCAGCAGATAAGG	180
Query	181	GACTCCTGCATTGTCAGTGGACTTTGAGCCTGAGTTTTTCTACTTGCATAGGTGAAAGTG	240
Sbjct	181	GACTCCTGCATTGTCAGTGGACTTTGAGCCTGAGTTTTTCTACTTGCATAGGTGAAAGTG	240
Query	241	GACTGCAATGCTAGTATAAATGCCGTATGATGACTAGTACCCCTTAGGGAGCTCCAGTTT	300
Sbjct	241	GACTGCAATGCTAGTATAAATGCCGTATGATGACTAGTACCCCTTAGGGAGCTCCAGTTT	300
Query	301	GCCTTCCTGGGGAACACAGACCCCAAGTGTAATTCCTGAGGACAGCCCGACTTCT	357
Sbjct	301	GCCTTCCTGGGGAACACAGACCCCAAGTGTAATTCCTGAGGACAGCCCGACTTCT	357

Sequence 506 matched with Sequence 147

Query= Sequence ID 506
Length=293

SEQ ID NO: 147

ALIGNMENTS

Identities = 293/293 (100%), Gaps = 0/293 (0%)

Query	1	GTTACTGTGAGCCTGTCAGTAGTGGGTACCAATCTTTTGTGACATATTGTCATGCTGAGG	60
Sbjct	1	GTTACTGTGAGCCTGTCAGTAGTGGGTACCAATCTTTTGTGACATATTGTCATGCTGAGG	60
Query	61	TGNGACACCTGCTGCACTCATCTGATGTAAAACCATCCCANAGCTGGCGAGAGGATGGAG	120
Sbjct	61	TGNGACACCTGCTGCACTCATCTGATGTAAAACCATCCCANAGCTGGCGAGAGGATGGAG	120
Query	121	CTGGGTGGAAACTGCTTTGCACTATCGTTTGCTTGGTGTGTTTGTGTTTAAACGCACAATTG	180
Sbjct	121	CTGGGTGGAAACTGCTTTGCACTATCGTTTGCTTGGTGTGTTTGTGTTTAAACGCACAATTG	180
Query	181	CTTGACAGTAAACTGTCTTCTGTACTATTAACTGTAAAATGGAATTTTGACTGATTTG	240
Sbjct	181	CTTGACAGTAAACTGTCTTCTGTACTATTAACTGTAAAATGGAATTTTGACTGATTTG	240
Query	241	TTACAATAATATAACTCTGAGATGTGTGaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	293
Sbjct	241	TTACAATAATATAACTCTGAGATGTGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	293

Sequence 507 matched with Sequence 148

Query= Sequence ID - 507
Length=521

nt: 521

SEQ ID NO: 148

nt: 521

ALIGNMENTS

Identities = 521/521 (100%), Gaps = 0/521 (0%)

Query	1	CTGCGGTGGAGCCGCCACCAAAATGCAGATTTTCGTGAAAACCCTTACGGGGAAGACCAT	60
Sbjct	1	CTGCGGTGGAGCCGCCACCAAAATGCAGATTTTCGTGAAAACCCTTACGGGGAAGACCAT	60
Query	61	CACCCTCGAGGTTGAACCCTCGGATACGATAGAAAATGTAAAGGCCAAGATCCAGGATAA	120
Sbjct	61	CACCCTCGAGGTTGAACCCTCGGATACGATAGAAAATGTAAAGGCCAAGATCCAGGATAA	120
Query	121	GGAAGGAATTCCTCCTGATCAGCAGAGACTGATCTTTGCTGGCAAGCAGCTGGAAGATGG	180
Sbjct	121	GGAAGGAATTCCTCCTGATCAGCAGAGACTGATCTTTGCTGGCAAGCAGCTGGAAGATGG	180
Query	181	ACGTACTTTGTCTGACTACAATATTCAAAAAGGAGTCTACTCTTCATCTTGTGTTGAGACT	240
Sbjct	181	ACGTACTTTGTCTGACTACAATATTCAAAAAGGAGTCTACTCTTCATCTTGTGTTGAGACT	240
Query	241	TCGTGGTGGTGCTaagaaaaggaagaagaagtcttacaccactcccaagaagaataagca	300
Sbjct	241	TCGTGGTGGTGCTAAGAAAAGGAAGAAGAAGTCTTACACCACTCCCAAGAAGAATAAGCA	300
Query	301	caagagaaagaagGTTAAGCTGGCTGTCCTGAAATATTATAAGGTGGATGAGAATGGCAA	360
Sbjct	301	CAAGAGAAAGAAGGTTAAGCTGGCTGTCCTGAAATATTATAAGGTGGATGAGAATGGCAA	360
Query	361	AATTAGTCGCCTTCGTCGAGAGTGCCCTTCTGATGAATGTGGTGCTGGGGTGTTTATGGC	420
Sbjct	361	AATTAGTCGCCTTCGTCGAGAGTGCCCTTCTGATGAATGTGGTGCTGGGGTGTTTATGGC	420
Query	421	AAGTCACTTTGACAGACATTATTGTGGCAAATGTTGTCTGACTTACTGTTTCAACAAACC	480
Sbjct	421	AAGTCACTTTGACAGACATTATTGTGGCAAATGTTGTCTGACTTACTGTTTCAACAAACC	480

```

Query    481  AGAAGACAAGTAACTGTATGAGTTAATAAAAGACATGAACT  521
        |||
Sbjct    481  AGAAGACAAGTAACTGTATGAGTTAATAAAAGACATGAACT  521

```

Sequence 508 matched with Sequence 149

Query= Sequence ID 508

Length=470

SEQ ID NO: 149

ALIGNMENTS

Identities = 470/470 (100%), Gaps = 0/470 (0%)

Query	1	AAGCTCATGATTTTAAATGTATTTTCTAATAAACTATACTCCCATTTAAAAATCACCAA	60
Sbjct	1	AAGCTCATGATTTTAAATGTATTTTCTAATAAACTATACTCCCATTTAAAAATCACCAA	60
Query	61	TACCTTAATGTTTCAATTATATAAGCTAATTAATAAAATAAAGGCTGGGCGTGGTGGCTCAC	120
Sbjct	61	TACCTTAATGTTTCAATTATATAAGCTAATTAATAAAATAAAGGCTGGGCGTGGTGGCTCAC	120
Query	121	TTTGGAAGACCGAGGCAGGCAGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGCCCAA	180
Sbjct	121	TTTGGAAGACCGAGGCAGGCAGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGCCCAA	180
Query	181	CATGGAGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGCACATGCC	240
Sbjct	181	CATGGAGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGCACATGCC	240
Query	241	CGTAATCCCAGCTACTGGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGCAGGG	300
Sbjct	241	CGTAATCCCAGCTACTGGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGCAGGG	300
Query	301	GCTGCAGTGAGCCGAGATCATGCCATTGCACTCCAGTCTGGGCAACAATAGTGGAACTCC	360
Sbjct	301	GCTGCAGTGAGCCGAGATCATGCCATTGCACTCCAGTCTGGGCAACAATAGTGGAACTCC	360
Query	361	ATCTCaaaaataataaaaaaaaaataaaataaaaaataaaattcaaacctaaaataGATGCTC	420
Sbjct	361	ATCTCAAAAATAATAAAAAAATAAAAATAAAAATAAAATTCAAACCTAAAATAGATGCTC	420
Query	421	TACTTCAGGAGTGGGCAAATTAATCACCTGCATCCTtttttttGGGCTTTC	470
Sbjct	421	TACTTCAGGAGTGGGCAAATTAATCACCTGCATCCTTTTTTTGGGCTTTC	470

Sequence 509 matched with Sequence 150

Query= Sequence ID - 509
Length=575

nt: 575

SEQ ID NO: 150

nt: 575

ALIGNMENTS

Identities = 575/575 (100%), Gaps = 0/575 (0%)

Query	1	tttttttCTAAATGGNGATTACTAATATATGTGGAGACTATTAATCTCTTTTCTGTTGCC	60
Sbjct	1	TTTTTTTCTAAATGGNGATTACTAATATATGTGGAGACTATTAATCTCTTTTCTGTTGCC	60
Query	61	ATTAGTTCATTTTCCCCAAAAGCCAATACATGTTCAATACaaaaatgaattataaaata	120
Sbjct	61	ATTAGTTCATTTTCCCCAAAAGCCAATACATGTTCAATACAAAAATGAATTATAAAATA	120
Query	121	taagttaaaagaaaaacataaaaaCCCTACAATCTTACCCACCCAGACAACACTACTATTAAT	180
Sbjct	121	TAAGTTAAAAGAAAAACATAAAACCCTACAATCTTACCCACCCAGACAACACTACTATTAAT	180
Query	181	ACCTTAGTATTAACATATACACATCATGTATATGTATAAATTTATCTTAAACAAAAATAA	240
Sbjct	181	ACCTTAGTATTAACATATACACATCATGTATATGTATAAATTTATCTTAAACAAAAATAA	240
Query	241	AATTATTCTTTACATATTGTTTTAAACCTATTTATCTGGCCAGGTGCCGTGGCTCACGC	300
Sbjct	241	AATTATTCTTTACATATTGTTTTAAACCTATTTATCTGGCCAGGTGCCGTGGCTCACGC	300
Query	301	TTGTAATCCCAGCACTTTGGGAGGCTGAGGCACGTGGATCACCTGAGGTCAGGAATTCGA	360
Sbjct	301	TTGTAATCCCAGCACTTTGGGAGGCTGAGGCACGTGGATCACCTGAGGTCAGGAATTCGA	360
Query	361	GACCAGCCCAGCCAACATGGTGAAACCCTGTCTCTAATGGTTTAAATACCAAAAAATTAG	420
Sbjct	361	GACCAGCCCAGCCAACATGGTGAAACCCTGTCTCTAATGGTTTAAATACCAAAAAATTAG	420
Query	421	CTGGGCATGGTGGCACATGCCTGTAATATCAGCTAACATGGGAGGCTGAGGCAGGAGAAT	480
Sbjct	421	CTGGGCATGGTGGCACATGCCTGTAATATCAGCTAACATGGGAGGCTGAGGCAGGAGAAT	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 CACTTGAACCANGGAGGGGGAGGTTGCAGTGAGCCGAAATCACACCACTTCACTGCAGCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 CACTTGAACCANGGAGGGGGAGGTTGCAGTGAGCCGAAATCACACCACTTCACTGCAGCC 540

Query 541 TGGGCAACAAAGCAAGACTGTCTCAAAAAGAAAAA 575
          ||||||||||||||||||||||||||||
Sbjct 541 TGGGCAACAAAGCAAGACTGTCTCAAAAAGAAAAA 575
```

Sequence 510 matched with Sequence 151

Query= Sequence ID 510

Length=430

SEQ ID NO: 151

ALIGNMENTS

Identities = 430/430 (100%), Gaps = 0/430 (0%)

Query	1	CACTGTCATTCCCAGGAGGCTTTGGAGTCAGAACTGGATTCAAATTCTGACTNTATGTTG	60
Sbjct	1	CACTGTCATTCCCAGGAGGCTTTGGAGTCAGAACTGGATTCAAATTCTGACTNTATGTTG	60
Query	61	TGTGACTTGGGCCAATAGCTTCTTTNTGTGCCTCAGTTTCTTTAGCTGTAAATANACGGG	120
Sbjct	61	TGTGACTTGGGCCAATAGCTTCTTTNTGTGCCTCAGTTTCTTTAGCTGTAAATANACGGG	120
Query	121	TAGGTCACCCCTTACCCCATAGGTTATGGGGAAAGTTACAGAAAATGGTCAGCTGGGCNC	180
Sbjct	121	TAGGTCACCCCTTACCCCATAGGTTATGGGGAAAGTTACAGAAAATGGTCAGCTGGGCNC	180
Query	181	AGTGGCTCAAGCCTGTGGTCCCAGCNCCTTGGGAGGCCAAGGTGAGCAGATTGCTTGAGC	240
Sbjct	181	AGTGGCTCAAGCCTGTGGTCCCAGCNCCTTGGGAGGCCAAGGTGAGCAGATTGCTTGAGC	240
Query	241	CCAGGAGTTTGACACCAGTNTGGCAACGTGACGAAACCCTATCNCTGTGAAAAATACAAA	300
Sbjct	241	CCAGGAGTTTGACACCAGTNTGGCAACGTGACGAAACCCTATCNCTGTGAAAAATACAAA	300
Query	301	AAATTAGCCAGGCATGGTGGTGTGTGTCTGTGGTTCCAGCTGCTTGAGAGTTTGAAGTGG	360
Sbjct	301	AAATTAGCCAGGCATGGTGGTGTGTGTCTGTGGTTCCAGCTGCTTGAGAGTTTGAAGTGG	360
Query	361	GAGGATCACCTGAGCCCAGAAGGTCGAGGCTGCAGTGAGCTGTGATCGCGTCACTGCACT	420
Sbjct	361	GAGGATCACCTGAGCCCAGAAGGTCGAGGCTGCAGTGAGCTGTGATCGCGTCACTGCACT	420
Query	421	CCAGCCTGGC	430
Sbjct	421	CCAGCCTGGC	430

Sequence 512 matched with Sequence 152

Query= Sequence ID 512
Length=631

SEQ ID NO: 152

ALIGNMENTS

Identities = 631/631 (100%), Gaps = 0/631 (0%)

Query	1	GTGAGCGGTGGTGGTTTATTCTTCCGTGGAGTTAAGGGCTCCGTGGACATCTCAGGTCTT	60
Sbjct	1	GTGAGCGGTGGTGGTTTATTCTTCCGTGGAGTTAAGGGCTCCGTGGACATCTCAGGTCTT	60
Query	61	CAGGGTCTTCCATCTGGAACATATAAAAGTTCAGAAAACATGTCTCGAAGATATGACTCC	120
Sbjct	61	CAGGGTCTTCCATCTGGAACATATAAAAGTTCAGAAAACATGTCTCGAAGATATGACTCC	120
Query	121	AGGACCACTATATTTTCTCCAGAAGGTCGCTTATACCAAGTTGAATATGCCATGGAAGCT	180
Sbjct	121	AGGACCACTATATTTTCTCCAGAAGGTCGCTTATACCAAGTTGAATATGCCATGGAAGCT	180
Query	181	ATTGGACATGCAGGCACCTGTTTGGGAATTTTAGCAAATGATGGTGTGTTTGCTTGCAGCA	240
Sbjct	181	ATTGGACATGCAGGCACCTGTTTGGGAATTTTAGCAAATGATGGTGTGTTTGCTTGCAGCA	240
Query	241	GAGAGACNCAACATCCACAAGCTTCTTGATGAAGTCtttttttCTGAAAAAATTTATAAA	300
Sbjct	241	GAGAGACNCAACATCCACAAGCTTCTTGATGAAGCTTTTTTTTCTGAAAAAATTTATAAA	300
Query	301	CTCAATGAGGACATGGCTTGCAAGTGTGGCAGGCATAACTTCTGATGCTAATGTTCTGACT	360
Sbjct	301	CTCAATGAGGACATGGCTTGCAAGTGTGGCAGGCATAACTTCTGATGCTAATGTTCTGACT	360
Query	361	AATGAACTAAGGCTCATTGCTCAAAGGTATTTATTACAGTATCAGGAGCCAATACCTTGT	420
Sbjct	361	AATGAACTAAGGCTCATTGCTCAAAGGTATTTATTACAGTATCAGGAGCCAATACCTTGT	420
Query	421	GAGCAGTTGGTTACAGCGCTGTGTGATATCAAACAAGCTTATACACAATTTGGAGGAAAA	480
Sbjct	421	GAGCAGTTGGTTACAGCGCTGTGTGATATCAAACAAGCTTATACACAATTTGGAGGAAAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CGTCCCTTTGGTGTTTCATTGCTGTACATTGGCTGGGATAAGCACTATGGCTTTCAGCTC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CGTCCCTTTGGTGTTTCATTGCTGTACATTGGCTGGGATAAGCACTATGGCTTTCAGCTC  540

Query  541  TATCAGAGTGACCCTAGTGGAATTTCGGGGGATGGGAAGGCCACATGCATTGGAAATAAT  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TATCAGAGTGACCCTAGTGGAATTTCGGGGGATGGGAAGGCCACATGCATTGGAAATAAT  600

Query  601  ANCGCTGCAGCTGTGTCAATGTTGAAACAAG  631
          |||||||||||||||||||||||||||
Sbjct  601  ANCGCTGCAGCTGTGTCAATGTTGAAACAAG  631
```

Sequence 513 matched with Sequence 153

Query= Sequence ID 513

Length=646

SEQ ID NO: 153

ALIGNMENTS

Identities = 646/646 (100%), Gaps = 0/646 (0%)

Query	1	tttttttttttATAAACTCCAATCATTTCAGAGCTACTTAGCTCAGCATCtttttttttCC	60
Sbjct	1	TTTTTTTTTTATAAACTCCAATCATTTCAGAGCTACTTAGCTCAGCATCTTTTTTTTCC	60
Query	61	ACGCTCTTAAGTTGTGTTTATACATTTTGTATACAGTTAGATTGTTTTGTTCACATTCTT	120
Sbjct	61	ACGCTCTTAAGTTGTGTTTATACATTTTGTATACAGTTAGATTGTTTTGTTCACATTCTT	120
Query	121	CATTCTATCCTGGGATCCCCAACCACCTAAGTGGATTTTTTGATAATTGTCATGCTTTA	180
Sbjct	121	CATTCTATCCTGGGATCCCCAACCACCTAAGTGGATTTTTTGATAATTGTCATGCTTTA	180
Query	181	AGGATAACTCTTCATTCTGNAAAGGGCTATGGGTTTTGGCAAATGCAGAGTCATGTATCC	240
Sbjct	181	AGGATAACTCTTCATTCTGNAAAGGGCTATGGGTTTTGGCAAATGCAGAGTCATGTATCC	240
Query	241	AAGATTACAATATCGCACAGAAGAGTTTCATCACTATATAAACTCACCAGTCTTCCTCC	300
Sbjct	241	AAGATTACAATATCGCACAGAAGAGTTTCATCACTATATAAACTCACCAGTCTTCCTCC	300
Query	301	TATTCAACCATCTCCATGCCTTCTTCCCAGCCCTAACTCCTTAAAACCACTCATATCTTT	360
Sbjct	301	TATTCAACCATCTCCATGCCTTCTTCCCAGCCCTAACTCCTTAAAACCACTCATATCTTT	360
Query	361	ACTATTGCTATAGTATTGCCTCTTCCACCATGTCATATAAATGGAAACATACAGTATTAG	420
Sbjct	361	ACTATTGCTATAGTATTGCCTCTTCCACCATGTCATATAAATGGAAACATACAGTATTAG	420
Query	421	TCTTCTCAAACCTAGTTTCTTTTACCTAACAACATGCATTTAAGATTCATAGTGTCTTTTA	480
Sbjct	421	TCTTCTCAAACCTAGTTTCTTTTACCTAACAACATGCATTTAAGATTCATAGTGTCTTTTA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATGACTTGATAGATTATTTCTTTGTAGCTGAATAATATTGCATCTTATAGATGTAACCGT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATGACTTGATAGATTATTTCTTTGTAGCTGAATAATATTGCATCTTATAGATGTAACCGT  540

Query  541  TTGTATATCCATATTTTCTCACAGCCTATGACTTGNCTTTTGATTCTCTGAACAGGCCAT  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TTGTATATCCATATTTTCTCACAGCCTATGACTTGNCTTTTGATTCTCTGAACAGGCCAT  600

Query  601  TCACAAAGCAGAAGTTTAAATTTTATAAAGCTAATGNATCAACTT  646
          |||||||||||||||||||||||||||||||||||||||
Sbjct  601  TCACAAAGCAGAAGTTTAAATTTTATAAAGCTAATGNATCAACTT  646
```

Sequence 515 matched with Sequence 154

Query= Sequence ID 515
Length=69

SEQ ID NO: 154

ALIGNMENTS

Identities = 69/69 (100%), Gaps = 0/69 (0%)

```
Query   1   CCTGGATGACAGCATATCTGTTTATAGCTCAGTTTACTGAATACTTTAAGCCCACTGTTG   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1   CCTGGATGACAGCATATCTGTTTATAGCTCAGTTTACTGAATACTTTAAGCCCACTGTTG   60

Query   61   AAACCTGCT   69
          |||||||
Sbjct   61   AAACCTGCT   69
```

Sequence 518 matched with Sequence 155

Query= Sequence ID - 518
Length=502

nt: 502

SEQ ID NO: 155

nt: 502

ALIGNMENTS

Identities = 499/499 (100%), Gaps = 0/499 (0%)

Query	1	GATGCATGTCCAGCATAGGCAGGATTGCTCGGTGGTGAGAAGGTTAGGTCCGGCTCAGAC	60
Sbjct	1	GATGCATGTCCAGCATAGGCAGGATTGCTCGGTGGTGAGAAGGTTAGGTCCGGCTCAGAC	60
Query	61	TGAATAAGAAGAGATAAAATTTGCCTTAAAACTTACCTGGCAGTGGCTTTGCTGCACGGT	120
Sbjct	61	TGAATAAGAAGAGATAAAATTTGCCTTAAAACTTACCTGGCAGTGGCTTTGCTGCACGGT	120
Query	121	CTGAAACACCTGTTCCCACCCTCTTGACCGAAATTTCTTTGTGACACAGAGAAGGGCAA	180
Sbjct	121	CTGAAACACCTGTTCCCACCCTCTTGACCGAAATTTCTTTGTGACACAGAGAAGGGCAA	180
Query	181	AGGTCTGAGCCCAGAGTTGACGGAGGGAGTATTTTCAGGGTTCACTTCAGGGGCTCCCAA	240
Sbjct	181	AGGTCTGAGCCCAGAGTTGACGGAGGGAGTATTTTCAGGGTTCACTTCAGGGGCTCCCAA	240
Query	241	GCGACAAGATCGTTAGGGAGAGAGGCCAGGGTGGGGACTGGGAATTTAAGGAGAGCTGG	300
Sbjct	241	GCGACAAGATCGTTAGGGAGAGAGGCCAGGGTGGGGACTGGGAATTTAAGGAGAGCTGG	300
Query	301	GAACGGATCCCTTAGGTTTCAGGAAGCTTCTGTGCAAGCTGCGAGGATGGCTTGGGCCGAA	360
Sbjct	301	GAACGGATCCCTTAGGTTTCAGGAAGCTTCTGTGCAAGCTGCGAGGATGGCTTGGGCCGAA	360
Query	361	GGGTTGCTCTGCCC GCCGCTAGCTGTGAGCTGAGCAAAGCCCTGGGCTCACAGCACCC	420
Sbjct	361	GGGTTGCTCTGCCC GCCGCTAGCTGTGAGCTGAGCAAAGCCCTGGGCTCACAGCACCC	420
Query	421	CAAAAGCCTGTGGCTTCAGTCCTGCGTCTGCACCACACATTCAAAAGGATCGTTTTGTTT	480
Sbjct	421	CAAAAGCCTGTGGCTTCAGTCCTGCGTCTGCACCACACATTCAAAAGGATCGTTTTGTTT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TGTTTTTAAAGAAAGGTGA	499
Sbjct	481	TGTTTTTAAAGAAAGGTGA	499

Sequence 519 matched with Sequence 156

Query= Sequence ID 519
Length=373

SEQ ID NO: 156

ALIGNMENTS

Identities = 373/373 (100%), Gaps = 0/373 (0%)

Query	1	CTGCGATNGAGTTTTGAGAGGAAGGANTAAAGTNCTCATCTCNGACGGTGAGAAAGATCA	60
Sbjct	1	CTGCGATNGAGTTTTGAGAGGAAGGANTAAAGTNCTCATCTCNGACGGTGAGAAAGATCA	60
Query	61	TNACTAAGGAAACGCAGGGTTGGAAGCAGTGCTGANTGTCCAGTTGAGTTTCATGANCAA	120
Sbjct	61	TNACTAAGGAAACGCAGGGTTGGAAGCAGTGCTGANTGTCCAGTTGAGTTTCATGANCAA	120
Query	121	ACATTTGCTGTGGGACCAGTTTTTCATGGNGGTTTGTCAATTTGTCCAGCTGCCTGGAGCT	180
Sbjct	121	ACATTTGCTGTGGGACCAGTTTTTCATGGNGGTTTGTCAATTTGTCCAGCTGCCTGGAGCT	180
Query	181	GCTTGGTTGAAGGCACAGAATAATCAGGATTAATTGTTNAACTTGTATGAATTTCTTTAT	240
Sbjct	181	GCTTGGTTGAAGGCACAGAATAATCAGGATTAATTGTTNAACTTGTATGAATTTCTTTAT	240
Query	241	TTTAAATAGGAATAATATCTGCCTTGGGAGCAAGTTGTAAGAGTTAACTGAAAGCTTNA	300
Sbjct	241	TTTAAATAGGAATAATATCTGCCTTGGGAGCAAGTTGTAAGAGTTAACTGAAAGCTTNA	300
Query	301	GGAAAACTTTCCCTTGCTATTTAAGTAGGGCTTTACAAGTTACAATTCTATCACAGTTT	360
Sbjct	301	GGAAAACTTTCCCTTGCTATTTAAGTAGGGCTTTACAAGTTACAATTCTATCACAGTTT	360
Query	361	TAAGATTATAAAC	373
Sbjct	361	TAAGATTATAAAC	373

Sequence 521 matched with Sequence 157

Query= Sequence ID 521
Length=155

SEQ ID NO: 157

ALIGNMENTS

Identities = 155/155 (100%), Gaps = 0/155 (0%)

Query	1	GCGGCGCANCTGCGGATCCANAAGGNCATAAACGANCNGAACCTGCCCAANNCGTGTGAT	60
Sbjct	1	GCGGCGCANCTGCGGATCCANAAGGNCATAAACGANCNGAACCTGCCCAANNCGTGTGAT	60
Query	61	ATCACCTTCTNAGATCCAGACNACCTCCTCAACTTCAAGCTGGTCATCTGTCCTGATGAG	120
Sbjct	61	ATCACCTTCTNAGATCCAGACNACCTCCTCAACTTCAAGCTGGTCATCTGTCCTGATGAG	120
Query	121	GGCTTCNACAAGAGTGGGAAGTTTGTCTCAAAAAA	155
Sbjct	121	GGCTTCNACAAGAGTGGGAAGTTTGTCTCAAAAAA	155

Sequence 523 matched with Sequence 158

Query= Sequence ID - 523
Length=585

nt: 585

SEQ ID NO: 158

nt: 585

ALIGNMENTS

Identities = 585/585 (100%), Gaps = 0/585 (0%)

Query	1	GATTTACTGTGGAATTTGCTCATGCAATTATGGAAACCTAGAAGTCCCATAATATGCCA	60
Sbjct	1	GATTTACTGTGGAATTTGCTCATGCAATTATGGAAACCTAGAAGTCCCATAATATGCCA	60
Query	61	TCTTCAAGCTGGAATCCCAGGAAAGCAGGTGGTGTAAATTCTGAGATTGAAGTCTTGAGAA	120
Sbjct	61	TCTTCAAGCTGGAATCCCAGGAAAGCAGGTGGTGTAAATTCTGAGATTGAAGTCTTGAGAA	120
Query	121	CCGGGGGAGTCAATGGTGTAACTCCCAATCTAGGGCTTAAGGCCCAAGGACCAGGGCTGC	180
Sbjct	121	CCGGGGGAGTCAATGGTGTAACTCCCAATCTAGGGCTTAAGGCCCAAGGACCAGGGCTGC	180
Query	181	TGGTGTGCAGATGCAAATCCTGGAGTTCAAAGGATTGAGAACCAGGAGCTCTGGTGTCTG	240
Sbjct	181	TGGTGTGCAGATGCAAATCCTGGAGTTCAAAGGATTGAGAACCAGGAGCTCTGGTGTCTG	240
Query	241	AGGGCAGTAGAAGATGGATGTTCCAGCTCAAGAAGGGAAAGTAAGAATCCGTCCTTCCTC	300
Sbjct	241	AGGGCAGTAGAAGATGGATGTTCCAGCTCAAGAAGGGAAAGTAAGAATCCGTCCTTCCTC	300
Query	301	CACTTTTTTGTCTATTTCAGATGAGCCCTCAATGGACTGAACGATGCTCACCCACACTGT	360
Sbjct	301	CACTTTTTTGTCTATTTCAGATGAGCCCTCAATGGACTGAACGATGCTCACCCACACTGT	360
Query	361	GAGGGCTGGTCTTCTTTATTCAATCCACTGACTTAAGTGCTGATCTTCTTGAAACACC	420
Sbjct	361	GAGGGCTGGTCTTCTTTATTCAATCCACTGACTTAAGTGCTGATCTTCTTGAAACACC	420
Query	421	TTCACAGACACACCCAGAAATAATGTTCTACCAGCCATGGGCCTGTTACTTAGCCCAGTC	480
Sbjct	421	TTCACAGACACACCCAGAAATAATGTTCTACCAGCCATGGGCCTGTTACTTAGCCCAGTC	480

PATENT SEQUENCE ALIGNMENT

Query	481	AAGTTGACACAGAAAATTAGCTATCACAACATCtgtgtgtgtatatatacatatgtatttgc	540
Sbjct	481	AAGTTGACACAGAAAATTAGCTATCACAACATCTGTGTGTGTATATACATATGTATTTGC	540
Query	541	atgtgtgtgtatatatggngtatatatatattcatgtgtgtgtatat	585
Sbjct	541	ATGTGTGTGTATATATGGNGTATATATATTTCATGTGTGTGTATAT	585

Sequence 524 matched with Sequence 159

Query= Sequence ID 524
Length=454

SEQ ID NO: 159

ALIGNMENTS

Identities = 454/454 (100%), Gaps = 0/454 (0%)

Query	1	CTTTTGCCAGTAGGCCCCCTGAGTAGGTCCTCTATCTTTTGGCATGACCCCAGAAGTCT	60
Sbjct	1	CTTTTGCCAGTAGGCCCCCTGAGTAGGTCCTCTATCTTTTGGCATGACCCCAGAAGTCT	60
Query	61	TTGATAACTTCCTTGCTTTCTGATGTGACAAGACATCCAGGGCCAGATTGTCCATATCCT	120
Sbjct	61	TTGATAACTTCCTTGCTTTCTGATGTGACAAGACATCCAGGGCCAGATTGTCCATATCCT	120
Query	121	GCCCCGGATGCACGATGCACTGTTTCTCCAAGAATCCCTGTGTCCTTTGCTGATGATGCC	180
Sbjct	121	GCCCCGGATGCACGATGCACTGTTTCTCCAAGAATCCCTGTGTCCTTTGCTGATGATGCC	180
Query	181	ATGATTTTAAGTTCTCTAATATAGTTTATCTCTTTGTTTCAGATAATGCTTTTGTGTTC	240
Sbjct	181	ATGATTTTAAGTTCTCTAATATAGTTTATCTCTTTGTTTCAGATAATGCTTTTGTGTTC	240
Query	241	TCACATGTCCTGctctctctctctctctcATTTTGGTGTTGATCAGTCTTCCATAAGAT	300
Sbjct	241	TCACATGTCCTGCTCTCTCTCTCTCTCATTTTGGTGTTGATCAGTCTTCCATAAGAT	300
Query	301	TGTTTATTTCACTAGTCCTTCATTCTTCTTTTTTCTAAATTTACTCTTCTTGACTAGTAT	360
Sbjct	301	TGTTTATTTCACTAGTCCTTCATTCTTCTTTTTTCTAAATTTACTCTTCTTGACTAGTAT	360
Query	361	CCTGTCACTTCTGAGGACTCATATTTTGGCAACTTGAAAATTATTCTTATTTATTTAAGT	420
Sbjct	361	CCTGTCACTTCTGAGGACTCATATTTTGGCAACTTGAAAATTATTCTTATTTATTTAAGT	420
Query	421	ATATGTTNCTGAAACTCTCATTAGACACATTTTG	454
Sbjct	421	ATATGTTNCTGAAACTCTCATTAGACACATTTTG	454

Length=346

SEQ ID NO: 160

Identities = 346/346 (100%), Gaps = 0/346 (0%)

[illegible]

nt: 516

nt: 516

Identities = 516/516 (100%), Gaps = 0/516 (0%)

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PATENT SEQUENCE ALIGNMENT

Query	481	ACACCCTCTGGGGAACACCCATGCACCTATGANATG	516
Sbjct	481	ACACCCTCTGGGGAACACCCATGCACCTATGANATG	516

Sequence 527 matched with Sequence 162

Query= Sequence ID 527

Length=385

SEQ ID NO: 162

ALIGNMENTS

Identities = 385/385 (100%), Gaps = 0/385 (0%)

Query	1	GACAAAAGCTGAGAGAA	ttttttt	CTTGAATATTTGCACTAAAAGATAGGTTAAAATTCT	60
Sbjct	1	GACAAAAGCTGAGAGAA	TTTTTTT	CTTGAATATTTGCACTAAAAGATAGGTTAAAATTCT	60
Query	61	TCAGGCTGAAGAGAGCATA	CCAGGTGGAGATTTGGATCTACAAAAAGGAAGGAAGATTTG	120	
Sbjct	61	TCAGGCTGAAGAGAGCATA	CCAGGTGGAGATTTGGATCTACAAAAAGGAAGGAAGATTTG	120	
Query	121	GAAATGGATTTGGCACCATT	GACTCAATTTCCAGAACAAGAAAGCAGGGACAGTTTTGGG	180	
Sbjct	121	GAAATGGATTTGGCACCATT	GACTCAATTTCCAGAACAAGAAAGCAGGGACAGTTTTGGG	180	
Query	181	AAGCTCAAGACACACTGCCC	ATGAGCAGCAATTTGGACCTCCTGCTGCATCCACTGTGCA	240	
Sbjct	181	AAGCTCAAGACACACTGCCC	ATGAGCAGCAATTTGGACCTCCTGCTGCATCCACTGTGCA	240	
Query	241	TCAAACACACACTGTACAG	ACAAAGACTCCCAGGAAAAGAAGTATAAACATGGACTAACA	300	
Sbjct	241	TCAAACACACACTGTACAG	ACAAAGACTCCCAGGAAAAGAAGTATAAACATGGACTAACA	300	
Query	301	CAGAGATGGGCAA	ACTACAGCCTGTGACCCAGCCACCTGTTTATGTAGAATCCAAAGTAA	360	
Sbjct	301	CAGAGATGGGCAA	ACTACAGCCTGTGACCCAGCCACCTGTTTATGTAGAATCCAAAGTAA	360	
Query	361	GAATCTTTAACTTACACATA	AACTT	385	
Sbjct	361	GAATCTTTAACTTACACATA	AACTT	385	

nt: 660

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nt:      660
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Identities = 660/660 (100%), Gaps = 0/660 (0%)

Query	1	GACAGCAGAGCACACAAGCTTNTAGGACAAGAGCCAGGAAGAAACCACCGGAAGGAACCA 	60
Sbjct	1	GACAGCAGAGCACACAAGCTTNTAGGACAAGAGCCAGGAAGAAACCACCGGAAGGAACCA	60
Query	61	TCTCACTGTGTGTAAACATGACTTCCAAGCTGGCCGTGGCTCTCTTGGCAGCCTTCCTGA 	120
Sbjct	61	TCTCACTGTGTGTAAACATGACTTCCAAGCTGGCCGTGGCTCTCTTGGCAGCCTTCCTGA	120
Query	121	TTTCTGCAGCTCTGTGTGAAGGTGCAGTTTTTGCCAAGGAGTGCTAAAGAACTTAGATGTC 	180
Sbjct	121	TTTCTGCAGCTCTGTGTGAAGGTGCAGTTTTTGCCAAGGAGTGCTAAAGAACTTAGATGTC	180
Query	181	AGTGCATAAAGACATACTCCAAACCTTTCCACCCCAAATTTATCAAAGAACTGAGAGTGA 	240
Sbjct	181	AGTGCATAAAGACATACTCCAAACCTTTCCACCCCAAATTTATCAAAGAACTGAGAGTGA	240
Query	241	TTGAGAGTGGACCACACTGCGCCAACACAGAAATTATTGTAAAGCTTTCTGATGGAAGAN 	300
Sbjct	241	TTGAGAGTGGACCACACTGCGCCAACACAGAAATTATTGTAAAGCTTTCTGATGGAAGAN	300
Query	301	AGCTCTGTCTGGACCCCAAGGAAAACCTGGGTGCANAGGGTTGTGGANAAGTTTTTTGAAGA 	360
Sbjct	301	AGCTCTGTCTGGACCCCAAGGAAAACCTGGGTGCANAGGGTTGTGGANAAGTTTTTTGAAGA	360
Query	361	GGGCTGAGAATTCATaaaaaaTTCATTCTCTGTGGTATCCAAGAATCAGTGAAGATGCC 	420
Sbjct	361	GGGCTGAGAATTCATAAAAAAATTCATTCTCTGTGGTATCCAAGAATCAGTGAAGATGCC	420
Query	421	AGTGAAACTTCAAGCAAATCTACTTCAACACTTCATGTATTGTGTGGGTCTGTTGTAGGG 	480
Sbjct	421	AGTGAAACTTCAAGCAAATCTACTTCAACACTTCATGTATTGTGTGGGTCTGTTGTAGGG	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTGCCAGATGCAATACAAGATTCCTGGTTAAATTTGAATTTTCAGTAAACAATGAATAGTT	540
Sbjct	481	TTGCCAGATGCAATACAAGATTCCTGGTTAAATTTGAATTTTCAGTAAACAATGAATAGTT	540
Query	541	TTTCATTGTACCATGAAATATCCAGAACATACTTATATGTAAAGTATTATTTATTTGAAT	600
Sbjct	541	TTTCATTGTACCATGAAATATCCAGAACATACTTATATGTAAAGTATTATTTATTTGAAT	600
Query	601	CTACAAAAAACAACAAATAATTTTTAGATATAAGGATTTTCCTGGATATTGCACGGGAGA	660
Sbjct	601	CTACAAAAAACAACAAATAATTTTTAGATATAAGGATTTTCCTGGATATTGCACGGGAGA	660

Sequence 532 matched with Sequence 166

Query= Sequence ID 532

Length=542

SEQ ID NO: 166

ALIGNMENTS

Identities = 542/542 (100%), Gaps = 0/542 (0%)

Query	1	GAATTGTGATAGTTCAGCTTGAATGTCTCTTAGAGGGTGGGCTTTTGTTGATGAGGGAGG	60
Sbjct	1	GAATTGTGATAGTTCAGCTTGAATGTCTCTTAGAGGGTGGGCTTTTGTTGATGAGGGAGG	60
Query	61	GGAAACtttttttttttCTATAGACTTTTTTCANATAACATCTTCTGAGTCATAACCAGC	120
Sbjct	61	GGAAACTTTTTTTTTTCTATAGACTTTTTTCANATAACATCTTCTGAGTCATAACCAGC	120
Query	121	CTGGCAGTATGATGGCCTANATGCAGAGAAAACAGCTCCTTGGTGAATTGATAAGTAAAG	180
Sbjct	121	CTGGCAGTATGATGGCCTANATGCAGAGAAAACAGCTCCTTGGTGAATTGATAAGTAAAG	180
Query	181	GCAGAAAAGATTATATGTCATACCTCCATTGGGGAATAAGCATAACCCTGAGATTCTTAC	240
Sbjct	181	GCAGAAAAGATTATATGTCATACCTCCATTGGGGAATAAGCATAACCCTGAGATTCTTAC	240
Query	241	TACTGATGAGAACATTATCTGCATATGCCAAAAAATTTTAAGCAAATGAAAGCTACCAAT	300
Sbjct	241	TACTGATGAGAACATTATCTGCATATGCCAAAAAATTTTAAGCAAATGAAAGCTACCAAT	300
Query	301	TTAAAGTTACGGAATCTACCATTTTAAAGTTAATTGCTTGTCAAGCTATAACCACAAAAA	360
Sbjct	301	TTAAAGTTACGGAATCTACCATTTTAAAGTTAATTGCTTGTCAAGCTATAACCACAAAAA	360
Query	361	TAATGAATTGATGAGAAATACAATGAAGAGGCAATGTCCATCTCAAATACTGCTTTTAC	420
Sbjct	361	TAATGAATTGATGAGAAATACAATGAAGAGGCAATGTCCATCTCAAATACTGCTTTTAC	420
Query	421	AAAAGCAGAATAAAAGCGAAAAGAAATGAAAATGTTACACTACATTAATCCTGGAATAAA	480
Sbjct	421	AAAAGCAGAATAAAAGCGAAAAGAAATGAAAATGTTACACTACATTAATCCTGGAATAAA	480

PATENT SEQUENCE ALIGNMENT

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Query  481  AGAAGCCGAAATAAATGAGAGATGAGTTGGGATCAAGTGGGATTGANGANGCTGTGCTGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGAAGCCGAAATAAATGAGAGATGAGTTGGGATCAAGTGGGATTGANGANGCTGTGCTGT  540

Query  541  GT    542
          ||
Sbjct  541  GT    542
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SEQ ID NO: 167

ALIGNMENTS

Identities = 421/421 (100%), Gaps = 0/421 (0%)

Query	1	CTTGAACCTCGGAGGCAGAGGTTGCAGTGAGCCGAGATCACGCCACTGCACTCCAGCCTC	60
Sbjct	1	CTTGAACCTCGGAGGCAGAGGTTGCAGTGAGCCGAGATCACGCCACTGCACTCCAGCCTC	60
Query	61	GGGGACAGAGCAAGACTCCATCTCAAAacacacacacacacacacacacacacacacaca	120
Sbjct	61	GGGGACAGAGCAAGACTCCATCTCAAAACACACACACACACACACACACACACACACA	120
Query	121	cacacaAAACAGATATATACTGAACACAGCACAAGTGGGACATAAGAGATTTAAAAGGGT	180
Sbjct	121	CACACAAAACAGATATATACTGAACACAGCACAAGTGGGACATAAGAGATTTAAAAGGGT	180
Query	181	TAGAGATGTAAAATGGATCTAGGAATGGAAACCATAAGGNGGGATTTATCAACTGGATTC	240
Sbjct	181	TAGAGATGTAAAATGGATCTAGGAATGGAAACCATAAGGNGGGATTTATCAACTGGATTC	240
Query	241	TGCANAATGCTGTTAAGGCCAGATGTTAGCAGGTGTTACATAAAAAAGGGATACCATGAG	300
Sbjct	241	TGCANAATGCTGTTAAGGCCAGATGTTAGCAGGTGTTACATAAAAAAGGGATACCATGAG	300
Query	301	CAAAAGTATTTGAACATGGGCAATGGTTGAAACAAGTTTAAACAGATTATNNTTTATTACC	360
Sbjct	301	CAAAAGTATTTGAACATGGGCAATGGTTGAAACAAGTTTAAACAGATTATNNTTTATTACC	360
Query	361	AAATCTCTCAAACCTTTAATATGCTATAAACATTGTGAAACAATaaaaaaCTTTCCAAA	420
Sbjct	361	AAATCTCTCAAACCTTTAATATGCTATAAACATTGTGAAACAATAAAAAAAGCTTTCCAAA	420
Query	421	A 421	
Sbjct	421	A 421	

Sequence 534 matched with Sequence 168

Query= Sequence ID 534
Length=472

SEQ ID NO: 168

ALIGNMENTS

Identities = 472/472 (100%), Gaps = 0/472 (0%)

Query	1	GGGAAGGGAGCTATGAggtgtgtgtgtgtgtATGGACTCACTCCCAGGTTACCTGGCCA	60
Sbjct	1	GGGAAGGGAGCTATGAGTGTGTGTGTTGTGTATGGACTCACTCCCAGGTTACCTGGCCA	60
Query	61	CAGGTGCACCCTTCCCACACCCTTTACATTCCCCAGAGCCAAGGGAGTTTAAGTTTGCAG	120
Sbjct	61	CAGGTGCACCCTTCCCACACCCTTTACATTCCCCAGAGCCAAGGGAGTTTAAGTTTGCAG	120
Query	121	TTACAGGCCAGTTCTCCAGCTCTCCATCTTANAGAGACAGGTACCTTGCAGGCCTGCTT	180
Sbjct	121	TTACAGGCCAGTTCTCCAGCTCTCCATCTTANAGAGACAGGTACCTTGCAGGCCTGCTT	180
Query	181	GCAGGAAATGAATCCAGCAGCCAACCTCGAATCCCCCTAGGGCTCAGGCACTGAGGGCCTG	240
Sbjct	181	GCAGGAAATGAATCCAGCAGCCAACCTCGAATCCCCCTAGGGCTCAGGCACTGAGGGCCTG	240
Query	241	GGGACAGTGGAGCATATGGGTGGGAGACAGATGGAGGGTACCCTATTTACAACCTGAGTCA	300
Sbjct	241	GGGACAGTGGAGCATATGGGTGGGAGACAGATGGAGGGTACCCTATTTACAACCTGAGTCA	300
Query	301	GCCAAGCCACTGATGGGAATATACAGATTTAGGTGCTAAACCGTTTATTTTCCACGGATG	360
Sbjct	301	GCCAAGCCACTGATGGGAATATACAGATTTAGGTGCTAAACCGTTTATTTTCCACGGATG	360
Query	361	AGTCACAATCTGAAGAATCAAACCTCCATCCTGAAAATCTATATGTTTCAAAACCACTTG	420
Sbjct	361	AGTCACAATCTGAAGAATCAAACCTCCATCCTGAAAATCTATATGTTTCAAAACCACTTG	420
Query	421	CCATCCTGTTAGATTGCCAGTTCCTGGGACCAGGCCTCANACTGTGAAAAGTA	472
Sbjct	421	CCATCCTGTTAGATTGCCAGTTCCTGGGACCAGGCCTCANACTGTGAAAAGTA	472

Sequence 560 matched with Sequence 169

Query= Sequence ID 560

Length=638

SEQ ID NO: 169

ALIGNMENTS

Identities = 638/638 (100%), Gaps = 0/638 (0%)

Query	1	GGCGGAGGTTGCAGTGAGCTGAGATGGCGCCATTGCTCTCCCAGCCTGGGTGACAAGAGC	60
Sbjct	1	GGCGGAGGTTGCAGTGAGCTGAGATGGCGCCATTGCTCTCCCAGCCTGGGTGACAAGAGC	60
Query	61	AAAAC TCCGTCTCaaaaaaaaaaaaaaaaaaaaaGCAATTTACTTAAAAACATACAAAC	120
Sbjct	61	AAAAC TCCGTCTCAAAAAAAAAAAAAAAAAAAAAAGCAATTTACTTAAAAACATACAAAC	120
Query	121	ACAGAGACAAGTATTTTTGAGAAACAAATACctttttcatttttATACCAATGTAACAA	180
Sbjct	121	ACAGAGACAAGTATTTTTGAGAAACAAATACCTTTTTTCATTTTTTATACCAATGTAACAA	180
Query	181	TAATCCATTAAACACACCTTTACTAACTGTTTTCTAGGAGTCTGATATGATGAGGAAATA	240
Sbjct	181	TAATCCATTAAACACACCTTTACTAACTGTTTTCTAGGAGTCTGATATGATGAGGAAATA	240
Query	241	GGTAAACCTTTAATAGCCAGTACTAAATTAGAGTGGCACAACCTTTCCTGGGAAAAAAGA	300
Sbjct	241	GGTAAACCTTTAATAGCCAGTACTAAATTAGAGTGGCACAACCTTTCCTGGGAAAAAAGA	300
Query	301	TGGGTATTTTACTTTTCTGTTTTAGAAAAGTGGCTTGACAACAGTATGCTTATGTCTTAG	360
Sbjct	301	TGGGTATTTTACTTTTCTGTTTTAGAAAAGTGGCTTGACAACAGTATGCTTATGTCTTAG	360
Query	361	AGTTTGAAATTCAAGTTCTTGAACATTATTAATGGCTACAATCATTCATACCCACATTGG	420
Sbjct	361	AGTTTGAAATTCAAGTTCTTGAACATTATTAATGGCTACAATCATTCATACCCACATTGG	420
Query	421	GCTGTATTCTTGATGAATCCAAAGTGATTTTCACCTCAACTCTGAATTTCAATTCTCCTCT	480
Sbjct	421	GCTGTATTCTTGATGAATCCAAAGTGATTTTCACCTCAACTCTGAATTTCAATTCTCCTCT	480

Sequence 561 matched with Sequence 170

Query= Sequence ID 561

Length=512

SEQ ID NO: 170

ALIGNMENTS

Identities = 512/512 (100%), Gaps = 0/512 (0%)

Query	1	CTCAGGGTGATCTCTGAACCCAAACTTGCCCCAAAGAAGGTTGCTCTGTCCTCTCCACAT	60
Sbjct	1	CTCAGGGTGATCTCTGAACCCAAACTTGCCCCAAAGAAGGTTGCTCTGTCCTCTCCACAT	60
Query	61	CCCCATCTCCTCCCTAGGGCCTTGTTGGGGAGAGGCTCCTCCATCTTTCCCAAGTCACAC	120
Sbjct	61	CCCCATCTCCTCCCTAGGGCCTTGTTGGGGAGAGGCTCCTCCATCTTTCCCAAGTCACAC	120
Query	121	CATCGTTTCCTACGTGGTCTGGACAAGAGCAAGAGCACACCTTGTCCTCCACCTTCTCCAG	180
Sbjct	121	CATCGTTTCCTACGTGGTCTGGACAAGAGCAAGAGCACACCTTGTCCTCCACCTTCTCCAG	180
Query	181	AGCAGCCAGAACCCACCTCAGGTGCCTTCCCCATCCGGTGCAGTTAAGGCACTTCTGCCA	240
Sbjct	181	AGCAGCCAGAACCCACCTCAGGTGCCTTCCCCATCCGGTGCAGTTAAGGCACTTCTGCCA	240
Query	241	GCACCATGGTATGAGCACTAGACTTGAGTTAAGATTTGAGAGCCCCCTCTGTCACTGTG	300
Sbjct	241	GCACCATGGTATGAGCACTAGACTTGAGTTAAGATTTGAGAGCCCCCTCTGTCACTGTG	300
Query	301	GAAGCTTGAGCATGTTGCTTGATCTCTCTGAACCTTGTTTCTCATCTGTGAAAGGTGA	360
Sbjct	301	GAAGCTTGAGCATGTTGCTTGATCTCTCTGAACCTTGTTTCTCATCTGTGAAAGGTGA	360
Query	361	TAATGTGGGGCTGCTGTGAGATTTAAAGGACATAATGCACCTACGGTCCAAGCACTGCCT	420
Sbjct	361	TAATGTGGGGCTGCTGTGAGATTTAAAGGACATAATGCACCTACGGTCCAAGCACTGCCT	420
Query	421	GGAATACAGCANAAGCTCAACAGATACTGGACAACCCATCCCCTTAGTAGAGGCACTAAC	480
Sbjct	421	GGAATACAGCANAAGCTCAACAGATACTGGACAACCCATCCCCTTAGTAGAGGCACTAAC	480

PATENT SEQUENCE ALIGNMENT

Query	481	CATGTGACCCAAGGCAAAAGTGCTTaaaaaaa	512
Sbjct	481	CATGTGACCCAAGGCAAAAGTGCTTAAAAAAA	512

Sequence 562 matched with Sequence 171

Query= Sequence ID - 562
Length=580

nt: 580

SEQ ID NO: 171

nt: 580

ALIGNMENTS

Identities = 580/580 (100%), Gaps = 0/580 (0%)

Query	1	ATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTG	60
Sbjct	1	ATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTG	60
Query	61	GAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGC	120
Sbjct	61	GAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGC	120
Query	121	AAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTTCGT	180
Sbjct	121	AAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTTCGT	180
Query	181	GATATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCACTGGACAAGAAGGCTGCTGGA	240
Sbjct	181	GATATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCACTGGACAAGAAGGCTGCTGGA	240
Query	241	GCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTA	300
Sbjct	241	GCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTA	300
Query	301	ATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTTCA	360
Sbjct	301	ATACCTGCCACCCCACTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTTCA	360
Query	361	ATTGGCCATTTAAGTTTAGTAGTAAAAGACTGGTTAATGATAACAATGCATCGTAAAACC	420
Sbjct	361	ATTGGCCATTTAAGTTTAGTAGTAAAAGACTGGTTAATGATAACAATGCATCGTAAAACC	420
Query	421	TTCAGAAAGGAAAGGAGAATgttttgtggaccactttggttttcttttttgcggtggcag	480
Sbjct	421	TTCAGAAAGGAAAGGAGAATGTTTTGTGGACCACTTTGGTTTTCTTTTTCGCTGTGGCAG	480

PATENT SEQUENCE ALIGNMENT

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Query  481  ttttaagttattagttttttaaatacagtactttttaATGGAAACAACCTGACCAAAAATT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTTTAAGTTATTAGTTTTTAAAATCAGTACTTTTAAATGGAAACAACCTGACCAAAAATT  540

Query  541  TGTCACAGAATTTTGAGACCCATTAAAAAAGTTAAATGAG  580
          |||||||||||||||||||||||||||||||||||
Sbjct  541  TGTCACAGAATTTTGAGACCCATTAAAAAAGTTAAATGAG  580
```

Sequence 563 matched with Sequence 172

Query= Sequence ID 563

Length=541

SEQ ID NO: 172

ALIGNMENTS

Identities = 541/541 (100%), Gaps = 0/541 (0%)

Query	1	GCAACCTGCACAACCCCGCCCTGTTTCGAGGGCCGGAGCCCTGCCGTGTGGGAGCTGGCCG	60
Sbjct	1	GCAACCTGCACAACCCCGCCCTGTTTCGAGGGCCGGAGCCCTGCCGTGTGGGAGCTGGCCG	60
Query	61	AGGAGTATCTGGACATCGTGC GGGAGCACCCCTGCCCCCTGTCCTACGTCCGGGGCCACC	120
Sbjct	61	AGGAGTATCTGGACATCGTGC GGGAGCACCCCTGCCCCCTGTCCTACGTCCGGGGCCACC	120
Query	121	TCTTCAAGCTGTGGCACCACACGCTGCAGGTGCACCAGGAGCTGCGAGAGGAGCTGGCCA	180
Sbjct	121	TCTTCAAGCTGTGGCACCACACGCTGCAGGTGCACCAGGAGCTGCGAGAGGAGCTGGCCA	180
Query	181	AGGTGAANACCCTGGAGGGCATCGCTGCTGTGAGCCAGGAGCTGAAGCTGCGGTGTCAGG	240
Sbjct	181	AGGTGAANACCCTGGAGGGCATCGCTGCTGTGAGCCAGGAGCTGAAGCTGCGGTGTCAGG	240
Query	241	AGGAGATATCCAGGCAGGAGGGAGCGAAGCCCACCGGCGACTTGCCCTTCCACTGGATCT	300
Sbjct	241	AGGAGATATCCAGGCAGGAGGGAGCGAAGCCCACCGGCGACTTGCCCTTCCACTGGATCT	300
Query	301	GCCAGCCCTACATCCGCGCGGGGGCCAGGGAGGGGAGCAAGGAGAAGGCAGGTGCGCGCA	360
Sbjct	301	GCCAGCCCTACATCCGCGCGGGGGCCAGGGAGGGGAGCAAGGAGAAGGCAGGTGCGCGCA	360
Query	361	GCAAGCGGGCCCTGGAGGAAGAGGAGGGTGGCACGGAGGTCCTGTCCAAGAACAAGCAAA	420
Sbjct	361	GCAAGCGGGCCCTGGAGGAAGAGGAGGGTGGCACGGAGGTCCTGTCCAAGAACAAGCAAA	420
Query	421	AGAAGCAGCTGAGGAACCCCCACAAGACCTTCGACCCCTCTCTGAACCAAAATATGCAAA	480
Sbjct	421	AGAAGCAGCTGAGGAACCCCCACAAGACCTTCGACCCCTCTCTGAACCAAAATATGCAAA	480

Sequence 564 matched with Sequence 173

Query= Sequence ID - 564
Length=671

nt: 671

SEQ ID NO: 173

nt: 671

ALIGNMENTS

Identities = 671/671 (100%), Gaps = 0/671 (0%)

Query	1	GGAATAGAAATTTTAAATAGTAATAACTGCTTGtttttttttGTGCAAGTACTTTTATACAT	60
Sbjct	1	GGAATAGAAATTTTAAATAGTAATAACTGCTTGTTTTTTTTGTGCAAGTACTTTTATACAT	60
Query	61	AAGATAAACAAAAACCTTACCACCAAACATACCAAATGCACCTCTTTCATAAGTGAGTT	120
Sbjct	61	AAGATAAACAAAAACCTTACCACCAAACATACCAAATGCACCTCTTTCATAAGTGAGTT	120
Query	121	ACTAAGATTTCTATACCTGGAATATCATGTATGTTTCATTTACTGGATGTTTACATTTTA	180
Sbjct	121	ACTAAGATTTCTATACCTGGAATATCATGTATGTTTCATTTACTGGATGTTTACATTTTA	180
Query	181	GGAAGGAAAATAGTTTTGTTTATTTAAACAACCTGAATACTTATAAACTGTTGTTCTGGA	240
Sbjct	181	GGAAGGAAAATAGTTTTGTTTATTTAAACAACCTGAATACTTATAAACTGTTGTTCTGGA	240
Query	241	AGTTATTTATTCCATAAAAAATTTGTTCTTTTGTTCATGAATTTATAATTCCTAAATGAAG	300
Sbjct	241	AGTTATTTATTCCATAAAAAATTTGTTCTTTTGTTCATGAATTTATAATTCCTAAATGAAG	300
Query	301	ACCAGAAAGTACAAATTGCTGGGAGGAAGAATAGGCTTTATTAATCAACTGATGTCTTGA	360
Sbjct	301	ACCAGAAAGTACAAATTGCTGGGAGGAAGAATAGGCTTTATTAATCAACTGATGTCTTGA	360
Query	361	TTTTTCTAAATGGGAAGATTGCTTTATTTTAACTAATTATGGGAGCAGATTCTTAGC	420
Sbjct	361	TTTTTCTAAATGGGAAGATTGCTTTATTTTAACTAATTATGGGAGCAGATTCTTAGC	420
Query	421	AAACTTCTTTGGAAGTTAATGTTATGATGTGCATTAGGCTGCCCCATCGTGTATATAA	480
Sbjct	421	AAACTTCTTTGGAAGTTAATGTTATGATGTGCATTAGGCTGCCCCATCGTGTATATAA	480

PATENT SEQUENCE ALIGNMENT

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Query  481  ATGAAGCAGATTTGATTTTTGTATTCTTACGTTTCTCTGCTTTGTAGTTGTGGCTGTACT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATGAAGCAGATTTGATTTTTGTATTCTTACGTTTCTCTGCTTTGTAGTTGTGGCTGTACT  540

Query  541  TAAAGAAATACAGAATTCATATATTTAAAAATGTTTAAAATGTGACCCACAGACATTGT  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TAAAGAAATACAGAATTCATATATTTAAAAATGTTTAAAATGTGACCCACAGACATTGT  600

Query  601  AAATGGATTNAAAACATAACATGAAAAATATTCAACCTAAAAGAATTCTTAACCTCACAAG  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  AAATGGATTNAAAACATAACATGAAAAATATTCAACCTAAAAGAATTCTTAACCTCACAAG  660

Query  661  TGTTTTACTTC  671
          |||||||||
Sbjct  661  TGTTTTACTTC  671
```


Sequence 565 matched with Sequence 174

Query= Sequence ID 565
Length=607

SEQ ID NO: 174

ALIGNMENTS

Identities = 607/607 (100%), Gaps = 0/607 (0%)

Query	1	CTTGGTTCCGCGTTCCTGCACAAAATGCCCGGCGAAGCCACAGAAACCGTCCCTGCTAC	60
Sbjct	1	CTTGGTTCCGCGTTCCTGCACAAAATGCCCGGCGAAGCCACAGAAACCGTCCCTGCTAC	60
Query	61	AGAGCAGGAGTTGCCGCAGCCCCAGGCTGAGACAGGGTCTGGAACAGAATCTGACAGTGA	120
Sbjct	61	AGAGCAGGAGTTGCCGCAGCCCCAGGCTGAGACAGGGTCTGGAACAGAATCTGACAGTGA	120
Query	121	TGAATCAGTACCAGAGCTTGAAGAACAGGATTCCACCCAGGCAACCACACAACAAGCCCA	180
Sbjct	121	TGAATCAGTACCAGAGCTTGAAGAACAGGATTCCACCCAGGCAACCACACAACAAGCCCA	180
Query	181	GCTGGCGGCAGCAGCTGAAATCGATGAAGAACCAGTCAGTAAAGCAAAAACAGAGTCGGAG	240
Sbjct	181	GCTGGCGGCAGCAGCTGAAATCGATGAAGAACCAGTCAGTAAAGCAAAAACAGAGTCGGAG	240
Query	241	TGAAAAGAAGGCACGGAAGGCTATGTCCAAACTGGGTCTTCGGCAGGTTACAGGAGTTAC	300
Sbjct	241	TGAAAAGAAGGCACGGAAGGCTATGTCCAAACTGGGTCTTCGGCAGGTTACAGGAGTTAC	300
Query	301	TAGAGTCACTATCCGGAAATCTAAGAATATCCTCTTTGTCATCACAAAACCAGATGTCTA	360
Sbjct	301	TAGAGTCACTATCCGGAAATCTAAGAATATCCTCTTTGTCATCACAAAACCAGATGTCTA	360
Query	361	CAAGAGCCCTGCTTCAGATACTTACATAGTTTTTGGGGAAGCCAAGATCGAAGATTTATC	420
Sbjct	361	CAAGAGCCCTGCTTCAGATACTTACATAGTTTTTGGGGAAGCCAAGATCGAAGATTTATC	420
Query	421	CCAGCAAGCACAACCTAGCAGCTGCTGAGAAATTCAAAGTTCAAGGTGAAGCTGTCTCAA	480
Sbjct	421	CCAGCAAGCACAACCTAGCAGCTGCTGAGAAATTCAAAGTTCAAGGTGAAGCTGTCTCAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CATTCAAGAAAACACACAGACTCCAAGTGTACAAGAGGAGAGTGAAGAGGAAGAGGTCGA	540
Sbjct	481	CATTCAAGAAAACACACAGACTCCAAGTGTACAAGAGGAGAGTGAAGAGGAAGAGGTCGA	540
Query	541	TGAAACAGGTGTAGAAAGTTAAGGACATAGAATTTGGTCATTGTCACAAAGCAAATGTGTC	600
Sbjct	541	TGAAACAGGTGTAGAAAGTTAAGGACATAGAATTTGGTCATTGTCACAAAGCAAATGTGTC	600
Query	601	GAGAGCA	607
Sbjct	601	GAGAGCA	607

Sequence 566 matched with Sequence 175

Query= Sequence ID 566
Length=583

SEQ ID NO: 175

ALIGNMENTS

Identities = 583/583 (100%), Gaps = 0/583 (0%)

Query	1	GTCACCAAGAGCTTGTTGTCAGGTTTTCACTTGCTATTTCGCAGAGAttttttttAAAGGC	60
Sbjct	1	GTCACCAAGAGCTTGTTGTCAGGTTTTCACTTGCTATTTCGCAGAGATTTTTTTTAAAGGC	60
Query	61	ACTATTTGTAGTGTTAAAAGGGTGAATTTATCANAAGGCATAATAATCATAAATGTGTAT	120
Sbjct	61	ACTATTTGTAGTGTTAAAAGGGTGAATTTATCANAAGGCATAATAATCATAAATGTGTAT	120
Query	121	ATGCCTAATAATAGAACTTTAAAAGGCATGAAGCAACACTCAAAAGGATTAAAGGGAGAT	180
Sbjct	121	ATGCCTAATAATAGAACTTTAAAAGGCATGAAGCAACACTCAAAAGGATTAAAGGGAGAT	180
Query	181	CATCTCACCCCCTTCTTACCAATTGATAGAATGATCTGATGAAAACAGTAAAATAACAAC	240
Sbjct	181	CATCTCACCCCCTTCTTACCAATTGATAGAATGATCTGATGAAAACAGTAAAATAACAAC	240
Query	241	AGATCTGAACACTGTCAACCATCTTGACAAATACTTATGCCTAGTGTTCCATTATTGGAA	300
Sbjct	241	AGATCTGAACACTGTCAACCATCTTGACAAATACTTATGCCTAGTGTTCCATTATTGGAA	300
Query	301	CACTAAACATGTGGAATGATTTATATCCTACTGCTCAAGGTCATCACCAAGGTCTAATTG	360
Sbjct	301	CACTAAACATGTGGAATGATTTATATCCTACTGCTCAAGGTCATCACCAAGGTCTAATTG	360
Query	361	TAAAATTTCAAAAAATTGCAACCTCAGGCATAAATGGGTAAATCGACATTTATAGCACAC	420
Sbjct	361	TAAAATTTCAAAAAATTGCAACCTCAGGCATAAATGGGTAAATCGACATTTATAGCACAC	420
Query	421	ACATGCAACATGTACCAGAGATTCCTTCTTTTCTATGAACATGGTACTTCCACCAAGATA	480
Sbjct	421	ACATGCAACATGTACCAGAGATTCCTTCTTTTCTATGAACATGGTACTTCCACCAAGATA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GACCACATTGTGAACTATAAAACAAATCTAAAAACATTTGAAATGAAGGAAATTATATAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GACCACATTGTGAACTATAAAACAAATCTAAAAACATTTGAAATGAAGGAAATTATATAA  540

Query  541  AATATGTTCTCTTGATCTCAATGAAATTAAATTAATACTATAT  583
          ||||||||||||||||||||||||||||||||||||
Sbjct  541  AATATGTTCTCTTGATCTCAATGAAATTAAATTAATACTATAT  583
```

Sequence 567 matched with Sequence 176

Query= Sequence ID 567

Length=549

SEQ ID NO: 176

ALIGNMENTS

Identities = 549/549 (100%), Gaps = 0/549 (0%)

Query	1	CTCATGGCGGCCAATGTAGGCCCAAACTTCCTCAAGTCAAACCTCCAGGCCACCTTC	60
Sbjct	1	CTCATGGCGGCCAATGTAGGCCCAAACTTCCTCAAGTCAAACCTCCAGGCCACCTTC	60
Query	61	TGCTTCCCGGTGGCATCAACAGGCCCAGCTTTGACTTGAGAACAGCCTCTGCAGGCCCTG	120
Sbjct	61	TGCTTCCCGGTGGCATCAACAGGCCCAGCTTTGACTTGAGAACAGCCTCTGCAGGCCCTG	120
Query	121	CTCTTGCTCCAGGGGCTTTTCCAGGCCCAGCTCTTGCTCATGGCAGCTGCCCCAGG	180
Sbjct	121	CTCTTGCTCCAGGGGCTTTTCCAGGCCCAGCTCTTGCTCATGGCAGCTGCCCCAGG	180
Query	181	CCAAATTTCTGCCTGCCTGCCAGCAGCCTCAACAGGCACAGCTCCTCCCTCACAGTGGCC	240
Sbjct	181	CCAAATTTCTGCCTGCCTGCCAGCAGCCTCAACAGGCACAGCTCCTCCCTCACAGTGGCC	240
Query	241	CATTTAGGCCCAACTCATGACTGTGAGGCCATTTCCAGGCCTAGTGCCTGCCTCGTGGCT	300
Sbjct	241	CATTTAGGCCCAACTCATGACTGTGAGGCCATTTCCAGGCCTAGTGCCTGCCTCGTGGCT	300
Query	301	GACTCTTGAAGCCCCAAACTTCCTCAAATCAGCCTTTTGCCCAACTTCTGTCTACTGTCTG	360
Sbjct	301	GACTCTTGAAGCCCCAAACTTCCTCAAATCAGCCTTTTGCCCAACTTCTGTCTACTGTCTG	360
Query	361	GACTCTACAGGTCAGCCTCTGCCTCACAGTGGACCCTCCAGACCCAGATGGTGTCTNCTG	420
Sbjct	361	GACTCTACAGGTCAGCCTCTGCCTCACAGTGGACCCTCCAGACCCAGATGGTGTCTNCTG	420
Query	421	TGGCATCCTCAGGCGAAGCTCCTGCCTTTCGGCAGCCTCTCCAGGCCCAGCTCCTCCTGC	480
Sbjct	421	TGGCATCCTCAGGCGAAGCTCCTGCCTTTCGGCAGCCTCTCCAGGCCCAGCTCCTCCTGC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TCCAGCCTTCTCTCCAGGCTCTGAACTTTCTCAGGTCTCCCTCTGTTGTCCAAGGCTGGA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TCCAGCCTTCTCTCCAGGCTCTGAACTTTCTCAGGTCTCCCTCTGTTGTCCAAGGCTGGA  540

Query  541  GTGTAGTAG  549
          ||||||||
Sbjct  541  GTGTAGTAG  549
```

Sequence 568 matched with Sequence 177

Query= Sequence ID 568
Length=662

SEQ ID NO: 177

ALIGNMENTS

Identities = 662/662 (100%), Gaps = 0/662 (0%)

Query	1	TATATATGTAATGCCCTTAACCTAGTGTGTTGGCATGATCGTTGCTGAAAGGGAAGCTTGT	60
Sbjct	1	TATATATGTAATGCCCTTAACCTAGTGTGTTGGCATGATCGTTGCTGAAAGGGAAGCTTGT	60
Query	61	GGGTACAGTGTCCCCTCAGAAGCCAAAGCCCAGGGAAGGTCGCCTGCCCAGGTCAGGCTC	120
Sbjct	61	GGGTACAGTGTCCCCTCAGAAGCCAAAGCCCAGGGAAGGTCGCCTGCCCAGGTCAGGCTC	120
Query	121	CCAGCGAGTTTGTCTGGGGAGGGGCCATTCATACCTCCAGGTCAGGACAGAGGCTCGGGC	180
Sbjct	121	CCAGCGAGTTTGTCTGGGGAGGGGCCATTCATACCTCCAGGTCAGGACAGAGGCTCGGGC	180
Query	181	TGAGGGAACCCTACACAGGTCCTGGAAGCAGATCCTTCCTGCCTAAGCCAGCAGGACAGC	240
Sbjct	181	TGAGGGAACCCTACACAGGTCCTGGAAGCAGATCCTTCCTGCCTAAGCCAGCAGGACAGC	240
Query	241	TCAACAGGAAGCATCTTCCAGCCACGGGAGGAGAGGCAGCACCTTTTTTGAACCATACA	300
Sbjct	241	TCAACAGGAAGCATCTTCCAGCCACGGGAGGAGAGGCAGCACCTTTTTTGAACCATACA	300
Query	301	GAGCTAAGAATGGTGGTACAAGTAATAGATTCTGTACTGGCAACCCCACTTGGTGGAGCA	360
Sbjct	301	GAGCTAAGAATGGTGGTACAAGTAATAGATTCTGTACTGGCAACCCCACTTGGTGGAGCA	360
Query	361	AGTTCTAGGAAAAGGGGGCTGTCCTTGAGTCAGCCATGGGGTCAGCCACACAGTCACCGC	420
Sbjct	361	AGTTCTAGGAAAAGGGGGCTGTCCTTGAGTCAGCCATGGGGTCAGCCACACAGTCACCGC	420
Query	421	AGCTGCTCTTTGGCACCGGGCGCTGGAAAGACCTAGGATGACACAGCCTGGAAAGAGCTT	480
Sbjct	421	AGCTGCTCTTTGGCACCGGGCGCTGGAAAGACCTAGGATGACACAGCCTGGAAAGAGCTT	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 GGGAAAAGCTCATCTTCCACAGAACTACCTGCTATACCAGCCAGGGCAGGTGCTTATTCC 540
          |||
Sbjct 481 GGGAAAAGCTCATCTTCCACAGAACTACCTGCTATACCAGCCAGGGCAGGTGCTTATTCC 540

Query 541 CACAACAGCCCTCTGTTGTAGGCGGCAGTGCCATCCTGAANGTGCCGTGGTACCTTCTGA 600
          |||
Sbjct 541 CACAACAGCCCTCTGTTGTAGGCGGCAGTGCCATCCTGAANGTGCCGTGGTACCTTCTGA 600

Query 601 ANACCCAGCTGAGGGCCTGTAATGGCACTTGCATGCCACATGGNACACCCTTTCCCGGTT 660
          |||
Sbjct 601 ANACCCAGCTGAGGGCCTGTAATGGCACTTGCATGCCACATGGNACACCCTTTCCCGGTT 660

Query 661 AA 662
          ||
Sbjct 661 AA 662
```


Sequence 570 matched with Sequence 178

Query= Sequence ID 570
Length=339

SEQ ID NO: 178

ALIGNMENTS

Identities = 339/339 (100%), Gaps = 0/339 (0%)

Query	1	ACCGCGGCCGCGTnaaaaaaaaaaaaaaaaaGAATTCCACTTGATCAACTTAATTCCTTNT	60
Sbjct	1	ACCGCGGCCGCGTNAANAAAAAAAAAAAAAGAATTCCACTTGATCAACTTAATTCCTTNT	60
Query	61	CTTTATCTTCCCTCCCTCACTTCCCTTTTCTCCCACCCTCTTTTCCAAGCTGTTTCGCTT	120
Sbjct	61	CTTTATCTTCCCTCCCTCACTTCCCTTTTCTCCCACCCTCTTTTCCAAGCTGTTTCGCTT	120
Query	121	TGCAATATATTACTGGTAATGAGTTGCAGGATAATGCAGTCATAACTTGTTTTCTCCTAA	180
Sbjct	121	TGCAATATATTACTGGTAATGAGTTGCAGGATAATGCAGTCATAACTTGTTTTCTCCTAA	180
Query	181	GTATTTGAGTTCAAACTCCTGTATCTAAAGAAATACGGTTGGGGTCATTAATAAGAAA	240
Sbjct	181	GTATTTGAGTTCAAACTCCTGTATCTAAAGAAATACGGTTGGGGTCATTAATAAGAAA	240
Query	241	ATCTTTCTATCTTaaa	300
Sbjct	241	ATCTTTCTATCTTAAA	300
Query	301	aaa	339
Sbjct	301	AAA	339

Sequence 571 matched with Sequence 179

Query= Sequence ID - 571
Length=457

nt: 457

SEQ ID NO: 179

nt: 457

ALIGNMENTS

Identities = 457/457 (100%), Gaps = 0/457 (0%)

Query	1	TTAGAGAGGTGAGGATCTGGTATTTCTGGACTAAATTCCTTGGGGAAGACGAAGGGA	60
Sbjct	1	TTAGAGAGGTGAGGATCTGGTATTTCTGGACTAAATTCCTTGGGGAAGACGAAGGGA	60
Query	61	TGCTGCAGTTCCAAAAGAGAAGGACTCTTCCAGAGTCATCTACCTGAGTCCCAAAGCTCC	120
Sbjct	61	TGCTGCAGTTCCAAAAGAGAAGGACTCTTCCAGAGTCATCTACCTGAGTCCCAAAGCTCC	120
Query	121	CTGTCCTGAAAGCCACAGACAATATGGTCCCAAATGACTGACTGCACCTTCTGTGCCTCA	180
Sbjct	121	CTGTCCTGAAAGCCACAGACAATATGGTCCCAAATGACTGACTGCACCTTCTGTGCCTCA	180
Query	181	GCCGTTCTTGACATCAAGAATCTTCTGTTCCACATCCACACAGCCAATACAATTAGTCAA	240
Sbjct	181	GCCGTTCTTGACATCAAGAATCTTCTGTTCCACATCCACACAGCCAATACAATTAGTCAA	240
Query	241	ACCACTGTTATTAACAGATGTAGCAACATGAGAAACGCTTATGTTACAGGTTACATGAGA	300
Sbjct	241	ACCACTGTTATTAACAGATGTAGCAACATGAGAAACGCTTATGTTACAGGTTACATGAGA	300
Query	301	GCAATCATGTAAGTCTATATGACTTCAGAAATGTTAAATAGACTAACCTCTAACAACAA	360
Sbjct	301	GCAATCATGTAAGTCTATATGACTTCAGAAATGTTAAATAGACTAACCTCTAACAACAA	360
Query	361	ATTAAAAGTGATTGTTTCAAGGTGATGCAATTATTGATGACCTATTTTATTTTCTATAA	420
Sbjct	361	ATTAAAAGTGATTGTTTCAAGGTGATGCAATTATTGATGACCTATTTTATTTTCTATAA	420
Query	421	TGATCATATATTACCTTTGTAATAAAACATTTTCCC	457
Sbjct	421	TGATCATATATTACCTTTGTAATAAAACATTTTCCC	457

Sequence 572 matched with Sequence 180

Query= Sequence ID 572
Length=658

SEQ ID NO: 180

ALIGNMENTS

Identities = 658/658 (100%), Gaps = 0/658 (0%)

Query	1	CGTCTATTTGNGTTTCTTCTCACAATTGGTAAGTTCTCTGTATTGATTGATGGCTAAGTT	60
Sbjct	1	CGTCTATTTGNGTTTCTTCTCACAATTGGTAAGTTCTCTGTATTGATTGATGGCTAAGTT	60
Query	61	TGATTAGTGTTTTCTCTAGTTGGTAATTATATTCTAGTATTTTATCATCTTATTGTTTA	120
Sbjct	61	TGATTAGTGTTTTCTCTAGTTGGTAATTATATTCTAGTATTTTATCATCTTATTGTTTA	120
Query	121	CTCAACTNAAAGTGNCACAGAAGAGTTGCCAGGTTTCTCTTTGATATGAGATCTCTNNTT	180
Sbjct	121	CTCAACTNAAAGTGNCACAGAAGAGTTGCCAGGTTTCTCTTTGATATGAGATCTCTNNTT	180
Query	181	GATTTGGAATGCAAATCANAAGTGTCATGTTTTGAATAAAGGGACCAGATGACTTATAGG	240
Sbjct	181	GATTTGGAATGCAAATCANAAGTGTCATGTTTTGAATAAAGGGACCAGATGACTTATAGG	240
Query	241	TATTCTTTCTCTAAATATAACTAAGGTAAGATTTTTGTTTTGAGGTACTTAATCTATATA	300
Sbjct	241	TATTCTTTCTCTAAATATAACTAAGGTAAGATTTTTGTTTTGAGGTACTTAATCTATATA	300
Query	301	AGTGGTAAAGAATTTACTTGAATTTCTCCAAATTCTCATGTCTAAAGTCTGATTGATTAA	360
Sbjct	301	AGTGGTAAAGAATTTACTTGAATTTCTCCAAATTCTCATGTCTAAAGTCTGATTGATTAA	360
Query	361	ATTCATTCTTGGTATTTTCAATTTGAAAAGAATGTAGCTTTAGCAAACCTCTTTGTATAAA	420
Sbjct	361	ATTCATTCTTGGTATTTTCAATTTGAAAAGAATGTAGCTTTAGCAAACCTCTTTGTATAAA	420
Query	421	TGCAGTGGGATTAAGGTCatttaaaaaattgttatatcattgtatttttaaaatttacca	480
Sbjct	421	TGCAGTGGGATTAAGGTCATTTAAAAAATTGTTATATCATTGTATTTTAAAATTTACCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	gtttttatTTTTctTTTTaccctttaGCCCCGGCCTCAGAAAGTGTGTTTGTGTCCATTTCT	540
Sbjct	481	GTTTTATTTTTCTTTTTACCCTTTAGCCCCGGCCTCAGAAAGTGTGTTTGTGTCCATTTCT	540
Query	541	CCCAGCGCACCTCTGCATATCTCTACCCACTTGTCATAATTCAGCATCCAGCAGAGGAA	600
Sbjct	541	CCCAGCGCACCTCTGCATATCTCTACCCACTTGTCATAATTCAGCATCCAGCAGAGGAA	600
Query	601	AACAAAGTGTGCGTACAGTTCCTCTACTAGCAGCATGCCTCCCCCAGGACAAGTGTA	658
Sbjct	601	AACAAAGTGTGCGTACAGTTCCTCTACTAGCAGCATGCCTCCCCCAGGACAAGTGTA	658

Sequence 574 matched with Sequence 181

Query= Sequence ID 574

Length=452

SEQ ID NO: 181

ALIGNMENTS

Identities = 452/452 (100%), Gaps = 0/452 (0%)

Query	1	TTATTGCTGACATAAAAAATGGTGCACATCGGCCAGGGCCCAGGATGAATCAGCCAATCTG	60
Sbjct	1	TTATTGCTGACATAAAAAATGGTGCACATCGGCCAGGGCCCAGGATGAATCAGCCAATCTG	60
Query	61	CACCATTTATACATGGAAGCTGGAGAACATTGTGCCAATAATCATTTAATATATGCCAAAT	120
Sbjct	61	CACCATTTATACATGGAAGCTGGAGAACATTGTGCCAATAATCATTTAATATATGCCAAAT	120
Query	121	CTTACACGTCTACTCTAAACTGCTCTAATGAAGTTTCAGTGACCTTGAGGGCTAAAGATT	180
Sbjct	121	CTTACACGTCTACTCTAAACTGCTCTAATGAAGTTTCAGTGACCTTGAGGGCTAAAGATT	180
Query	181	GTTCTTCTGGGTAAGAGCTCTTGGGCTGGTTTTTTCANAGCAGAGTTCTTGTTGTGGGTAG	240
Sbjct	181	GTTCTTCTGGGTAAGAGCTCTTGGGCTGGTTTTTTCANAGCAGAGTTCTTGTTGTGGGTAG	240
Query	241	ACTGTGACTAGGTTACAGCCTTTGTGGAACATTCCGTATAACGGCATTGTGGAAGCAAT	300
Sbjct	241	ACTGTGACTAGGTTACAGCCTTTGTGGAACATTCCGTATAACGGCATTGTGGAAGCAAT	300
Query	301	AACTAGTTCCTATGAAAGAACCAGAGCTGGGAAGATGGCTGGGAAGCCAGGCCAAAGTGG	360
Sbjct	301	AACTAGTTCCTATGAAAGAACCAGAGCTGGGAAGATGGCTGGGAAGCCAGGCCAAAGTGG	360
Query	361	GGGCAACAGCTTGCTTCTCTTTCTCTTCTCACCCTCAGTTTGTATGGGAAAATGGAGATG	420
Sbjct	361	GGGCAACAGCTTGCTTCTCTTTCTCTTCTCACCCTCAGTTTGTATGGGAAAATGGAGATG	420
Query	421	TCCTCTCCACTTTATCCCACGATATCTAAATG	452
Sbjct	421	TCCTCTCCACTTTATCCCACGATATCTAAATG	452

Sequence 575 matched with Sequence 182

Query= Sequence ID - 575 nt: 209
Length=188

SEQ ID NO: 182 nt: 209

ALIGNMENTS

Identities = 188/188 (100%), Gaps = 0/188 (0%)

Query	1	CAGGATATCGAGACCATCCCAGACAGCATGGTGAAACTCCGTCTCTACTGGAATACAAAA	60
Sbjct	1	CAGGATATCGAGACCATCCCAGACAGCATGGTGAAACTCCGTCTCTACTGGAATACAAAA	60
Query	61	AGTTAGCCGTGTGTGGTGGCACGCGCCTCTAATCCCAGCTATTCGGGAGGCTTAGGCAGG	120
Sbjct	61	AGTTAGCCGTGTGTGGTGGCACGCGCCTCTAATCCCAGCTATTCGGGAGGCTTAGGCAGG	120
Query	121	AGAATTACTTGAACCCGGGAGGCGAAGGTTGCAGTGAGCTGAGATCGCACCATTGCACTC	180
Sbjct	121	AGAATTACTTGAACCCGGGAGGCGAAGGTTGCAGTGAGCTGAGATCGCACCATTGCACTC	180
Query	181	CACCCTGG	188
Sbjct	181	CACCCTGG	188

Sequence 576 matched with Sequence 183

Query= Sequence ID - 576
Length=541

nt: 541

SEQ ID NO: 183

nt: 541

ALIGNMENTS

Identities = 541/541 (100%), Gaps = 0/541 (0%)

Query	1	CAGCCAACCCAGAAGGAGCCAGTCTACAACTATGCCTGATCCTCCTCATGGCAGGCCACG	60
Sbjct	1	CAGCCAACCCAGAAGGAGCCAGTCTACAACTATGCCTGATCCTCCTCATGGCAGGCCACG	60
Query	61	AAGCATTGCTGCCATGTGTTGAATTATAAAACCCACATTGCTTTTTGAACCCTGTTGCGG	120
Sbjct	61	AAGCATTGCTGCCATGTGTTGAATTATAAAACCCACATTGCTTTTTGAACCCTGTTGCGG	120
Query	121	GTAAAAATAACCAAATTATCAGTCCTTGGAACCCAGGCAATCAAGTGAGTACAAGGTAA	180
Sbjct	121	GTAAAAATAACCAAATTATCAGTCCTTGGAACCCAGGCAATCAAGTGAGTACAAGGTAA	180
Query	181	AGATAAGTATGGTTTAGAGGAGAAATTATGTTTCCTGAACTGGTGTCTTTGATGGCAGCG	240
Sbjct	181	AGATAAGTATGGTTTAGAGGAGAAATTATGTTTCCTGAACTGGTGTCTTTGATGGCAGCG	240
Query	241	TCAGCCTTGCTAAGTCAGAGTAGAGGGAGCAGTGACCTTAATAAGCTTTGGTGAGCATCA	300
Sbjct	241	TCAGCCTTGCTAAGTCAGAGTAGAGGGAGCAGTGACCTTAATAAGCTTTGGTGAGCATCA	300
Query	301	TGTGCACGCGTGGGTGGGAGTCCCTTTCACTGATGCTTTTAAAAGTGCTTTTGCAGACCC	360
Sbjct	301	TGTGCACGCGTGGGTGGGAGTCCCTTTCACTGATGCTTTTAAAAGTGCTTTTGCAGACCC	360
Query	361	TGGAAGGGATCCTCCACACATATGAGGTGTGGGACAGGTAGGCCAGAGAGGATTAGCCCT	420
Sbjct	361	TGGAAGGGATCCTCCACACATATGAGGTGTGGGACAGGTAGGCCAGAGAGGATTAGCCCT	420
Query	421	GCTTTTCGAGACTAGAAATCTACAGTCCTGAAGGAGCAGTAATTAATTGGTACACCTGTCA	480
Sbjct	421	GCTTTTCGAGACTAGAAATCTACAGTCCTGAAGGAGCAGTAATTAATTGGTACACCTGTCA	480

Sequence 577 matched with Sequence 184

Query= Sequence ID 577
Length=640

SEQ ID NO: 184

ALIGNMENTS

Identities = 640/640 (100%), Gaps = 0/640 (0%)

Query	1	CTTTAATTTTCAAGTGTTTAAAAACAATTTTATACTTAAGCCAGCCTTGAAGATAAGC	60
Sbjct	1	CTTTAATTTTCAAGTGTTTAAAAACAATTTTATACTTAAGCCAGCCTTGAAGATAAGC	60
Query	61	ACAAAATTTACCAGTTTACATTTaaaaaacaacaaaaaCGACAACAACTCAAGCACCC	120
Sbjct	61	ACAAAATTTACCAGTTTACATTTAAAAACAACAAAAACGACAACAACTCAAGCACCC	120
Query	121	GCTCTGTGCATAGCACTATTCTAGGTGCAATAAAAGGGAATCTTAACCTTAGAAATATGA	180
Sbjct	121	GCTCTGTGCATAGCACTATTCTAGGTGCAATAAAAGGGAATCTTAACCTTAGAAATATGA	180
Query	181	GTTCACTTTCTGGAATTGTATTATCTCCTTTTCCAGAGAGTAAAAATAAATAAAATCACC	240
Sbjct	181	GTTCACTTTCTGGAATTGTATTATCTCCTTTTCCAGAGAGTAAAAATAAATAAAATCACC	240
Query	241	ATTGTTTACTACAGATCTGCCCCAAACCACATCTGGTTCACAGAAAGGCTAATTTCTGCC	300
Sbjct	241	ATTGTTTACTACAGATCTGCCCCAAACCACATCTGGTTCACAGAAAGGCTAATTTCTGCC	300
Query	301	AAATTAAAGATGTAATGAACTCAGTTCCTGCTTTCCCAAAAACACGAAAGCAGAATTCCT	360
Sbjct	301	AAATTAAAGATGTAATGAACTCAGTTCCTGCTTTCCCAAAAACACGAAAGCAGAATTCCT	360
Query	361	TTTCACTGaaaaaaaTAAACAGTTTCCATGCAAGGGCAGTTTGCTTCTAATAAGTAttt	420
Sbjct	361	TTTCACTGAAAAAATAAACAGTTTCCATGCAAGGGCAGTTTGCTTCTAATAAGTATTT	420
Query	421	tttaaaaaatttttttttCCTCTAGCTTTTCTTTAAATTTTCTTCCTCTAATATTGCCTT	480
Sbjct	421	TTTAAAAAATTTTTTTTCTCTAGCTTTTCTTTAAATTTTCTTCCTCTAATATTGCCTT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTCTTGTACAAGGCAGACCAGGTATCTTTTATGCTGTTTTTCCTTTACTAAGAAAAGTA	540
Sbjct	481	TTCTTGTACAAGGCAGACCAGGTATCTTTTATGCTGTTTTTCCTTTACTAAGAAAAGTA	540
Query	541	TTGCATCTTGAAGACAAACCATTTCCCAGAGTAGTGATAAAAAATAACACTaaaaaaCT	600
Sbjct	541	TTGCATCTTGAAGACAAACCATTTCCCAGAGTAGTGATAAAAAATAACACTAAAAAACT	600
Query	601	TTAAAGGTGAGTCACTTCATCACCTTGATGAAGTAAAAAA	640
Sbjct	601	TTAAAGGTGAGTCACTTCATCACCTTGATGAAGTAAAAAA	640

Sequence 578 matched with Sequence 185

Query= Sequence ID 578

Length=633

SEQ ID NO: 185

ALIGNMENTS

Identities = 633/633 (100%), Gaps = 0/633 (0%)

Query	1	GGAAAAAATATTTCCACTTAGATATTTTACATGGTTTTGTTTAAAATTACCATTACTTGT	60
Sbjct	1	GGAAAAAATATTTCCACTTAGATATTTTACATGGTTTTGTTTAAAATTACCATTACTTGT	60
Query	61	TTTTTAAAAACACATGACCACATATGTATATGTATATCTACCTAAACATTGTATCATGGT	120
Sbjct	61	TTTTTAAAAACACATGACCACATATGTATATGTATATCTACCTAAACATTGTATCATGGT	120
Query	121	TTCAGTATGTTATTCATGTATTACTGGGAGATGCTACCAAGAAACCAACCCAAAGAAAAT	180
Sbjct	121	TTCAGTATGTTATTCATGTATTACTGGGAGATGCTACCAAGAAACCAACCCAAAGAAAAT	180
Query	181	TCTGGAAAAATACATTTCTATTTATAGAATAAATGTTTCATTTATATAAAAGCAAAAGAAC	240
Sbjct	181	TCTGGAAAAATACATTTCTATTTATAGAATAAATGTTTCATTTATATAAAAGCAAAAGAAC	240
Query	241	TTAGAGTTCTAATAAATGGGATGTCTAATAAATTATGAAGTTACTGATTTGAATATATTA	300
Sbjct	241	TTAGAGTTCTAATAAATGGGATGTCTAATAAATTATGAAGTTACTGATTTGAATATATTA	300
Query	301	TATTTTATAACTTCCTTGCCAAAGTCCTGATTTAGTACATTAGAGAACCTGTGTTTCCT	360
Sbjct	301	TATTTTATAACTTCCTTGCCAAAGTCCTGATTTAGTACATTAGAGAACCTGTGTTTCCT	360
Query	361	CTCTCCTCTACCATTCTCTCTCTCCATACAGTCATTTGGGCTTTTTACTCAAAGAGAA	420
Sbjct	361	CTCTCCTCTACCATTCTCTCTCTCCATACAGTCATTTGGGCTTTTTACTCAAAGAGAA	420
Query	421	TCAAGAAATAATAAGGTATAACAAGCTTGGCAAAGTGTTGGCTTTTTTaaaaaaaatttt	480
Sbjct	421	TCAAGAAATAATAAGGTATAACAAGCTTGGCAAAGTGTTGGCTTTTTTAAAAAAAAATTTT	480

PATENT SEQUENCE ALIGNMENT

Query	481	tttAATCTCTAGCAGTTTGGTAATTTAGCAGCATCATTTATTTGGGATTCTTTTATCTGA	540
Sbjct	481	TTTAATCTCTAGCAGTTTGGTAATTTAGCAGCATCATTTATTTGGGATTCTTTTATCTGA	540
Query	541	TTTCAACAGTGAAAAACATCCCTATGATAAAGCCTAATGACCCATTTC AAAAGATGGAA	600
Sbjct	541	TTTCAACAGTGAAAAACATCCCTATGATAAAGCCTAATGACCCATTTC AAAAGATGGAA	600
Query	601	TTGCCCTTCCTAGAAAATATGACGGAGAAAAGT	633
Sbjct	601	TTGCCCTTCCTAGAAAATATGACGGAGAAAAGT	633

Sequence 579 matched with Sequence 186

Query= Sequence ID - 579
Length=502

nt: 502

SEQ ID NO: 186

nt: 502

ALIGNMENTS

Identities = 502/502 (100%), Gaps = 0/502 (0%)

Query	1	CGAATAGCCAAGTGGTCTGACAAGATCGAGAGTAATGAGGCCCATACTTTAGTACAGTCT	60
Sbjct	1	CGAATAGCCAAGTGGTCTGACAAGATCGAGAGTAATGAGGCCCATACTTTAGTACAGTCT	60
Query	61	TGAATGGCCAGATGGTGTCTGGGCATACCCCAACCAGAGATATGTAAGTCTTTATGTTGTC	120
Sbjct	61	TGAATGGCCAGATGGTGTCTGGGCATACCCCAACCAGAGATATGTAAGTCTTTATGTTGTC	120
Query	121	AAAATTTCCCAGAAACATGAATTTCCCACTAAGATTCATTAAGGAAAACTAGAATGAAAA	180
Sbjct	121	AAAATTTCCCAGAAACATGAATTTCCCACTAAGATTCATTAAGGAAAACTAGAATGAAAA	180
Query	181	CAAAAACGTTTCCTTGATAATATTCATTANAAAGAAATGAAGAAGGCCGGGCATGGTGGC	240
Sbjct	181	CAAAAACGTTTCCTTGATAATATTCATTANAAAGAAATGAAGAAGGCCGGGCATGGTGGC	240
Query	241	TCACGCCTGTAATCCCAGCACTTTGAGAGGCCAAGGTAGGCAGATCATGAGGTCAGGAGT	300
Sbjct	241	TCACGCCTGTAATCCCAGCACTTTGAGAGGCCAAGGTAGGCAGATCATGAGGTCAGGAGT	300
Query	301	TTGAGACCAGCCTGGCCAACATAGTGAAATCCCGTCTCTACCAAAAAATACaaaaaaTTA	360
Sbjct	301	TTGAGACCAGCCTGGCCAACATAGTGAAATCCCGTCTCTACCAAAAAATACAAAAAATTA	360
Query	361	GCCGGGCATGGTGGCACACACCTGTCATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAT	420
Sbjct	361	GCCGGGCATGGTGGCACACACCTGTCATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAT	420
Query	421	TGCTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCTGAGATTGCACCACTGTACTACAGCC	480
Sbjct	421	TGCTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCTGAGATTGCACCACTGTACTACAGCC	480

PATENT SEQUENCE ALIGNMENT

Query	481	TAGGTGACAGTGCAAGACTCTG	502
Sbjct	481	TAGGTGACAGTGCAAGACTCTG	502

Sequence 580 matched with Sequence 187

Query= Sequence ID - 580
Length=316

nt: 316

SEQ ID NO: 187

nt: 316

ALIGNMENTS

Identities = 316/316 (100%), Gaps = 0/316 (0%)

Query	1	CCTATGCCAAACTAAAGAAAGCTTGCCTGGCCTACAGGCCTAAAGGTTCAAATGNGGATT	60
Sbjct	1	CCTATGCCAAACTAAAGAAAGCTTGCCTGGCCTACAGGCCTAAAGGTTCAAATGNGGATT	60
Query	61	aaaaaaaaCACAGTAGTCACATAAAATGTCTGCTGGCTGGCTGGAATTCCATCACCTACAA	120
Sbjct	61	AAAAAAACACAGTAGTCACATAAAATGTCTGCTGGCTGGCTGGAATTCCATCACCTACAA	120
Query	121	TTTACCTGCTTTCAAAAACTGTGTTCAACATTGAGAAAACAGAAAACCACTTATCTTGAG	180
Sbjct	121	TTTACCTGCTTTCAAAAACTGTGTTCAACATTGAGAAAACAGAAAACCACTTATCTTGAG	180
Query	181	CTTAATATGGGCTTCTTTTTCTTAACTGTAGAACACTTACTGAAATATCAAATCAATGG	240
Sbjct	181	CTTAATATGGGCTTCTTTTTCTTAACTGTAGAACACTTACTGAAATATCAAATCAATGG	240
Query	241	TTAGGATATGTATCCTAGGCAGGCCTAAACCATTAACACTTGGTTTAAGCACTTTGTAT	300
Sbjct	241	TTAGGATATGTATCCTAGGCAGGCCTAAACCATTAACACTTGGTTTAAGCACTTTGTAT	300
Query	301	AATTNACCTCCTAAAT	316
Sbjct	301	AATTNACCTCCTAAAT	316

Sequence 581 matched with Sequence 188

Query= Sequence ID 581
Length=94

SEQ ID NO: 188

ALIGNMENTS

Identities = 94/94 (100%), Gaps = 0/94 (0%)

```
Query   1   CTTCATGAGTGCCCGGTTGCCCAAGTCAAAAACCTGGGAGTGATATAAACTCCCCACACA   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1   CTTCATGAGTGCCCGGTTGCCCAAGTCAAAAACCTGGGAGTGATATAAACTCCCCACACA   60

Query   61  TCCAGTCAGTCACTCATCAACTCTATTGATTCTG   94
          ||||||||||||||||||||||||||||||||
Sbjct   61  TCCAGTCAGTCACTCATCAACTCTATTGATTCTG   94
```

Length=644

Identities = 644/644 (100%), Gaps = 0/644 (0%)

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PATENT SEQUENCE ALIGNMENT

Query	481	TTCACTGCATTTTTGTGGGCTGCACTTACCTTTCAGGTAACAACAACACTGGCCCCTCTT	540
Sbjct	481	TTCACTGCATTTTTGTGGGCTGCACTTACCTTTCAGGTAACAACAACACTGGCCCCTCTT	540
Query	541	GCCCTTCTAGTCAGAAGTGCCAAAATGATGAGAGCTAGCCATGACAAACCCACAGCCAAC	600
Sbjct	541	GCCCTTCTAGTCAGAAGTGCCAAAATGATGAGAGCTAGCCATGACAAACCCACAGCCAAC	600
Query	601	ATTACACTGAATGTGCAAACTGGAAGGGCATCCAAACAGAGGA	644
Sbjct	601	ATTACACTGAATGTGCAAACTGGAAGGGCATCCAAACAGAGGA	644

nt: 631

nt: 631

Identities = 631/631 (100%), Gaps = 0/631 (0%)

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PATENT SEQUENCE ALIGNMENT

```
Query  481  TAAAACCGGTTACTGTCCAGAAAATGATAAGAATCCCTGGGTTCCAAATCCTTCATAAGG  540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TAAAACCGGTTACTGTCCAGAAAATGATAAGAATCCCTGGGTTCCAAATCCTTCATAAGG  540

Query  541  TATTTATTCATTTATTTATTCAACACATTTACTCAATGCCTCCGCTCTGCTGCAACTACA  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TATTTATTCATTTATTTATTCAACACATTTACTCAATGCCTCCGCTCTGCTGCAACTACA  600

Query  601  CTGACATTCTGCTTCTAATCTAACCGAAAAAT  631
        ||||||||||||||||||||||||||||
Sbjct  601  CTGACATTCTGCTTCTAATCTAACCGAAAAAT  631
```

Sequence 585 matched with Sequence 191

Query= Sequence ID 585
Length=638

SEQ ID NO: 191

ALIGNMENTS

Identities = 638/638 (100%), Gaps = 0/638 (0%)

Query	1	TTTCAAATTGTACAATAACACAAACAACCTTTGTTAAGGCCATGTTTTATTTGCTGATTAA	60
Sbjct	1	TTTCAAATTGTACAATAACACAAACAACCTTTGTTAAGGCCATGTTTTATTTGCTGATTAA	60
Query	61	TGGACAAAAGGCAATGTAATTTATTTTCAAGTATTTTCTTGAAAGTCTGTGCTCATAAAA	120
Sbjct	61	TGGACAAAAGGCAATGTAATTTATTTTCAAGTATTTTCTTGAAAGTCTGTGCTCATAAAA	120
Query	121	ATCATGAAAAGTTGGAAAGACTGTTAAATCACTGAAACTTCAAATATATCTTACACAATC	180
Sbjct	121	ATCATGAAAAGTTGGAAAGACTGTTAAATCACTGAAACTTCAAATATATCTTACACAATC	180
Query	181	TTGTTTGTACAAAAATACAAGTTAAATATAAACATAAAGCAATCATGGTAATTTTATGCA	240
Sbjct	181	TTGTTTGTACAAAAATACAAGTTAAATATAAACATAAAGCAATCATGGTAATTTTATGCA	240
Query	241	AATCTGTTTTATGTGATCATCAGTTATATATAAAAGTTTCTCAGTTCTGTTATTTGTGAA	300
Sbjct	241	AATCTGTTTTATGTGATCATCAGTTATATATAAAAGTTTCTCAGTTCTGTTATTTGTGAA	300
Query	301	AAGATCAATACCAGATTGAATGACTACCTATTGGCAAAGGGCCCTAAAAAGCTTACTTTA	360
Sbjct	301	AAGATCAATACCAGATTGAATGACTACCTATTGGCAAAGGGCCCTAAAAAGCTTACTTTA	360
Query	361	GCACTCATCTTTTACATGGTTAAATGCATTTCTTAATTTGAGATCACCTAAACACTGGAA	420
Sbjct	361	GCACTCATCTTTTACATGGTTAAATGCATTTCTTAATTTGAGATCACCTAAACACTGGAA	420
Query	421	AAGaaaaaaaTGAAAGGGCAGTATGTCCATAAACCAACAAATAATTTGGCTGTAATGTA	480
Sbjct	421	AAGAAAAAAAAATGAAAGGGCAGTATGTCCATAAACCAACAAATAATTTGGCTGTAATGTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCATaaaacacaaacccccacacatctgtacaataaacattatgtattacatacacacaac	540
Sbjct	481	TCATAAAACACAAACCCCACACATCTGTACAATAAACATTATGTATTACATACACACAAC	540
Query	541	acacacCCAGTCATAAAGCCTAATGATGTGCTGCTTCCAGTTCAATATTCAGCTGTGCAT	600
Sbjct	541	ACACACCCAGTCATAAAGCCTAATGATGTGCTGCTTCCAGTTCAATATTCAGCTGTGCAT	600
Query	601	TTTTTCTTATTTTCATCAAATGAATAGCTTTTTTGTACC	638
Sbjct	601	TTTTTCTTATTTTCATCAAATGAATAGCTTTTTTGTACC	638

Sequence 586 matched with Sequence 192

Query= Sequence ID 586
Length=283

SEQ ID NO: 192

ALIGNMENTS

Identities = 283/283 (100%), Gaps = 0/283 (0%)

Query	1	GTAAACTGTTCTCTCCGAGGGAAAAAATGGAAGTTATCCTCACAGTTCAGTCCCGTGGTA	60
Sbjct	1	GTAAACTGTTCTCTCCGAGGGAAAAAATGGAAGTTATCCTCACAGTTCAGTCCCGTGGTA	60
Query	61	TTTCTTCTGTCCCATGCTTTGCATGACTGCCATGGTACAGCCTTGTTTCAAAGTTCAC	120
Sbjct	61	TTTCTTCTGTCCCATGCTTTGCATGACTGCCATGGTACAGCCTTGTTTCAAAGTTCAC	120
Query	121	TGTGATCTGTGGGTCTTTGAGTTTCAGTGAGTTTGCTGAAATGTGGAAGAAGTAGTTCCA	180
Sbjct	121	TGTGATCTGTGGGTCTTTGAGTTTCAGTGAGTTTGCTGAAATGTGGAAGAAGTAGTTCCA	180
Query	181	AACTTCAATGTTCAATGAAATTTTGTTCAGTTTGAAATGGAGAGAGCAGCTTTAAAAG	240
Sbjct	181	AACTTCAATGTTCAATGAAATTTTGTTCAGTTTGAAATGGAGAGAGCAGCTTTAAAAG	240
Query	241	GTACTAAGCCTTTTACAAATTGGTGAGTACTGGCACATGAGAT	283
Sbjct	241	GTACTAAGCCTTTTACAAATTGGTGAGTACTGGCACATGAGAT	283

Sequence 587 matched with Sequence 193

Query= Sequence ID 587

Length=613

SEQ ID NO: 193

ALIGNMENTS

Identities = 613/613 (100%), Gaps = 0/613 (0%)

Query	1	tttttttttttCCTTAAAAGGTAACCCCTAAACACAGCTAAAACTATGCCATCAGCTGAC	60
Sbjct	1	TTTTTTTTTTTCCTTAAAAGGTAACCCCTAAACACAGCTAAAACTATGCCATCAGCTGAC	60
Query	61	TCCAAGGNACACACAGTCCTGTATCTGGAAGTACTGAGTGGCAGGCATCTTTCTCTGCCT	120
Sbjct	61	TCCAAGGNACACACAGTCCTGTATCTGGAAGTACTGAGTGGCAGGCATCTTTCTCTGCCT	120
Query	121	CTGACAGTGGAGTCCCCATCACTGCAGAGCATAGCCAAAGGAGTCAAAGGTCTCAGCGGG	180
Sbjct	121	CTGACAGTGGAGTCCCCATCACTGCAGAGCATAGCCAAAGGAGTCAAAGGTCTCAGCGGG	180
Query	181	TCACTGCCTTATCAACCCTCACCAGTCCCTTATGTTTTTTAATATTTTATAATCTTGACA	240
Sbjct	181	TCACTGCCTTATCAACCCTCACCAGTCCCTTATGTTTTTTAATATTTTATAATCTTGACA	240
Query	241	TGACACCAAGATGCTTTAATAAAAAAGCACCTCTAACTCGGTCTTGATTCACTTACCTT	300
Sbjct	241	TGACACCAAGATGCTTTAATAAAAAAGCACCTCTAACTCGGTCTTGATTCACTTACCTT	300
Query	301	GAGCCTGGGACTTCTCTAGGCTCCTGAGGCAAAAACAGGTAGAGGGGAGATGGTGGAAACA	360
Sbjct	301	GAGCCTGGGACTTCTCTAGGCTCCTGAGGCAAAAACAGGTAGAGGGGAGATGGTGGAAACA	360
Query	361	TAAACACAAATTTTGCTTGGCACCCACCTTGGCGTCTGTCCCCATGACCAGGTCTTTCAA	420
Sbjct	361	TAAACACAAATTTTGCTTGGCACCCACCTTGGCGTCTGTCCCCATGACCAGGTCTTTCAA	420
Query	421	TTCGATGATTTTGTCAATTGATGGAGGAGCGATATCGTTTCTCAATGATATTATGGGTTGT	480
Sbjct	421	TTCGATGATTTTGTCAATTGATGGAGGAGCGATATCGTTTCTCAATGATATTATGGGTTGT	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCGCCTTTCTCCTTCTTTGGGGGGCTCAAGCTGCTTGACTCCCCCAGGTACCTGCTTAAT	540
Sbjct	481	CCGCCTTTCTCCTTCTTTGGGGGGCTCAAGCTGCTTGACTCCCCCAGGTACCTGCTTAAT	540
Query	541	GGGGCACTTTCTCTTGCCCCATCATTACAGGCATTGTGGTCAGAATGGTCCCACTGCTGC	600
Sbjct	541	GGGGCACTTTCTCTTGCCCCATCATTACAGGCATTGTGGTCAGAATGGTCCCACTGCTGC	600
Query	601	CCACCAGGGTCTA	613
Sbjct	601	CCACCAGGGTCTA	613

Sequence 588 matched with Sequence 194

Query= Sequence ID 588

Length=350

SEQ ID NO: 194

ALIGNMENTS

Identities = 350/350 (100%), Gaps = 0/350 (0%)

Query	1	CTAGTCTTTTCATAGTCTGCATAGAGTCTGGCCATTACCATCAGTTTTTAAGATGTCCAT	60
Sbjct	1	CTAGTCTTTTCATAGTCTGCATAGAGTCTGGCCATTACCATCAGTTTTTAAGATGTCCAT	60
Query	61	ATTGTGGCCGGGCGCGGTGGCTCACGCCTGGTAGTCCCAGCACTTTGGGAGGCTGAGGCA	120
Sbjct	61	ATTGTGGCCGGGCGCGGTGGCTCACGCCTGGTAGTCCCAGCACTTTGGGAGGCTGAGGCA	120
Query	121	GGTGGATCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCGTCTCT	180
Sbjct	121	GGTGGATCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCGTCTCT	180
Query	181	ACTaaaaaaaaatattaaaaaaTTGGCCAGGCCTGGTGGTGGGCGCCTGTGGTCCCGGCTG	240
Sbjct	181	ACTAAAAAAAAATATTAaaaaaTTGGCCAGGCCTGGTGGTGGGCGCCTGTGGTCCCGGCTG	240
Query	241	CTTGGGAGGCTGAGGCAGGANAATGGTGTGAACCCGGAAGTCGGAGGTTGCAGTGAGCCA	300
Sbjct	241	CTTGGGAGGCTGAGGCAGGANAATGGTGTGAACCCGGAAGTCGGAGGTTGCAGTGAGCCA	300
Query	301	AGATTGCACCTGGGCAACACAGCGAGACTCCGTCTCaaaaaaaaaaaaaaaaa	350
Sbjct	301	AGATTGCACCTGGGCAACACAGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAA	350

Sequence 589 matched with Sequence 195

Query= Sequence ID 589
Length=541

SEQ ID NO: 195

ALIGNMENTS

Identities = 541/541 (100%), Gaps = 0/541 (0%)

Query	1	CAATTATTTATTACCTTTCCATTTGTTTCGCCTGATGATGTGACAATGCATGGTCTTTGTG	60
Sbjct	1	CAATTATTTATTACCTTTCCATTTGTTTCGCCTGATGATGTGACAATGCATGGTCTTTGTG	60
Query	61	CATGCTGCTAGACACTTTTCTTTCCCAGCCGAAAAGTCTATTATGTAATTTTACATTCA	120
Sbjct	61	CATGCTGCTAGACACTTTTCTTTCCCAGCCGAAAAGTCTATTATGTAATTTTACATTCA	120
Query	121	TAATTTTAATGTGGATGATCAGGATTAAATCAAGATATATATCTGGAACCTCTTATAAAT	180
Sbjct	121	TAATTTTAATGTGGATGATCAGGATTAAATCAAGATATATATCTGGAACCTCTTATAAAT	180
Query	181	GGAGCACTTAGAAATTTGTTGTTCTGCACTTAACCTAGAGAGAGAAAAAATGCTTTTCTT	240
Sbjct	181	GGAGCACTTAGAAATTTGTTGTTCTGCACTTAACCTAGAGAGAGAAAAAATGCTTTTCTT	240
Query	241	TGTGAAAAATCTGAATTCCTGTCTGACCTTCTGTGATGTGGAAACCCTAGGCTCTGAGA	300
Sbjct	241	TGTGAAAAATCTGAATTCCTGTCTGACCTTCTGTGATGTGGAAACCCTAGGCTCTGAGA	300
Query	301	CACACTCTCTGGTGTCTGAGACAGAACCAAAGCAATAACGTTGTGATGCCCACAGGCCTG	360
Sbjct	301	CACACTCTCTGGTGTCTGAGACAGAACCAAAGCAATAACGTTGTGATGCCCACAGGCCTG	360
Query	361	GAGCCAGCTAGCGACCTTGTGCCGCCAGCTGTCCATGGCCCGTGCAGAGCAGAGGACAG	420
Sbjct	361	GAGCCAGCTAGCGACCTTGTGCCGCCAGCTGTCCATGGCCCGTGCAGAGCAGAGGACAG	420
Query	421	TGAGTGTCTGCACTGAGAACCTTAAACCACAGTTGAACATAACCCACACCTGTTTGTCTTA	480
Sbjct	421	TGAGTGTCTGCACTGAGAACCTTAAACCACAGTTGAACATAACCCACACCTGTTTGTCTTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGCTATAGTGTA	AAAA	CAAAGTTTGGGCTCTG	AAAATTTAACTG	AAAAAGATTTCCTTGT	540
Sbjct	481	AGCTATAGTGTA	AAAA	CAAAGTTTGGGCTCTG	AAAATTTAACTG	AAAAAGATTTCCTTGT	540
Query	541	T	541				
Sbjct	541	T	541				

Sequence 590 matched with Sequence 196

Query= Sequence ID 590

Length=336

SEQ ID NO: 196

ALIGNMENTS

Identities = 336/336 (100%), Gaps = 0/336 (0%)

Query	1	GTGGCAGCAGGCGCAGCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGGACCT	60
Sbjct	1	GTGGCAGCAGGCGCAGCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGGACCT	60
Query	61	GTACGTGCCGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCACGCATC	120
Sbjct	61	GTACGTGCCGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCACGCATC	120
Query	121	CATCCAGATGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAATGGCCAGTTTAA	180
Sbjct	121	CATCCAGATGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAATGGCCAGTTTAA	180
Query	181	AACTTATGCTATCTGCGGGGCCATTTCGTAGGATGGGTGAGTCAGATGATTCCATTCTCCG	240
Sbjct	181	AACTTATGCTATCTGCGGGGCCATTTCGTAGGATGGGTGAGTCAGATGATTCCATTCTCCG	240
Query	241	ATTGGCCAAGGCCGATGGCATCGTCTCAAAGAACTTTTGGAGAGAGAATCACAGATGT	300
Sbjct	241	ATTGGCCAAGGCCGATGGCATCGTCTCAAAGAACTTTTGGAGAGAGAATCACAGATGT	300
Query	301	GGAATATTTGTCATAAATAAATAATGAAAACCTAAA	336
Sbjct	301	GGAATATTTGTCATAAATAAATAATGAAAACCTAAA	336

Sequence 591 matched with Sequence 197

Query= Sequence ID 591
Length=377

SEQ ID NO: 197

ALIGNMENTS

Identities = 377/377 (100%), Gaps = 0/377 (0%)

Query	1	CAGCAGCAGAAATGTTTGCAAGATAGGCCAAAATGAGTACAAAAGGTCTGTCTTCCATCA	60
Sbjct	1	CAGCAGCAGAAATGTTTGCAAGATAGGCCAAAATGAGTACAAAAGGTCTGTCTTCCATCA	60
Query	61	GACCCAGTGATGCTGCGACTCACACGCTTCAATTCAAGACCTGACCGCTAGTAGGGAGGT	120
Sbjct	61	GACCCAGTGATGCTGCGACTCACACGCTTCAATTCAAGACCTGACCGCTAGTAGGGAGGT	120
Query	121	TTATTCANATCGCTGGCAGCCTCGGCTGAGCAGATGCACAGAGGGGATCACTGTGCAGTG	180
Sbjct	121	TTATTCANATCGCTGGCAGCCTCGGCTGAGCAGATGCACAGAGGGGATCACTGTGCAGTG	180
Query	181	GGACCACCCTCACTGGCCTTCTGCAGCAGGGTTCTGGGATGTTTTCACTGGTCAAAATAC	240
Sbjct	181	GGACCACCCTCACTGGCCTTCTGCAGCAGGGTTCTGGGATGTTTTCACTGGTCAAAATAC	240
Query	241	TCTGTTTAGAGCAAGGGCTCAGAAAACAGAAATACTGTCATGGAGGTGCTGAACACAGGG	300
Sbjct	241	TCTGTTTAGAGCAAGGGCTCAGAAAACAGAAATACTGTCATGGAGGTGCTGAACACAGGG	300
Query	301	AAGGTCTGGTACATATTGGAATTATGAGCAGAACAAATACTCAACTAAATGCACAAAGT	360
Sbjct	301	AAGGTCTGGTACATATTGGAATTATGAGCAGAACAAATACTCAACTAAATGCACAAAGT	360
Query	361	ATAAAGTGTAGCCATGT	377
Sbjct	361	ATAAAGTGTAGCCATGT	377

Sequence 592 matched with Sequence 198

Query= Sequence ID 592
Length=63

SEQ ID NO: 198

ALIGNMENTS

Identities = 63/63 (100%), Gaps = 0/63 (0%)

Query	1	TACTCAATGAAAAACCATGATAATTCTTTGTATATAAAATAAACATTTGaaaaaaaaa	60
Sbjct	1	TACTCAATGAAAAACCATGATAATTCTTTGTATATAAAATAAACATTTGAAAAAAAAA	60
Query	61	aaa	63
Sbjct	61	AAA	63

Sequence 593 matched with Sequence 199

Query= Sequence ID - 593
Length=565

nt: 565

SEQ ID NO: 199

nt: 565

ALIGNMENTS

Identities = 565/565 (100%), Gaps = 0/565 (0%)

Query	1	CAGGATCAAGGTGAAAAGGAGAACCCCATGCGGGAACCTTCGCATCCGCAAACCTGTGTCTC	60
Sbjct	1	CAGGATCAAGGTGAAAAGGAGAACCCCATGCGGGAACCTTCGCATCCGCAAACCTGTGTCTC	60
Query	61	AACATCTGTGTTGGGGAGAGTGGAGACAGACTGACGCGAGCAGCCAAGGTGTTGGAGCAG	120
Sbjct	61	AACATCTGTGTTGGGGAGAGTGGAGACAGACTGACGCGAGCAGCCAAGGTGTTGGAGCAG	120
Query	121	CTCACAGGGCAGACCCCTGTGTTTTCCAAAGCTAGATACACTGTCAGATCCTTTGGCATC	180
Sbjct	121	CTCACAGGGCAGACCCCTGTGTTTTCCAAAGCTAGATACACTGTCAGATCCTTTGGCATC	180
Query	181	CGGAGAAATGAAAAGATTGCTGTCCACTGCACAGTTCGAGGGGCCAAGGCAGAAGAAATC	240
Sbjct	181	CGGAGAAATGAAAAGATTGCTGTCCACTGCACAGTTCGAGGGGCCAAGGCAGAAGAAATC	240
Query	241	TTGGAGAAGGGTCTAAAGGTGCGGGAGTATGAGTTAAGAAAAACAACCTTCTCAGATACT	300
Sbjct	241	TTGGAGAAGGGTCTAAAGGTGCGGGAGTATGAGTTAAGAAAAACAACCTTCTCAGATACT	300
Query	301	GGAAACTTTGGTTTTGGGATCCAGGAACACATCGATCTGGGTATCAAATATGACCCAAGC	360
Sbjct	301	GGAAACTTTGGTTTTGGGATCCAGGAACACATCGATCTGGGTATCAAATATGACCCAAGC	360
Query	361	ATTGGTATCTACGGCCTGGACTTCTATGTGGTGCTGGGTAGGCCAGGTTTCAGCATCGCA	420
Sbjct	361	ATTGGTATCTACGGCCTGGACTTCTATGTGGTGCTGGGTAGGCCAGGTTTCAGCATCGCA	420
Query	421	GACAAGAAGCGCAGGACAGGCTGCATTGGGGCCAAACACAGAATCAGCAAAGAGGAGGCC	480
Sbjct	421	GACAAGAAGCGCAGGACAGGCTGCATTGGGGCCAAACACAGAATCAGCAAAGAGGAGGCC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATGCGCTGGTTCCAGCAGAAGTATGATGGGATCATCCTTCCTGGCAAATAAATTCCCGTT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATGCGCTGGTTCCAGCAGAAGTATGATGGGATCATCCTTCCTGGCAAATAAATTCCCGTT  540

Query  541  TCTATCCAAAAGAGCAATAAAAAGT  565
          ||||||||||||||||||
Sbjct  541  TCTATCCAAAAGAGCAATAAAAAGT  565
```

Sequence 594 matched with Sequence 200

Query= Sequence ID 594
Length=629

SEQ ID NO: 200

ALIGNMENTS

Identities = 629/629 (100%), Gaps = 0/629 (0%)

Query	1	CAGAAGAGTAAGCAAATCTCaaagcagcgaaaggaagaaactaaaaaggtagagcaga	60
Sbjct	1	CAGAAGAGTAAGCAAATCTCAAAGCAGCGAAAGGGAAGAACTAAAAAAGGTAGAGCAGA	60
Query	61	aataagagaaaaatagagaagagacaattgagaaaaataattgaaacccaaaGGTGGTTC	120
Sbjct	61	AATAAGAGAAAAATAGAGAAGAGAACAATTGAGAAAAATAATTGAAACCAAAGGTGGTTC	120
Query	121	TTTGAAGCCTAACAAAATGGACACATCTTTAGTTAGAGTGACCAAGAAAAAGGGCAG	180
Sbjct	121	TTTGAAGCCTAACAAAATGGACACATCTTTAGTTAGAGTGACCAAGAAAAAGGGCAG	180
Query	181	TGACTCAGATTACTTCATTCAAGAGTGAAAGAGGGCACATCACTACCAATTTACAGAAAT	240
Sbjct	181	TGACTCAGATTACTTCATTCAAGAGTGAAAGAGGGCACATCACTACCAATTTACAGAAAT	240
Query	241	AAAAAGGATTATGAGGAAATACTACAGATAATTGATGACATTAAGTTAGAAGAATATATT	300
Sbjct	241	AAAAAGGATTATGAGGAAATACTACAGATAATTGATGACATTAAGTTAGAAGAATATATT	300
Query	301	TCAAGAAAGACACAACTACTGAAACCGACTCAAGAAGAAACAGAAAATCTGAACAGACC	360
Sbjct	301	TCAAGAAAGACACAACTACTGAAACCGACTCAAGAAGAAACAGAAAATCTGAACAGACC	360
Query	361	TATAAAAAATAGAGATTTAATTGATATTCAGAAAGTTTCCCAAAAAGAAAAGCACTGGCC	420
Sbjct	361	TATAAAAAATAGAGATTTAATTGATATTCAGAAAGTTTCCCAAAAAGAAAAGCACTGGCC	420
Query	421	AAGATGACTTCACTGGTGAATTCTATCAAGTGTCAAAGATGAATTACTGACATTCATTCA	480
Sbjct	421	AAGATGACTTCACTGGTGAATTCTATCAAGTGTCAAAGATGAATTACTGACATTCATTCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CACTCCTTTAAGAAATAGAAGAGGGGACATCACTTTTCAAAGCATCGACATTCTAATCAT	540
Sbjct	481	CACTCCTTTAAGAAATAGAAGAGGGGACATCACTTTTCAAAGCATCGACATTCTAATCAT	540
Query	541	TAGTCCCTTGGTTTCCTGCTCCCAAAGCCAGGTGATGTATCACaaaaaaCCCCTACAGA	600
Sbjct	541	TAGTCCCTTGGTTTCCTGCTCCCAAAGCCAGGTGATGTATCACAAAAAACCCCTACAGA	600
Query	601	CCCACTGGGCACAATGGCTTTATGCCTAT	629
Sbjct	601	CCCACTGGGCACAATGGCTTTATGCCTAT	629

Sequence 595 matched with Sequence 201

Query= Sequence ID - 595 nt: 98
Length=98

SEQ ID NO: 201 nt: 98

ALIGNMENTS

Identities = 98/98 (100%), Gaps = 0/98 (0%)

```
Query 1 CTTTGCTCGAATNGTCAGATAAGGATTCTGTGAANGGAGATGAGATTCCATCCATGCTG 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 CTTTGCTCGAATNGTCAGATAAGGATTCTGTGAANGGAGATGAGATTCCATCCATGCTG 60

Query 61 ACTTTGANAATACATGTTCCCGAATTGGGGNCCCCAAA 98
      ||||||||||||||||||||||||||||||||||||
Sbjct 61 ACTTTGANAATACATGTTCCCGAATTGGGGNCCCCAAA 98
```

Sequence 596 matched with Sequence 202

Query= Sequence ID 596
Length=224

SEQ ID NO: 202

ALIGNMENTS

Identities = 224/224 (100%), Gaps = 0/224 (0%)

Query	1	CTCAAGTGTTCCCTCAGCTTAGGCTTTGTTTAAATGATCCCACCCAGGGGCGATGGTAGG	60
Sbjct	1	CTCAAGTGTTCCCTCAGCTTAGGCTTTGTTTAAATGATCCCACCCAGGGGCGATGGTAGG	60
Query	61	GAACAACAGGGTCACTAAACTATTTGGCTGGCTACAACCTCTGGGAAATGGTAAGACAGGG	120
Sbjct	61	GAACAACAGGGTCACTAAACTATTTGGCTGGCTACAACCTCTGGGAAATGGTAAGACAGGG	120
Query	121	AAAGGCCATGTTGTTTCATTCCCTTGTGCAGATCTAGGGAGAACCGCAGAGAGAACAGTTA	180
Sbjct	121	AAAGGCCATGTTGTTTCATTCCCTTGTGCAGATCTAGGGAGAACCGCAGAGAGAACAGTTA	180
Query	181	GCATTTCTTGTTCAATGAATTATCCTATTAAGAACACTGGATGT	224
Sbjct	181	GCATTTCTTGTTCAATGAATTATCCTATTAAGAACACTGGATGT	224

Sequence 597 matched with Sequence 203

Query= Sequence ID 597
Length=81

SEQ ID NO: 203

ALIGNMENTS

Identities = 81/81 (100%), Gaps = 0/81 (0%)

```
Query   1   CGGNCGCGGTCGACGCTACTCCTACCTATCTCCCCTTTTATACTAATAATCTTATAaaaa 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1   CGGNCGCGGTCGACGCTACTCCTACCTATCTCCCCTTTTATACTAATAATCTTATAAAAA 60

Query   61  aaaaaaaaaaaaaaaaaaaaaa 81
          ||||||||||||||||||
Sbjct   61  AAAAAAAAAAAAAAAAAAAAAA 81
```


Sequence 598 matched with Sequence 204

Query= Sequence ID - 598
Length=362

nt: 362

SEQ ID NO: 204

nt: 362

ALIGNMENTS

Identities = 362/362 (100%), Gaps = 0/362 (0%)

Query	1	GGCATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCAAGAGTTCAA	60
Sbjct	1	GGCATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCAAGAGTTCAA	60
Query	61	GGCTGCAACAAGCTTTGATTGCGCCACTGCACTCCANCCTTGGCGACAGACTAAAACGCT	120
Sbjct	61	GGCTGCAACAAGCTTTGATTGCGCCACTGCACTCCANCCTTGGCGACAGACTAAAACGCT	120
Query	121	GTCTCaaaaaaaaaacaacgacnaaaaaaaaaacagaaaaaTTAACTTAGGC	180
Sbjct	121	GTCTCAAAAAAAAAAACAAACGACNAAAAAAAAACAAACAGAAAAATTACTTAGGC	180
Query	181	AATGACAGTCCCTGGCAAATGCTGGGAGGGAGGCAACANTGGTCAAGGAAGGTAACCCTG	240
Sbjct	181	AATGACAGTCCCTGGCAAATGCTGGGAGGGAGGCAACANTGGTCAAGGAAGGTAACCCTG	240
Query	241	AANCAGGACTTGTAAGCAAATAANATTGGGAGGCCAAGGTGGGTGGATCACNAGGTCAG	300
Sbjct	241	AANCAGGACTTGTAAGCAAATAANATTGGGAGGCCAAGGTGGGTGGATCACNAGGTCAG	300
Query	301	GAGTTCGAGACCAACCTGGCCAACATAGTGAAACCCCGTCTTTCTAAAAATACaaaaaa	360
Sbjct	301	GAGTTCGAGACCAACCTGGCCAACATAGTGAAACCCCGTCTTTCTAAAAATACAAAAAA	360
Query	361	TT 362	
Sbjct	361	TT 362	

Sequence 599 matched with Sequence 205

Query= Sequence ID 599

Length=581

SEQ ID NO: 205

ALIGNMENTS

Identities = 581/581 (100%), Gaps = 0/581 (0%)

Query	1	GACAAAAGAACCATTTGGATACATAGGTATGGTCTGAGCTATGATATCAATTGGCTTCCT	60
Sbjct	1	GACAAAAGAACCATTTGGATACATAGGTATGGTCTGAGCTATGATATCAATTGGCTTCCT	60
Query	61	AGGGTTTATCGTGTGAGCACACCATATATTTACAGTAGGAATAGACGTAGACACACGAGC	120
Sbjct	61	AGGGTTTATCGTGTGAGCACACCATATATTTACAGTAGGAATAGACGTAGACACACGAGC	120
Query	121	ATATTTACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAAGTATTTAGCTG	180
Sbjct	121	ATATTTACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAAGTATTTAGCTG	180
Query	181	ACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTCTGAGCCCTAGG	240
Sbjct	181	ACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTCTGAGCCCTAGG	240
Query	241	ATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGCATTGTATTAGCAAACATCACT	300
Sbjct	241	ATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGCATTGTATTAGCAAACATCACT	300
Query	301	AGACATCGTACTACACGACACGTACTACGTTGTAGCTCACTTCCACTATGTCCTATCAAT	360
Sbjct	301	AGACATCGTACTACACGACACGTACTACGTTGTAGCTCACTTCCACTATGTCCTATCAAT	360
Query	361	AGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTATTCTCAGGCTA	420
Sbjct	361	AGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTATTCTCAGGCTA	420
Query	421	CACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATCGGCGTAAATCT	480
Sbjct	421	CACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATCGGCGTAAATCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AACTTTCTTCCCACAACACTTTCTCGGCCTGTCCGGAATGCCCCGACGTTACTCGGACTA  540
          |||
Sbjct  481  AACTTTCTTCCCACAACACTTTCTCGGCCTGTCCGGAATGCCCCGACGTTACTCGGACTA  540

Query  541  CCCCgatgcatacaccacatgaaacatcctatcatctggag  581
          |||
Sbjct  541  CCCCgatgcatacaccacatgaaacatcctatcatctggag  581
```

Sequence 600 matched with Sequence 206

Query= Sequence ID - 600
Length=595

nt: 595

SEQ ID NO: 206

nt: 595

ALIGNMENTS

Identities = 595/595 (100%), Gaps = 0/595 (0%)

Query	1	TTCAAATTCTTGNTAANAGTCTTTGTTCTGAATTTTACTTTGTCTGTTATTCCTATAGCC	60
Sbjct	1	TTCAAATTCTTGNTAANAGTCTTTGTTCTGAATTTTACTTTGTCTGTTATTCCTATAGCC	60
Query	61	TTTCCAATTTTCTTTTCGCTTGGAttttacgtgataagttttttcccccattttactttta	120
Sbjct	61	TTTCCAATTTTCTTTTCGCTTGGATTTTACGTGATAAGTTTTTCCCCATTTTACTTTTA	120
Query	121	ncaactctatatattttttaGTTGAGGTTGGGTTTCTTGTAACAGCATATAATTTGGGTTT	180
Sbjct	121	NCAACTCTATATTTTTTTAGTTGAGGTTGGGTTTCTTGTAACAGCATATAATTTGGGTTT	180
Query	181	TTTAATCCAATCTGAAAATTAATGTCCTTAATTTTGTGTTTATACCATTTACACATAATG	240
Sbjct	181	TTTAATCCAATCTGAAAATTAATGTCCTTAATTTTGTGTTTATACCATTTACACATAATG	240
Query	241	TACTCATATATAAGGTTTAACTGAAACCTACTATCTTGCTAGTTGTGCTCTACTTGAAtt	300
Sbjct	241	TACTCATATATAAGGTTTAACTGAAACCTACTATCTTGCTAGTTGTGCTCTACTTGAATT	300
Query	301	tttttttAGTATTCTGTTTTAATTGACCAACATTTGACTGTATCTCTTTGTGTAATTCTT	360
Sbjct	301	TTTTTTTAGTATTCTGTTTTAATTGACCAACATTTGACTGTATCTCTTTGTGTAATTCTT	360
Query	361	TTACAGGTTGCTGTAGGCATGACAATATATACACTTAACTTTTCTCAGTACACTGAGAGT	420
Sbjct	361	TTACAGGTTGCTGTAGGCATGACAATATATACACTTAACTTTTCTCAGTACACTGAGAGT	420
Query	421	TGAAATTGTAGTACTTCGAGGAAAACATAGAAAACCTTGCAATGATATCGGTTACATTTTA	480
Sbjct	421	TGAAATTGTAGTACTTCGAGGAAAACATAGAAAACCTTGCAATGATATCGGTTACATTTTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCACCTCCATATGTTGCAATTATTAAATGTATTAGATCTGCCTACCTCGAAAACCCATCA	540
Sbjct	481	CCACCTCCATATGTTGCAATTATTAAATGTATTAGATCTGCCTACCTCGAAAACCCATCA	540
Query	541	GTCTTTTAACTTTGCTCTCAATGGTGATTCATATTTTaaaaaaaCTTGAGGCAA	595
Sbjct	541	GTCTTTTAACTTTGCTCTCAATGGTGATTCATATTTTAAAAAACTTGAGGCAA	595

Sequence 601 matched with Sequence 207

Query= Sequence ID - 601
Length=522

nt: 522

SEQ ID NO: 207

nt: 522

ALIGNMENTS

Identities = 522/522 (100%), Gaps = 0/522 (0%)

Query	1	TCGACCGGGTTTGGAGCAGTGCCTTGTTGCTGTGCAGCGGATACTCTACAGGTACATTT	60
Sbjct	1	TCGACCGGGTTTGGAGCAGTGCCTTGTTGCTGTGCAGCGGATACTCTACAGGTACATTT	60
Query	61	CCTTTTTGGAACCAAAAGGGAGGGATTTGACAATATTGATGGTAGATCTTTTTCTTTAG	120
Sbjct	61	CCTTTTTGGAACCAAAAGGGAGGGATTTGACAATATTGATGGTAGATCTTTTTCTTTAG	120
Query	121	CAAGAATTAAGGATTTTGGTGGGTGGGGGAGGCTTCTGTGGGGACCAAGACAATGTACT	180
Sbjct	121	CAAGAATTAAGGATTTTGGTGGGTGGGGGAGGCTTCTGTGGGGACCAAGACAATGTACT	180
Query	181	GTCAGTCAGGATTTAAGTCGAACTACCTCATCCCTTGCCCCAGAGAACAGTTGATCGTGT	240
Sbjct	181	GTCAGTCAGGATTTAAGTCGAACTACCTCATCCCTTGCCCCAGAGAACAGTTGATCGTGT	240
Query	241	TTTAAACCAAAAAGGTGCGGAATGGAGAGAGGGAGGCGGTGCATTGCAGCTTCCGATAGAG	300
Sbjct	241	TTTAAACCAAAAAGGTGCGGAATGGAGAGAGGGAGGCGGTGCATTGCAGCTTCCGATAGAG	300
Query	301	CTTTTTATTTTGGATATCAGGAACCAATTTTGAAGATTTCTTAAGAAAGTCATTTACAT	360
Sbjct	301	CTTTTTATTTTGGATATCAGGAACCAATTTTGAAGATTTCTTAAGAAAGTCATTTACAT	360
Query	361	CAGGGACATGAAGAGCAAAGTAGGTATTTTGGTCAGTACTTGAATTTGATAGGCTTTAT	420
Sbjct	361	CAGGGACATGAAGAGCAAAGTAGGTATTTTGGTCAGTACTTGAATTTGATAGGCTTTAT	420
Query	421	GCAAACAACCTCTCCCTCTGCTGGAGTCTGGCAAGTTTGCTTTTCACTGGACGCTAATTCA	480
Sbjct	421	GCAAACAACCTCTCCCTCTGCTGGAGTCTGGCAAGTTTGCTTTTCACTGGACGCTAATTCA	480

```
Query    481  AGTGCCATACAAAAC TAAAATAANAGTTTTACTTATAACACA  522
        |||
Sbjct    481  AGTGCCATACAAAAC TAAAATAANAGTTTTACTTATAACACA  522
```

Sequence 602 matched with Sequence 208

Query= Sequence ID 602

Length=585

SEQ ID NO: 208

ALIGNMENTS

Identities = 585/585 (100%), Gaps = 0/585 (0%)

Query	1	CAGAAATCGCAATTGAAGACCAGATTTGTCAAGGTTTGAAACTGACATTTGATACTACCT	60
Sbjct	1	CAGAAATCGCAATTGAAGACCAGATTTGTCAAGGTTTGAAACTGACATTTGATACTACCT	60
Query	61	TCTCACCAAACACAGGAAAGAAAAGTGGTAAAATCAAGTCTTCTTACAAGAGGGAGTGTA	120
Sbjct	61	TCTCACCAAACACAGGAAAGAAAAGTGGTAAAATCAAGTCTTCTTACAAGAGGGAGTGTA	120
Query	121	TAAACCTTGTTGTGATGTTGACTTTGATTTTGCTGGACCTGCAATCCATGGTTCAGCTG	180
Sbjct	121	TAAACCTTGTTGTGATGTTGACTTTGATTTTGCTGGACCTGCAATCCATGGTTCAGCTG	180
Query	181	TCTTTGGTTATGAGGGCTGGCTTGCTGGCTACCAGATGACCTTTGACAGTGCCAAATCAA	240
Sbjct	181	TCTTTGGTTATGAGGGCTGGCTTGCTGGCTACCAGATGACCTTTGACAGTGCCAAATCAA	240
Query	241	AGCTGACAAGGAATAACTTTGCAGTGGGCTACAGGACTGGGGACTTCCAGCTACACACTA	300
Sbjct	241	AGCTGACAAGGAATAACTTTGCAGTGGGCTACAGGACTGGGGACTTCCAGCTACACACTA	300
Query	301	ATGTCAATGATGGGACAGAATTTGGAGGATCAATTTATCAGAAAGTTTGTGAAGATCTTG	360
Sbjct	301	ATGTCAATGATGGGACAGAATTTGGAGGATCAATTTATCAGAAAGTTTGTGAAGATCTTG	360
Query	361	ACACTTCAGTAAACCTTGCTTGGACATCAGGTACCAACTGCACTCGTTTTGGCATTGCAG	420
Sbjct	361	ACACTTCAGTAAACCTTGCTTGGACATCAGGTACCAACTGCACTCGTTTTGGCATTGCAG	420
Query	421	CTAAATATCAGTTGGATCCCACTGCTTCCATTTCTGCAAAAGTCAACAACCTCTAGCTTAA	480
Sbjct	421	CTAAATATCAGTTGGATCCCACTGCTTCCATTTCTGCAAAAGTCAACAACCTCTAGCTTAA	480

PATENT SEQUENCE ALIGNMENT

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Query  481  TTGGAGTAGGCTATACTCAGACTCTGAGGCCTGGTGTGAAGCTTACACTCTCTGCTCTGG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTGGAGTAGGCTATACTCAGACTCTGAGGCCTGGTGTGAAGCTTACACTCTCTGCTCTGG  540

Query  541  TAGATGGGAAGAGCATTAATGCTGGAGGCCACAAGGTTGGGCTCG  585
          ||||||||||||||||||||||||||||||||||||
Sbjct  541  TAGATGGGAAGAGCATTAATGCTGGAGGCCACAAGGTTGGGCTCG  585
```

Sequence 603 matched with Sequence 209

Query= Sequence ID - 603
Length=624

nt: 624

SEQ ID NO: 209

nt: 624

ALIGNMENTS

Identities = 624/624 (100%), Gaps = 0/624 (0%)

Query	1	GACACACGAGCATATTTACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAA	60
Sbjct	1	GACACACGAGCATATTTACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAA	60
Query	61	GTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTC	120
Sbjct	61	GTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTC	120
Query	121	TGAGCCCTAGGATTCATCTTTCTTTTACCCGTAGGTGGCCTGACTGGCATTGTATTAGCA	180
Sbjct	121	TGAGCCCTAGGATTCATCTTTCTTTTACCCGTAGGTGGCCTGACTGGCATTGTATTAGCA	180
Query	181	AACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGTAGCCCACTTCCACTAT	240
Sbjct	181	AACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGTAGCCCACTTCCACTAT	240
Query	241	GTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTA	300
Sbjct	241	GTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTA	300
Query	301	TTCTCAGGCTACACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATC	360
Sbjct	301	TTCTCAGGCTACACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATC	360
Query	361	GGCGTAAATCTAACTTTCTTCCCACAACACTTTCTCGGCCTATCCGGAATGCCCCGACGT	420
Sbjct	361	GGCGTAAATCTAACTTTCTTCCCACAACACTTTCTCGGCCTATCCGGAATGCCCCGACGT	420
Query	421	TACTCGGACTACCCCGATGCATACACCACATGAAACATCCTATCATCTGTAGGCTCATTC	480
Sbjct	421	TACTCGGACTACCCCGATGCATACACCACATGAAACATCCTATCATCTGTAGGCTCATTC	480

Query	481	ATTTCTCTAACAGCAGTAATATTAATAATTTTCATGATTGAGAAGCCTTCGCTTCGAAG	540
Sbjct	481	ATTTCTCTAACAGCAGTAATATTAATAATTTTCATGATTGAGAAGCCTTCGCTTCGAAG	540
Query	541	CGAAAAGTCCTAATAGTAGAAGAACCCTCCATAAACCTGGAGTGA	600
		CTATATGGATGCCCC	
Sbjct	541	CGAAAAGTCCTAATAGTAGAAGAACCCTCCATAAACCTGGAGTGA	600
		CTATATGGATGCCCC	
Query	601	CCACCCTACCACACATT	624
		CGAAGAA	
Sbjct	601	CCACCCTACCACACATT	624
		CGAAGAA	

Sequence 605 matched with Sequence 210

Query= Sequence ID - 605
Length=338

nt: 338

SEQ ID NO: 210

nt: 338

ALIGNMENTS

Identities = 338/338 (100%), Gaps = 0/338 (0%)

Query	1	ACCTGAGGCCTCGGTGGGGCCAGTGCGACGCTGGCTTAAGGAGCTGGAGGGGTTCTAAT	60
Sbjct	1	ACCTGAGGCCTCGGTGGGGCCAGTGCGACGCTGGCTTAAGGAGCTGGAGGGGTTCTAAT	60
Query	61	ACACATTTAATTCAGTTTCTCTTCCCTAAGAGGCTGCCGGAGTTGGGGCCTCCTCCAGCA	120
Sbjct	61	ACACATTTAATTCAGTTTCTCTTCCCTAAGAGGCTGCCGGAGTTGGGGCCTCCTCCAGCA	120
Query	121	GAGACCCTCGGACCCCTGCAGGGCCTGGACTTGGGGTGAACAGGGCTTCAGTCAGCGCAA	180
Sbjct	121	GAGACCCTCGGACCCCTGCAGGGCCTGGACTTGGGGTGAACAGGGCTTCAGTCAGCGCAA	180
Query	181	GTATTCCATTTGCATTTGGTAATTTTTCATGCCACCTATTTATGAATATATAAATCTTTA	240
Sbjct	181	GTATTCCATTTGCATTTGGTAATTTTTCATGCCACCTATTTATGAATATATAAATCTTTA	240
Query	241	TACCAAATCTATTTTTTAAAACATGGAAAAGTTGCCTTTATGGAACTTGGCAGAGCCAG	300
Sbjct	241	TACCAAATCTATTTTTTAAAACATGGAAAAGTTGCCTTTATGGAACTTGGCAGAGCCAG	300
Query	301	AGTGTACACATTCCTAAACCATTAACAGATTTCTATA	338
Sbjct	301	AGTGTACACATTCCTAAACCATTAACAGATTTCTATA	338

Sequence 606 matched with Sequence 211

Query= Sequence ID - 606
Length=556

nt: 556

SEQ ID NO: 211

nt: 556

ALIGNMENTS

Identities = 556/556 (100%), Gaps = 0/556 (0%)

Query	1	GGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAGTACTTGAGTGTGCAGCTGCATG	60
Sbjct	1	GGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAGTACTTGAGTGTGCAGCTGCATG	60
Query	61	AGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGAAGCTATACCAGTAGGACAAGGCAGGA	120
Sbjct	61	AGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGAAGCTATACCAGTAGGACAAGGCAGGA	120
Query	121	AAATACTACACTTTCAGGATCAAGCCCCTCTGACTCTCATTTGGAAACTGGATGTTTGCT	180
Sbjct	121	AAATACTACACTTTCAGGATCAAGCCCCTCTGACTCTCATTTGGAAACTGGATGTTTGCT	180
Query	181	AAGCACCTGCTTCTTAAGGATGCCGAGGGATTTAATGATACTCCCAGAAACCTGGAGAGA	240
Sbjct	181	AAGCACCTGCTTCTTAAGGATGCCGAGGGATTTAATGATACTCCCAGAAACCTGGAGAGA	240
Query	241	TTAATGGGGCCTATGGAGAAGTGCTCTGAACTCAGTGTTGGGACTTGAATAAAATTAACC	300
Sbjct	241	TTAATGGGGCCTATGGAGAAGTGCTCTGAACTCAGTGTTGGGACTTGAATAAAATTAACC	300
Query	301	ATTGTCATGTTTTCAGAACAACCTAAGCTGTTTTATATTTTCATGTGCATGAAAGCCCTAGA	360
Sbjct	301	ATTGTCATGTTTTCAGAACAACCTAAGCTGTTTTATATTTTCATGTGCATGAAAGCCCTAGA	360
Query	361	ACTAAGTTGTGTTATTTCCAGAAATGAAATAGATCCCACAGTTAGATGATGTGGCCATTA	420
Sbjct	361	ACTAAGTTGTGTTATTTCCAGAAATGAAATAGATCCCACAGTTAGATGATGTGGCCATTA	420
Query	421	GGAAGTACCAAATTTATAAAAATCACTGGAGGTCTGTCTGAGCAGTACCTAATAAAATAT	480
Sbjct	421	GGAAGTACCAAATTTATAAAAATCACTGGAGGTCTGTCTGAGCAGTACCTAATAAAATAT	480

PATENT SEQUENCE ALIGNMENT

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Query  481  AGTATACTGAAAGTGAACAGATCTTTGTCTCTTTCTTTGGCTGCTTGATACTTTATCTGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGTATACTGAAAGTGAACAGATCTTTGTCTCTTTCTTTGGCTGCTTGATACTTTATCTGT  540

Query  541  GTCTGCCGGACAGTGC  556
          |||||||||||||
Sbjct  541  GTCTGCCGGACAGTGC  556
```

Sequence 607 matched with Sequence 212

Query= Sequence ID 607
Length=305

SEQ ID NO: 212

ALIGNMENTS

Identities = 305/305 (100%), Gaps = 0/305 (0%)

Query	1	CAATAAAAGCAGGTTAACCTCAATGATAGCAGTTAAAATGTTCTATCTTATGTATTTCTT	60
Sbjct	1	CAATAAAAGCAGGTTAACCTCAATGATAGCAGTTAAAATGTTCTATCTTATGTATTTCTT	60
Query	61	TTAAGTATTACCATTATGGTGCTACTGAGCGTTTTCTTTTGGTAAAAAGAAAAATGCCAT	120
Sbjct	61	TTAAGTATTACCATTATGGTGCTACTGAGCGTTTTCTTTTGGTAAAAAGAAAAATGCCAT	120
Query	121	GGGCTGCAGTCTTCTTCCATCACTTTTCCCTACCAGGTCCATTAATATGCTTATAACACT	180
Sbjct	121	GGGCTGCAGTCTTCTTCCATCACTTTTCCCTACCAGGTCCATTAATATGCTTATAACACT	180
Query	181	AGTGCCAGTTATTTTATTTGATAATGCTTATGGTATTTGTATATTTGTTTGCATTCCAAT	240
Sbjct	181	AGTGCCAGTTATTTTATTTGATAATGCTTATGGTATTTGTATATTTGTTTGCATTCCAAT	240
Query	241	TTTGTTTAATAATGAGTGTGTAAACTGCATACGTAAATAAATGTAAATACTAATGTACT	300
Sbjct	241	TTTGTTTAATAATGAGTGTGTAAACTGCATACGTAAATAAATGTAAATACTAATGTACT	300
Query	301	GCTGC 305	
Sbjct	301	GCTGC 305	

Sequence 609 matched with Sequence 213

Query= Sequence ID 609
Length=495

SEQ ID NO: 213

ALIGNMENTS

Identities = 495/495 (100%), Gaps = 0/495 (0%)

Query	1	TTTTATTACCCAAGTTTAACTCTGTCTGGTGATttgttggttggttggtgtngttgt	60
Sbjct	1	TTTTATTACCCAAGTTTAACTCTGTCTGGTGATTTGTTGTTGTTGTTGTTGTNGTTGT	60
Query	61	tgttgAAGTTCAGGCTGCATGTGGGATAGGTTTGCTCAGGCATACTTCTTAGGAAGTAGT	120
Sbjct	61	TGTTGAAGTTCAGGCTGCATGTGGGATAGGTTTGCTCAGGCATACTTCTTAGGAAGTAGT	120
Query	121	CACTTGCATGACTGTTTTTGGGATAACTCTTTGAGTATTTGGAGAGGTCTATTGTAACCTT	180
Sbjct	121	CACTTGCATGACTGTTTTTGGGATAACTCTTTGAGTATTTGGAGAGGTCTATTGTAACCTT	180
Query	181	CTGAAAGGCATTGTTTTTACGTATGAATGTTCTAAAATTCACTTCTAAATGGTCATGAAAA	240
Sbjct	181	CTGAAAGGCATTGTTTTTACGTATGAATGTTCTAAAATTCACTTCTAAATGGTCATGAAAA	240
Query	241	GAAAAGGATTCACATTTTAGAATGGCAATAGTCCCTGAGGACTATTATGTCTTTTAGATT	300
Sbjct	241	GAAAAGGATTCACATTTTAGAATGGCAATAGTCCCTGAGGACTATTATGTCTTTTAGATT	300
Query	301	TCCTGTGGGTTTCTAGGAATGTTAGTGTAACCTTANATTTCCACCTACCTGATTTCTGGAT	360
Sbjct	301	TCCTGTGGGTTTCTAGGAATGTTAGTGTAACCTTANATTTCCACCTACCTGATTTCTGGAT	360
Query	361	GTGCCTATTGGAACCTTGCTGAGATCtttttttttCCTTAACATGTTGTCCCCTTGACCCG	420
Sbjct	361	GTGCCTATTGGAACCTTGCTGAGATCTTTTTTTTCCTTAACATGTTGTCCCCTTGACCCG	420
Query	421	TACTTCGAAACTAAACATATTATTTTATTTGCTTACACTTCAGGAGGCAATTGGCAGACA	480
Sbjct	421	TACTTCGAAACTAAACATATTATTTTATTTGCTTACACTTCAGGAGGCAATTGGCAGACA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCAGGCCAACAGTCT	495
Sbjct	481	CCAGGCCAACAGTCT	495

Sequence 610 matched with Sequence 214

Query= Sequence ID 610

Length=507

SEQ ID NO: 214

ALIGNMENTS

Identities = 507/507 (100%), Gaps = 0/507 (0%)

Query	1	GCTCTGACCCCAAGTTGGAAATGTATCTGTACTTTGTCCGGCTTCCACTCAAGGACCATT	60
Sbjct	1	GCTCTGACCCCAAGTTGGAAATGTATCTGTACTTTGTCCGGCTTCCACTCAAGGACCATT	60
Query	61	ATGACATTGCTTGGTGTCTGAGCTGACAGGGGCTCTGGCCACAGCTTGTGGGGATGACGCGA	120
Sbjct	61	ATGACATTGCTTGGTGTCTGAGCTGACAGGGGCTCTGGCCACAGCTTGTGGGGATGACGCGA	120
Query	121	TCCGCGTGTTTCAGGAGGATCCCAACTCGGATCCACAGCAGCCACCTTCTCCCTGACAG	180
Sbjct	121	TCCGCGTGTTTCAGGAGGATCCCAACTCGGATCCACAGCAGCCACCTTCTCCCTGACAG	180
Query	181	CCCACTTGTCATCAGGCCCATTCCAGGATGTCAACTGTGTGGCCTGGAACCCCAAGGAGC	240
Sbjct	181	CCCACTTGTCATCAGGCCCATTCCAGGATGTCAACTGTGTGGCCTGGAACCCCAAGGAGC	240
Query	241	CAGGGCTACTGGCCTCCTGCAGTGATGATGGGGAGGTGGCCTTCTGGAAGTATCAGCGGC	300
Sbjct	241	CAGGGCTACTGGCCTCCTGCAGTGATGATGGGGAGGTGGCCTTCTGGAAGTATCAGCGGC	300
Query	301	CTGAAGGCCTCTGAGCTACCTCGACTTTGGACAGAGTAATGACTCCCCAGAAAACGTCAT	360
Sbjct	301	CTGAAGGCCTCTGAGCTACCTCGACTTTGGACAGAGTAATGACTCCCCAGAAAACGTCAT	360
Query	361	ATAAGACTTTACCAGCCCCTGAGAGGACCAGGAGGAGCATCCTTGACCTTCATTAACTT	420
Sbjct	361	ATAAGACTTTACCAGCCCCTGAGAGGACCAGGAGGAGCATCCTTGACCTTCATTAACTT	420
Query	421	GGCTCACTTCTCTTCANACTTGGGTAGAAAGTGCAGAGCCACAAAATTGCTTTCCTTCCCC	480
Sbjct	421	GGCTCACTTCTCTTCANACTTGGGTAGAAAGTGCAGAGCCACAAAATTGCTTTCCTTCCCC	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCCTTTGACATGAGGCCTTCAGTAAAG	507
Sbjct	481	GCCTTTGACATGAGGCCTTCAGTAAAG	507

Sequence 611 matched with Sequence 215

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 611
Length=17

SEQ ID NO: 215	34.2	1e-08
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ALIGNMENTS

Identities = 17/17 (100%), Gaps = 0/17 (0%)

Query	1	TGCAGGATCCGTCGACT	17
Sbjct	1	TGCAGGATCCGTCGACT	17

Sequence 612 matched with Sequence 216

Query= Sequence ID - 612
Length=576

nt: 576

SEQ ID NO: 216

nt: 576

ALIGNMENTS

Identities = 576/576 (100%), Gaps = 0/576 (0%)

Query	1	GAGAAATATAAGATTATGTATAGATCAAATCTACCTCTATTTGGTGTCTGAAAGAGATG	60
Sbjct	1	GAGAAATATAAGATTATGTATAGATCAAATCTACCTCTATTTGGTGTCTGAAAGAGATG	60
Query	61	AGGAGAATGGGACAACTTGGAAGCTTATTTCAAGATAACATTCCTGAGAACTTCCCA	120
Sbjct	61	AGGAGAATGGGACAACTTGGAAGCTTATTTCAAGATAACATTCCTGAGAACTTCCCA	120
Query	121	ATCTTGCTAGAGAGGCCAACATTAATAATTCAGTAAATGCTGAAAACTCCAGTAAGATATT	180
Sbjct	121	ATCTTGCTAGAGAGGCCAACATTAATAATTCAGTAAATGCTGAAAACTCCAGTAAGATATT	180
Query	181	TCTTAAGAAAAATTATTCCCAAGATATATACTCATCAAATTATCTAAGGTCAAATGAAGGA	240
Sbjct	181	TCTTAAGAAAAATTATTCCCAAGATATATACTCATCAAATTATCTAAGGTCAAATGAAGGA	240
Query	241	AAAAATTTTATAGGCAGCTAGAGAGAAATGTCAGGTCACCTACAAAGAGAATGGCATAAG	300
Sbjct	241	AAAAATTTTATAGGCAGCTAGAGAGAAATGTCAGGTCACCTACAAAGAGAATGGCATAAG	300
Query	301	ACAAAAAGTAGAACTCCCAGCAGAACTCTAAAAGCCAGAAGAGATTAGGGGCCAATATT	360
Sbjct	301	ACAAAAAGTAGAACTCCCAGCAGAACTCTAAAAGCCAGAAGAGATTAGGGGCCAATATT	360
Query	361	TAACATTCTGAAAGAAATTCCAACAAGGAATTTTCATATCCAGCCAACTAAGCTTCATAA	420
Sbjct	361	TAACATTCTGAAAGAAATTCCAACAAGGAATTTTCATATCCAGCCAACTAAGCTTCATAA	420
Query	421	TTGAAGGAGAAATAAGATATTTTCCAGACAAGCAAATGCTGATGAAATCCATCACCACCA	480
Sbjct	421	TTGAAGGAGAAATAAGATATTTTCCAGACAAGCAAATGCTGATGAAATCCATCACCACCA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GACCTGCCTTATAAGAGCTCCTGAGGGAAGCACTAAATATTGAAAGGGAAGAACTTTATG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GACCTGCCTTATAAGAGCTCCTGAGGGAAGCACTAAATATTGAAAGGGAAGAACTTTATG  540

Query  541  AACCATTTCAAAAACACATTTAAGTNCACAAAGCAG  576
          |||||||||||||||||||||||||||||||
Sbjct  541  AACCATTTCAAAAACACATTTAAGTNCACAAAGCAG  576
```

Sequence 613 matched with Sequence 217

Query= Sequence ID - 613
Length=341

nt: 341

SEQ ID NO: 217

nt: 341

ALIGNMENTS

Identities = 341/341 (100%), Gaps = 0/341 (0%)

Query	1	CCTTATTTTACAGGTGAAAAACCAACGAATCAGATAGATTTTATTTGCCCAAGTCACATA	60
Sbjct	1	CCTTATTTTACAGGTGAAAAACCAACGAATCAGATAGATTTTATTTGCCCAAGTCACATA	60
Query	61	ATATTAAGAACAGGCCAAGTGTGGTGGCTCATGTCTGTAATCTGAGCACTTTGGGAGGCT	120
Sbjct	61	ATATTAAGAACAGGCCAAGTGTGGTGGCTCATGTCTGTAATCTGAGCACTTTGGGAGGCT	120
Query	121	AAGGCGGGTGGATTTCTGAGCCTAGGAGTTTGAGATCAGCCTGGGCAACATGGCGAAAC	180
Sbjct	121	AAGGCGGGTGGATTTCTGAGCCTAGGAGTTTGAGATCAGCCTGGGCAACATGGCGAAAC	180
Query	181	CTCATCTCTACAAAACATACAAAAATTAGTCAGTGTGGTGGTGAGAGCCTGTAGTCCTGG	240
Sbjct	181	CTCATCTCTACAAAACATACAAAAATTAGTCAGTGTGGTGGTGAGAGCCTGTAGTCCTGG	240
Query	241	CTACTCGTGAGGCTGAGGTGGGAGCATCACCTGAGCCTGGGAAGTCGAGGCTGCAGTGGC	300
Sbjct	241	CTACTCGTGAGGCTGAGGTGGGAGCATCACCTGAGCCTGGGAAGTCGAGGCTGCAGTGGC	300
Query	301	AACAGAATGGGTAACCTGGACATCAGAGTGAGACCCTGTCT	341
Sbjct	301	AACAGAATGGGTAACCTGGACATCAGAGTGAGACCCTGTCT	341

Sequence 614 matched with Sequence 218

Query= Sequence ID 614
Length=494

SEQ ID NO: 218

ALIGNMENTS

Identities = 494/494 (100%), Gaps = 0/494 (0%)

Query	1	CTCACACCTGTAATTCCATTACTTTGGAAGGCTGAGAGAGGAGGATCAGTGGAGCCCAGG	60
Sbjct	1	CTCACACCTGTAATTCCATTACTTTGGAAGGCTGAGAGAGGAGGATCAGTGGAGCCCAGG	60
Query	61	AGTTTGAGACCAGCCTGGGCAATATAGGGAGACCCTGTCTCTACAAAAATGAAATAGCCA	120
Sbjct	61	AGTTTGAGACCAGCCTGGGCAATATAGGGAGACCCTGTCTCTACAAAAATGAAATAGCCA	120
Query	121	GGCGAGGTGGCATGTGCCTGTGGTCCCAGCTACTTGGGAGACTGAGGTGGAAGGCTGCCT	180
Sbjct	121	GGCGAGGTGGCATGTGCCTGTGGTCCCAGCTACTTGGGAGACTGAGGTGGAAGGCTGCCT	180
Query	181	TGAGCCCAGGAGTTCCAGGCTGCAGTGAGCCATCATTATGCCACTGCACTCCAACCTGGG	240
Sbjct	181	TGAGCCCAGGAGTTCCAGGCTGCAGTGAGCCATCATTATGCCACTGCACTCCAACCTGGG	240
Query	241	AGACAGAGTGAGAGAGACCCTGTCTCAAACAAACAAACCCAAAAATAGGCCAGGCACAGTG	300
Sbjct	241	AGACAGAGTGAGAGAGACCCTGTCTCAAACAAACAAACCCAAAAATAGGCCAGGCACAGTG	300
Query	301	ACTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAAATAGGCGGATCATTTGAGGTCAG	360
Sbjct	301	ACTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAAATAGGCGGATCATTTGAGGTCAG	360
Query	361	GAGTTCAAATTCAAGACCAGCCCGGCCAACATGGCAAAACCACATCTCTACTACAAATAA	420
Sbjct	361	GAGTTCAAATTCAAGACCAGCCCGGCCAACATGGCAAAACCACATCTCTACTACAAATAA	420
Query	421	AAAATTAGTTGGGTGTGGNGGAGCATTTCCTGTAATCACAGCTATTCAGGAGGCTGAGGCA	480
Sbjct	421	AAAATTAGTTGGGTGTGGNGGAGCATTTCCTGTAATCACAGCTATTCAGGAGGCTGAGGCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TGANAACCGCTTCA	494
Sbjct	481	TGANAACCGCTTCA	494

Sequence 615 matched with Sequence 219

Query= Sequence ID - 615 nt: 379
Length=379

SEQ ID NO: 219 nt: 379

ALIGNMENTS

Identities = 379/379 (100%), Gaps = 0/379 (0%)

Query	1	TAAATTTAAAACATTTTAATTAGCTGGCATGATGGCATGCACCTGTAGTCCTACCTACTT	60
Sbjct	1	TAAATTTAAAACATTTTAATTAGCTGGCATGATGGCATGCACCTGTAGTCCTACCTACTT	60
Query	61	GGGAGGCCAAGGCAGGAAGATTGCTTGAGCCCAGGAGTTTGAGCTTACTGTGAGCTGTGA	120
Sbjct	61	GGGAGGCCAAGGCAGGAAGATTGCTTGAGCCCAGGAGTTTGAGCTTACTGTGAGCTGTGA	120
Query	121	TCACACCACTGCACTCCAGCCTGGGTGACAAAGGAAGACCGTATTTCTaaaaataaaaa	180
Sbjct	121	TCACACCACTGCACTCCAGCCTGGGTGACAAAGGAAGACCGTATTTCTAAAAAATAAAAA	180
Query	181	aTACAAATACAACACTACAACTAGCACTAGACCAACAGTGACTATGTACCATGAACTGAGG	240
Sbjct	181	ATACAAATACAACACTACAACTAGCACTAGACCAACAGTGACTATGTACCATGAACTGAGG	240
Query	241	AATATTATTAATTCCACCATTTGCATCTGAGGTTAACAATATGTCAATGACTTAAATAAC	300
Sbjct	241	AATATTATTAATTCCACCATTTGCATCTGAGGTTAACAATATGTCAATGACTTAAATAAC	300
Query	301	ATCATATCTCTGAGAGTAATTTCTCCTATATTTCCATGACAAATGTTAGATAATTTTCCA	360
Sbjct	301	ATCATATCTCTGAGAGTAATTTCTCCTATATTTCCATGACAAATGTTAGATAATTTTCCA	360
Query	361	TTTTTTCCATTCAACAAAA 379	
Sbjct	361	TTTTTTCCATTCAACAAAA 379	

Sequence 617 matched with Sequence 220

Query= Sequence ID 617
Length=421

SEQ ID NO: 220

ALIGNMENTS

Identities = 421/421 (100%), Gaps = 0/421 (0%)

Query	1	TTTTCAGGCATGTCAGAGAAGGGAGGACTCACTAGAATTAGCAAACAAAACCACCCTGAC	60
Sbjct	1	TTTTCAGGCATGTCAGAGAAGGGAGGACTCACTAGAATTAGCAAACAAAACCACCCTGAC	60
Query	61	ATCCTCCTTCAGGAACACGGGGAGCAGAGGCCAAAGCACTAAGGGGAGGGCGCATACCCG	120
Sbjct	61	ATCCTCCTTCAGGAACACGGGGAGCAGAGGCCAAAGCACTAAGGGGAGGGCGCATACCCG	120
Query	121	AGACGATTGTATGAAGAAAATATGGAGGAACTGTTACATGTTCCGGTACTAAGTCATTTTC	180
Sbjct	121	AGACGATTGTATGAAGAAAATATGGAGGAACTGTTACATGTTCCGGTACTAAGTCATTTTC	180
Query	181	AGGGGATTGAAAGACTATTGCTGGATTTTCATGATGCTGACTGGCGTTAGCTGATTAACCC	240
Sbjct	181	AGGGGATTGAAAGACTATTGCTGGATTTTCATGATGCTGACTGGCGTTAGCTGATTAACCC	240
Query	241	ATGTAAATAGGCACTTAAATAGAAGCAGGAAAGGGAGACAAAGACTGGCTTCTGGACTTC	300
Sbjct	241	ATGTAAATAGGCACTTAAATAGAAGCAGGAAAGGGAGACAAAGACTGGCTTCTGGACTTC	300
Query	301	CTCCCTGATCCCCACTCTTACTCATCACCTGCAGTGGCCAGAATTAGGGACTCAGAATCA	360
Sbjct	301	CTCCCTGATCCCCACTCTTACTCATCACCTGCAGTGGCCAGAATTAGGGACTCAGAATCA	360
Query	361	AACCAGTGTAAGGCAGTGCTGGCTGCCATTGCCTGGTCACATTGAAATTGGTGGCTTCAT	420
Sbjct	361	AACCAGTGTAAGGCAGTGCTGGCTGCCATTGCCTGGTCACATTGAAATTGGTGGCTTCAT	420
Query	421	T 421	
Sbjct	421	T 421	

Sequence 618 matched with Sequence 221

Query= Sequence ID - 618
Length=598

nt: 598

SEQ ID NO: 221

nt: 598

ALIGNMENTS

Identities = 598/598 (100%), Gaps = 0/598 (0%)

Query	1	GATTAAC	TTTCATTTTAAGCTCTTCTCTACTAATTCTGTTTCGTATGTTTATTCATTTTGC	60
Sbjct	1	GATTAAC	TTTCATTTTAAGCTCTTCTCTACTAATTCTGTTTCGTATGTTTATTCATTTTGC	60
Query	61	GTTGATCATATTTTGTACACCAGGCACTCTTCTCAGTTTTATATGTGTGTTAATTTACTC	120	
Sbjct	61	GTTGATCATATTTTGTACACCAGGCACTCTTCTCAGTTTTATATGTGTGTTAATTTACTC	120	
Query	121	CTTTCAAGAGCCCTATGATACATGAATTTATCTCCATTTTATAGATGAGGAAATTAAGAC	180	
Sbjct	121	CTTTCAAGAGCCCTATGATACATGAATTTATCTCCATTTTATAGATGAGGAAATTAAGAC	180	
Query	181	CTAGAGTTACTGAACTTGCCCAAGGTTATACAGCTGATGGGTAGGGCCAGAACTTTGCCT	240	
Sbjct	181	CTAGAGTTACTGAACTTGCCCAAGGTTATACAGCTGATGGGTAGGGCCAGAACTTTGCCT	240	
Query	241	CAGAGAATCTGAATTTCCAAAAATAACCTAAAAGAGAAATTTAAGTACTAATTAGTAAG	300	
Sbjct	241	CAGAGAATCTGAATTTCCAAAAATAACCTAAAAGAGAAATTTAAGTACTAATTAGTAAG	300	
Query	301	CAAAGAAATGCACATTTAAGGAAGACAGTGCACATTTAAGGAAGACAGTAACCTTTTATC	360	
Sbjct	301	CAAAGAAATGCACATTTAAGGAAGACAGTGCACATTTAAGGAAGACAGTAACCTTTTATC	360	
Query	361	TATTAGAGAAAAACACACATTCTGTCTTTAACACACACATAAATCTTATATTGGCAGGGA	420	
Sbjct	361	TATTAGAGAAAAACACACATTCTGTCTTTAACACACACATAAATCTTATATTGGCAGGGA	420	
Query	421	TTTTCTTTATTCAGCAATTATTTATTGGTTGTCTGCTTTGTGGTACACATAAATGCTGGG	480	
Sbjct	421	TTTTCTTTATTCAGCAATTATTTATTGGTTGTCTGCTTTGTGGTACACATAAATGCTGGG	480	

PATENT SEQUENCE ALIGNMENT

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Query  481  GATAAACACTTAATAAAATATACTTCCTTCTCTTGAATATCTTGCACTTTAAGTGGGAAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GATAAACACTTAATAAAATATACTTCCTTCTCTTGAATATCTTGCACTTTAAGTGGGAAG  540

Query  541  GTAAGTCAACAGAGTAGAGGTGATATATCCAAGTGATAGACTGTTTCATTGCCAGTAG  598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GTAAGTCAACAGAGTAGAGGTGATATATCCAAGTGATAGACTGTTTCATTGCCAGTAG  598
```

Sequence 619 matched with Sequence 222

Query= Sequence ID 619

Length=473

SEQ ID NO: 222

ALIGNMENTS

Identities = 473/473 (100%), Gaps = 0/473 (0%)

Query	1	GTTGCCTGAGAGTGACCTTTGCATCTGCCTGTCCAGCCAGCATGGAACCAAAGCGGATCA	60
Sbjct	1	GTTGCCTGAGAGTGACCTTTGCATCTGCCTGTCCAGCCAGCATGGAACCAAAGCGGATCA	60
Query	61	GAGAGGGCTACCTTGTGAAGAAGGGGAGCGTGTTCAATACGTGGAAACCCATGTGGGTTG	120
Sbjct	61	GAGAGGGCTACCTTGTGAAGAAGGGGAGCGTGTTCAATACGTGGAAACCCATGTGGGTTG	120
Query	121	TATTGTTAGAAGATGGAATTGAATTCTATAAGAAGAAAAGTGACAACAGCCCCAAAGGAA	180
Sbjct	121	TATTGTTAGAAGATGGAATTGAATTCTATAAGAAGAAAAGTGACAACAGCCCCAAAGGAA	180
Query	181	TGATCCCGCTGAAAGGGAGCACTCTGACTAGCCCTTGTCAAGACTTTGGCAAAAGGATGT	240
Sbjct	181	TGATCCCGCTGAAAGGGAGCACTCTGACTAGCCCTTGTCAAGACTTTGGCAAAAGGATGT	240
Query	241	TTGTGTTTAAGATCACTATGACCAAACAGCAGGACCACTTCTTCCAGGCAGCCTTCCTGG	300
Sbjct	241	TTGTGTTTAAGATCACTATGACCAAACAGCAGGACCACTTCTTCCAGGCAGCCTTCCTGG	300
Query	301	AGGAGAGAGATGCCTGGGTTCTGGGATATCAATAAGGCCATTAAATGCATTGAAGGAGGCC	360
Sbjct	301	AGGAGAGAGATGCCTGGGTTCTGGGATATCAATAAGGCCATTAAATGCATTGAAGGAGGCC	360
Query	361	AGAAATTTGCCAGGAAATCTACCAGGAGGTCCATTCGACTGCCAGAAACCATTGACTTAG	420
Sbjct	361	AGAAATTTGCCAGGAAATCTACCAGGAGGTCCATTCGACTGCCAGAAACCATTGACTTAG	420
Query	421	GTGCCTTATATTTGTCCATGAAAGACACTGAAAAAGGAATAAAAGAACTGAAT	473
Sbjct	421	GTGCCTTATATTTGTCCATGAAAGACACTGAAAAAGGAATAAAAGAACTGAAT	473

Sequence 621 matched with Sequence 223

Query= Sequence ID 621
Length=392

SEQ ID NO: 223

ALIGNMENTS

Identities = 392/392 (100%), Gaps = 0/392 (0%)

Query	1	TGGTACTGAACCTACGAGTACACCGACTACGGCGGACTAATCTTCAACTCCTACATACTT	60
Sbjct	1	TGGTACTGAACCTACGAGTACACCGACTACGGCGGACTAATCTTCAACTCCTACATACTT	60
Query	61	CCCCATTATTCCTAGAACCCAGGCGACCTGCGACTCCTTGACGTTGACAATCGAGTAGTA	120
Sbjct	61	CCCCATTATTCCTAGAACCCAGGCGACCTGCGACTCCTTGACGTTGACAATCGAGTAGTA	120
Query	121	CTCCCGATTGAAGCCCCCATTTCGTATAATAATTACATCACAAGACGTCTTGCACTCATGA	180
Sbjct	121	CTCCCGATTGAAGCCCCCATTTCGTATAATAATTACATCACAAGACGTCTTGCACTCATGA	180
Query	181	GCTGTCCCCACATTAGGCTTAAAAACAGATGCAATTCCCGGACGTCTAAACCAAACCACT	240
Sbjct	181	GCTGTCCCCACATTAGGCTTAAAAACAGATGCAATTCCCGGACGTCTAAACCAAACCACT	240
Query	241	TTCACCGCTACACGACCGGGGTATACTACGGTCAATGCTCTGAAATCTGTGGAGCAAAC	300
Sbjct	241	TTCACCGCTACACGACCGGGGTATACTACGGTCAATGCTCTGAAATCTGTGGAGCAAAC	300
Query	301	CACAGTTTCATGCCCATCGTCCTAGAATTAATTCCTTAAAAATCTTTGAAATAGGGCCC	360
Sbjct	301	CACAGTTTCATGCCCATCGTCCTAGAATTAATTCCTTAAAAATCTTTGAAATAGGGCCC	360
Query	361	GTATTTACCCTATAGCACCCCTCTACCCCT	392
Sbjct	361	GTATTTACCCTATAGCACCCCTCTACCCCT	392

Sequence 622 matched with Sequence 224

Query= Sequence ID 622
Length=618

SEQ ID NO: 224

ALIGNMENTS

Identities = 618/618 (100%), Gaps = 0/618 (0%)

Query	1	TTTTTCTTGTTTTGTGTGTCTACCTTGGCATATACTAAAGGAAGGTGTGTATTCATTTA	60
Sbjct	1	TTTTTCTTGTTTTGTGTGTCTACCTTGGCATATACTAAAGGAAGGTGTGTATTCATTTA	60
Query	61	TTACATGATATCTCTGGGTTATAATTATTTACATATATGAATTTGAAAGAAAGATTGAGA	120
Sbjct	61	TTACATGATATCTCTGGGTTATAATTATTTACATATATGAATTTGAAAGAAAGATTGAGA	120
Query	121	GGGATATGTGTGACCTTTGTTTCATTATGATCATTTACATGACTAAAGATAAAGATCATA	180
Sbjct	121	GGGATATGTGTGACCTTTGTTTCATTATGATCATTTACATGACTAAAGATAAAGATCATA	180
Query	181	TGTCTGATTTTCAGTTTAATGGCAAGTTACTTAAAATAAATGAAATATGTTTTTATTGTT	240
Sbjct	181	TGTCTGATTTTCAGTTTAATGGCAAGTTACTTAAAATAAATGAAATATGTTTTTATTGTT	240
Query	241	TTCGTGGGTTTGATGCTTTGTGTTTTATTTCAAGTAACTTGAGAATGCATTGTGTTTGGT	300
Sbjct	241	TTCGTGGGTTTGATGCTTTGTGTTTTATTTCAAGTAACTTGAGAATGCATTGTGTTTGGT	300
Query	301	ACTGTTTTTTATGAATATCATTAAAAATTTATTTAAGGAGAGAGTAATTTTGCaataata	360
Sbjct	301	ACTGTTTTTTATGAATATCATTAAAAATTTATTTAAGGAGAGAGTAATTTTGCAATAATA	360
Query	361	tttttgattttatttgaaaataaaaattcaagataaatgaaataattgaaattttCTAAAGA	420
Sbjct	361	TTTTTGATTATTTGAAAATAAAATTCAAGATAAATGAAATAATTGAAATTTTCTAAAGA	420
Query	421	AGGAATTGAATATATTTTTACATTTGAATGAACTAAGGATTAAGTGAACCATTTATATAT	480
Sbjct	421	AGGAATTGAATATATTTTTACATTTGAATGAACTAAGGATTAAGTGAACCATTTATATAT	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGTACTTTCAGAACTGAATGTCTTAAATGATAAAGCTCTAATTGGTTAAAGTGA	540
Sbjct	481	AGTACTTTCAGAACTGAATGTCTTAAATGATAAAGCTCTAATTGGTTAAAGTGA	540
Query	541	TTCAAGTCAAAGAACCCAGAACTGAATAGATGATCTAACTACTGCCACTGAGGTT	600
Sbjct	541	TTCAAGTCAAAGAACCCAGAACTGAATAGATGATCTAACTACTGCCACTGAGGTT	600
Query	601	ATTAGTGAGTATAAATTT	618
Sbjct	601	ATTAGTGAGTATAAATTT	618

Sequence 624 matched with Sequence 225

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 624
Length=17

SEQ ID NO: 225	34.2	1e-08
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ALIGNMENTS

Identities = 17/17 (100%), Gaps = 0/17 (0%)

Query	1	TGCAGGATCCGTCGACT	17
Sbjct	1	TGCAGGATCCGTCGACT	17

Sequence 625 matched with Sequence 226

Query= Sequence ID 625

Length=396

SEQ ID NO: 226

ALIGNMENTS

Identities = 396/396 (100%), Gaps = 0/396 (0%)

Query	1	GACAATCAGAGCAGATCTTGGGCTTCTGTGGCTCATCTCAGCCCTTTATAACTGGCCTGA	60
Sbjct	1	GACAATCAGAGCAGATCTTGGGCTTCTGTGGCTCATCTCAGCCCTTTATAACTGGCCTGA	60
Query	61	GAAGAGGGTTTATCTACTTGTGCAAGTGGCCCAGAAATCTCACTCGTACATGAGGCTTTG	120
Sbjct	61	GAAGAGGGTTTATCTACTTGTGCAAGTGGCCCAGAAATCTCACTCGTACATGAGGCTTTG	120
Query	121	GAACATCCTTGCAAAGGTACGCTGAAAGCAAATTGCTGTTTTCTGGTGGTTCTGCACGT	180
Sbjct	121	GAACATCCTTGCAAAGGTACGCTGAAAGCAAATTGCTGTTTTCTGGTGGTTCTGCACGT	180
Query	181	TTCCTAACTTTTATCATAGTTTGATTTTCATTATTTAAGaaaaataaaaaaTCCAAAGA	240
Sbjct	181	TTCCTAACTTTTATCATAGTTTGATTTTCATTATTTAAGAAAAAATAAAAAATCCAAAGA	240
Query	241	CCATAAGATGGCATTAGATTTTTTACCATTA AATTATTAATGCCTATTTGGTGCTCATAA	300
Sbjct	241	CCATAAGATGGCATTAGATTTTTTACCATTA AATTATTAATGCCTATTTGGTGCTCATAA	300
Query	301	AGATTAATCATGTCACGCATGTTTCCAATCTTTCTTTTGCAGTATATTATTTTCTAAAAA	360
Sbjct	301	AGATTAATCATGTCACGCATGTTTCCAATCTTTCTTTTGCAGTATATTATTTTCTAAAAA	360
Query	361	TTGTTACATGCAAATTTAAACCAAGATTTATCAGTA	396
Sbjct	361	TTGTTACATGCAAATTTAAACCAAGATTTATCAGTA	396

Sequence 626 matched with Sequence 227

Query= Sequence ID 626

Length=535

SEQ ID NO: 227

ALIGNMENTS

Identities = 535/535 (100%), Gaps = 0/535 (0%)

Query	1	TTGGAAGAAATAAACCAAGGCAGAAAAATTTTAAATGGCCAAAATAAATTGTATTGCTAA	60
Sbjct	1	TTGGAAGAAATAAACCAAGGCAGAAAAATTTTAAATGGCCAAAATAAATTGTATTGCTAA	60
Query	61	CTTAGATGGCCACAGATGGGGGCAGGGGTGGAGAGAGGAGAAATTGAAAACNCCACAAAG	120
Sbjct	61	CTTAGATGGCCACAGATGGGGGCAGGGGTGGAGAGAGGAGAAATTGAAAACNCCACAAAG	120
Query	121	ACCCCGCAATGGCTAGAACTTGAAATCTCTGGATATTGCAACAATAGCAGCCTCCTTAAG	180
Sbjct	121	ACCCCGCAATGGCTAGAACTTGAAATCTCTGGATATTGCAACAATAGCAGCCTCCTTAAG	180
Query	181	TCAGCAAAAAGATAAAGATTGATCCAATGTTCTATATTACAGAACAGAGCAGATTGTCAA	240
Sbjct	181	TCAGCAAAAAGATAAAGATTGATCCAATGTTCTATATTACAGAACAGAGCAGATTGTCAA	240
Query	241	TATAGCAAATAAAGTTACCGTTGAGTGGACTGCGCTGTNTAAGCTGCTTGGTTGGCCTTA	300
Sbjct	241	TATAGCAAATAAAGTTACCGTTGAGTGGACTGCGCTGTNTAAGCTGCTTGGTTGGCCTTA	300
Query	301	AGTGCCGACAATTAAGAGATGAAGGCAATGAGAACTGAAACAAACATTTAAGTTCAAGAC	360
Sbjct	301	AGTGCCGACAATTAAGAGATGAAGGCAATGAGAACTGAAACAAACATTTAAGTTCAAGAC	360
Query	361	CCAGTTTACTGACACTGGGACTATTACTATATCTCTTTGGGCCTCAGTTTACTTATCTGT	420
Sbjct	361	CCAGTTTACTGACACTGGGACTATTACTATATCTCTTTGGGCCTCAGTTTACTTATCTGT	420
Query	421	AACATTAAGAGGTTGGATTACATGATGTCTCACGATTCTtttttttttATTTAGAGATGGG	480
Sbjct	421	AACATTAAGAGGTTGGATTACATGATGTCTCACGATTCTTTTTTTTATTTAGAGATGGG	480

Query	481	GTTTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCATGATCATAGCTCACAGCAG	535
Sbjct	481	GTTTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCATGATCATAGCTCACAGCAG	535

Sequence 627 matched with Sequence 228

Query= Sequence ID 627
Length=392

SEQ ID NO: 228

ALIGNMENTS

Identities = 392/392 (100%), Gaps = 0/392 (0%)

Query	1	CCAGCCTGTCACTGGCCTGGCCAAGGAGGAGAGACAGGCCAGGGATTCTGGTCCTAACTC	60
Sbjct	1	CCAGCCTGTCACTGGCCTGGCCAAGGAGGAGAGACAGGCCAGGGATTCTGGTCCTAACTC	60
Query	61	TACTGGCCACACTGTGTGGCCTGAGACCCCCCTTTCCTCCCAAGCCCCTGCCTCCGCAT	120
Sbjct	61	TACTGGCCACACTGTGTGGCCTGAGACCCCCCTTTCCTCCCAAGCCCCTGCCTCCGCAT	120
Query	121	CTGCGTGGTGAAGGCCATTGGCCCTCATCGGTGGATCTGCGTTTCCTCGGGCCTACACTG	180
Sbjct	121	CTGCGTGGTGAAGGCCATTGGCCCTCATCGGTGGATCTGCGTTTCCTCGGGCCTACACTG	180
Query	181	TCTAGGATTGTGCGGGGCTGGTGAGAGAACAAGATCTCTTCCGTGTTCAAGGCAGACTTC	240
Sbjct	181	TCTAGGATTGTGCGGGGCTGGTGAGAGAACAAGATCTCTTCCGTGTTCAAGGCAGACTTC	240
Query	241	CTGCCCCCTGCACCCTGCTCTCTCCCAGGCCTTGAGGTCAGTGTGAGCCCCAAGGGCAAG	300
Sbjct	241	CTGCCCCCTGCACCCTGCTCTCTCCCAGGCCTTGAGGTCAGTGTGAGCCCCAAGGGCAAG	300
Query	301	AACACTTCTGGAAGGGAGAGTGGATTTGGCTGGGCCATCTGGATGGAAGGTaaaaaaaG	360
Sbjct	301	AACACTTCTGGAAGGGAGAGTGGATTTGGCTGGGCCATCTGGATGGAAGGTAAAAAAAAG	360
Query	361	AAAATCCCTTGAAAGGAGATTGAGGGAAGTTT	392
Sbjct	361	AAAATCCCTTGAAAGGAGATTGAGGGAAGTTT	392

nt: 419

nt: 419

Identities = 419/419 (100%), Gaps = 0/419 (0%)

Query	1	AAGAGAAAGGACTCAGTGTGTGATCCGTTTCTTTTTTGCTCGCCCCTGTTTTTTGTAGAA	60
Sbjct	1	AAGAGAAAGGACTCAGTGTGTGATCCGTTTCTTTTTTGCTCGCCCCTGTTTTTTGTAGAA	60
Query	61	TCTCTTCATGCTTGACATACCTACCAGTATTATTCCCGACGACACATATACATATGAGAA	120
Sbjct	61	TCTCTTCATGCTTGACATACCTACCAGTATTATTCCCGACGACACATATACATATGAGAA	120
Query	121	TATACCTTATTTATTTTTGTGTAGGTGTCTGCCTTCACAAATGTCATTGTCTACTCCTAG	180
Sbjct	121	TATACCTTATTTATTTTTGTGTAGGTGTCTGCCTTCACAAATGTCATTGTCTACTCCTAG	180
Query	181	AAGAACCAAATACCTCAATTTTTGTTTTTGAGTACTGTACTATCCTGTAAATATATCTTA	240
Sbjct	181	AAGAACCAAATACCTCAATTTTTGTTTTTGAGTACTGTACTATCCTGTAAATATATCTTA	240
Query	241	AGCAGGTTTGTTCAGCACTGATGGAAAATACCAGTGTTGGGtttttttttAGTTGCCA	300
Sbjct	241	AGCAGGTTTGTTCAGCACTGATGGAAAATACCAGTGTTGGGTTTTTTTTTAGTTGCCA	300
Query	301	ACAGTTGTATGTTTGCTGATTATTTATGACCTGAAATAATATATTTCTTCTTAAGAAG	360
Sbjct	301	ACAGTTGTATGTTTGCTGATTATTTATGACCTGAAATAATATATTTCTTCTTCTAAGAAG	360
Query	361	ACATTTTGTTACATAAGGATGACTTTTTTATACAATGGGAATAAATTATGGCATTTTTTT	419
Sbjct	361	ACATTTTGTTACATAAGGATGACTTTTTTATACAATGGGAATAAATTATGGCATTTTTTT	419

Length=622

Identities = 622/622 (100%), Gaps = 0/622 (0%)

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PATENT SEQUENCE ALIGNMENT

Query	481	ATGAAATCCAGGTTTCAACAGGACTGGGTTCCCTTCTAGCTCATT	CAGCTACCTGGCTCA	540
Sbjct	481	ATGAAATCCAGGTTTCAACAGGACTGGGTTCCCTTCTAGCTCATT	CAGCTACCTGGCTCA	540
Query	541	TTCAGGTTGTNGGCAGAATATACTTCCATGAAACTGTAGGGCTGAGACCCCGTTCCTTCC	600	
Sbjct	541	TTCAGGTTGTNGGCAGAATATACTTCCATGAAACTGTAGGGCTGAGACCCCGTTCCTTCC	600	
Query	601	TGGCTATCATCTGAAAAC TTTC	622	
Sbjct	601	TGGCTATCATCTGAAAAC TTTC	622	

Sequence 630 matched with Sequence 231

Query= Sequence ID 630
Length=350

SEQ ID NO: 231

ALIGNMENTS

Identities = 350/350 (100%), Gaps = 0/350 (0%)

Query	1	AGGCGCAGCCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGGACCTGTACGTGC	60
Sbjct	1	AGGCGCAGCCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGGACCTGTACGTGC	60
Query	61	CGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCACGCATCCATCCAGA	120
Sbjct	61	CGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCACGCATCCATCCAGA	120
Query	121	TGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAATGGCCAGTTTAAACTTATG	180
Sbjct	121	TGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAATGGCCAGTTTAAACTTATG	180
Query	181	CTATCTGCGGGGCCATTTCGTAGGATGGGTGAGTCAGATGATTCCATTCTCCGATTGGCCA	240
Sbjct	181	CTATCTGCGGGGCCATTTCGTAGGATGGGTGAGTCAGATGATTCCATTCTCCGATTGGCCA	240
Query	241	AGGCCGATGGCATCGTCTCAAAGAACTTTTGGAGAGAGAATCACAGATGTGGAATATT	300
Sbjct	241	AGGCCGATGGCATCGTCTCAAAGAACTTTTGGAGAGAGAATCACAGATGTGGAATATT	300
Query	301	TGTCATAAAATAAATAATGAAAACCTaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	350
Sbjct	301	TGTCATAAAATAAATAATGAAAACCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	350

Sequence 631 matched with Sequence 232

Query= Sequence ID 631
Length=493

SEQ ID NO: 232

ALIGNMENTS

Identities = 491/491 (100%), Gaps = 0/491 (0%)

Query	3	CACTCACACACTCCCAAACCTTAACAAACACATACATGTGCAGCCAACCCAATGGGCCAG	62
Sbjct	3	CACTCACACACTCCCAAACCTTAACAAACACATACATGTGCAGCCAACCCAATGGGCCAG	62
Query	63	CCTCTTTTATGCTCCTCACATGTTTCCTTTAACTGGAATACCCATGACAGCTCCCTACAT	122
Sbjct	63	CCTCTTTTATGCTCCTCACATGTTTCCTTTAACTGGAATACCCATGACAGCTCCCTACAT	122
Query	123	AGTTACTTGTAACCTCCTCCTCTGTATAAGTTTTCTGAAttttttGATAAAATTAA	182
Sbjct	123	AGTTACTTGTAACCTCCTCCTCTGTATAAGTTTTCTGAATTTTTTGTATAAAATTAA	182
Query	183	GTTGTGCCACCCCTTTATGCTCTCTTANAACCTTGTCTGTTCTCATGGCTGTTCTGCAA	242
Sbjct	183	GTTGTGCCACCCCTTTATGCTCTCTTANAACCTTGTCTGTTCTCATGGCTGTTCTGCAA	242
Query	243	CGAATCTCATTGTGTTCTCCTACTCAATTACATTCCTGCGTCTCCCACTAGATGGCAGAC	302
Sbjct	243	CGAATCTCATTGTGTTCTCCTACTCAATTACATTCCTGCGTCTCCCACTAGATGGCAGAC	302
Query	303	TCTTTGAGAGTAGGAGATTCCCTTGTTATCTCTGGATCCCTGGCACTTGCAGAAAGCCTG	362
Sbjct	303	TCTTTGAGAGTAGGAGATTCCCTTGTTATCTCTGGATCCCTGGCACTTGCAGAAAGCCTG	362
Query	363	TTACGTAATAATTGCTCAACAATTAGTTTTTAAATAAATGAATTATTTTAAACGCCAA	422
Sbjct	363	TTACGTAATAATTGCTCAACAATTAGTTTTTAAATAAATGAATTATTTTAAACGCCAA	422
Query	423	AATTACAATGATTGTGCATTAAGTGAAAGATGACCATCTAAAAACATAAAGCCATGCTTC	482
Sbjct	423	AATTACAATGATTGTGCATTAAGTGAAAGATGACCATCTAAAAACATAAAGCCATGCTTC	482

PATENT SEQUENCE ALIGNMENT

Query	483	ATGACATTGGC	493
Sbjct	483	ATGACATTGGC	493

Sequence 632 matched with Sequence 233

Query= Sequence ID 632

Length=577

SEQ ID NO: 233

ALIGNMENTS

Identities = 577/577 (100%), Gaps = 0/577 (0%)

Query	1	GACCATTTCAGGGAAATTTTATAAAAAATGCAGATACTGTCTTGAGCAGATCGAAATGCCG	60
Sbjct	1	GACCATTTCAGGGAAATTTTATAAAAAATGCAGATACTGTCTTGAGCAGATCGAAATGCCG	60
Query	61	ATGAGGTGGATGCAATTTCTTTTGTGCAAGCAGTGCACGGTGccccccctCGGGTGTC	120
Sbjct	61	ATGAGGTGGATGCAATTTCTTTTGTGCAAGCAGTGCACGGTGCCCCCCCCTCGGGTGTC	120
Query	121	CGTGCTGTGCCTTAGCTTCCCCAGGTGCCGGGACTCACACCTGCTAGGGGCTGGGCAAGG	180
Sbjct	121	CGTGCTGTGCCTTAGCTTCCCCAGGTGCCGGGACTCACACCTGCTAGGGGCTGGGCAAGG	180
Query	181	CCCCGGCTCTGCTTTCTCTGAAGGGCTTGTCCTCAAGTTCATTGCCCTGTTACAGGTGGTCA	240
Sbjct	181	CCCCGGCTCTGCTTTCTCTGAAGGGCTTGTCCTCAAGTTCATTGCCCTGTTACAGGTGGTCA	240
Query	241	AGACGTCCGGCCGCCTTGACCCAGGCTACCCTTAGCCAATATCCTCTGCCCCTGGGTGGT	300
Sbjct	241	AGACGTCCGGCCGCCTTGACCCAGGCTACCCTTAGCCAATATCCTCTGCCCCTGGGTGGT	300
Query	301	TGGTGGCTGGGCCTCAGGGTGGGCAACGTTAGGGGTTTGGCGAAAGCCCGCCCCATGGGA	360
Sbjct	301	TGGTGGCTGGGCCTCAGGGTGGGCAACGTTAGGGGTTTGGCGAAAGCCCGCCCCATGGGA	360
Query	361	TTGAGGGACGGGGCTGCACTCCAACCGTCTGCACCTGCTCTTCCCCACCCCTGTGGGAC	420
Sbjct	361	TTGAGGGACGGGGCTGCACTCCAACCGTCTGCACCTGCTCTTCCCCACCCCTGTGGGAC	420
Query	421	CTCATCTTCACGTGCCATGTGTGCTGAAGGCCAGGGCCCAGCAGGGGGCAGTGGCACCT	480
Sbjct	421	CTCATCTTCACGTGCCATGTGTGCTGAAGGCCAGGGCCCAGCAGGGGGCAGTGGCACCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GTTGACGGAAAAGCCGAGGTGCTTACCAATGGACCTTCTGGCCCGCCCTCCCCTGTACTT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTTGACGGAAAAGCCGAGGTGCTTACCAATGGACCTTCTGGCCCGCCCTCCCCTGTACTT  540

Query  541  GTCGGGCATTCAGGGCCCCGACCTGTGCCTACCCGCA  577
          ||||||||||||||||||||||||||||
Sbjct  541  GTCGGGCATTCAGGGCCCCGACCTGTGCCTACCCGCA  577
```


Sequence 633 matched with Sequence 234

Query= Sequence ID 633

Length=568

SEQ ID NO: 234

ALIGNMENTS

Identities = 568/568 (100%), Gaps = 0/568 (0%)

Query	1	CAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAA	60
Sbjct	1	CAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAA	60
Query	61	GTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGCCCT	120
Sbjct	61	GTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGCCCT	120
Query	121	GGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGGGATCT	180
Sbjct	121	GGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGGGATCT	180
Query	181	GTCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGTGCT	240
Sbjct	181	GTCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGTGCT	240
Query	241	CGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCACACT	300
Sbjct	241	CGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCACACT	300
Query	301	GAGTGAGCTGCACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGCTCCTGGGCAA	360
Sbjct	301	GAGTGAGCTGCACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGCTCCTGGGCAA	360
Query	361	CGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCACCAAGTGCAGGC	420
Sbjct	361	CGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCACCAAGTGCAGGC	420
Query	421	TGCCTATCANAAAGTGGTGGCTGGTGTGGGCTAATGCCTGGCCCCACAAGTATCACTAAG	480
Sbjct	421	TGCCTATCANAAAGTGGTGGCTGGTGTGGGCTAATGCCTGGCCCCACAAGTATCACTAAG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTCCTTTGTTCCCTAAGTCCAACACTACT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTCCTTTGTTCCCTAAGTCCAACACTACT  540

Query  541  AAAGTGGGGGATATTATGAAGGGCCTTG  568
          ||||||||||||||||||||
Sbjct  541  AAAGTGGGGGATATTATGAAGGGCCTTG  568
```

Sequence 634 matched with Sequence 235

Query= Sequence ID - 634
Length=511

nt: 511

SEQ ID NO: 235

nt: 511

ALIGNMENTS

Identities = 511/511 (100%), Gaps = 0/511 (0%)

Query	1	TTTTTTAATTCACCAAATTTGTTGACGTCCCTTGATTTGCTGATAGGGACAATAATTA	60
Sbjct	1	TTTTTTAATTCACCAAATTTGTTGACGTCCCTTGATTTGCTGATAGGGACAATAATTA	60
Query	61	AATATTTTCCACTTGTTTTTATAAAAACTGTAATGGTGATTTGTTTAACAGATGTTGACT	120
Sbjct	61	AATATTTTCCACTTGTTTTTATAAAAACTGTAATGGTGATTTGTTTAACAGATGTTGACT	120
Query	121	TAGCACCTTCTCTCttttttttttttttttttttGAGTTGGAGTCTTGCTCTGTCACCCAG	180
Sbjct	121	TAGCACCTTCTCTCTTTTTTTTTTTTTTTTTTTTGGAGTTGGAGTCTTGCTCTGTCACCCAG	180
Query	181	CTGGAGTGCAGTGGCACGATTTTCGGCTCACTGCAACCTCCGCCTCCCAGGTTCTGGGCGCT	240
Sbjct	181	CTGGAGTGCAGTGGCACGATTTTCGGCTCACTGCAACCTCCGCCTCCCAGGTTCTGGGCGCT	240
Query	241	TCTCCTGCCTCAGCCTCCCANATAGTTGGGATTACAGGTGCATGCCGCCACNCCTAGCTA	300
Sbjct	241	TCTCCTGCCTCAGCCTCCCANATAGTTGGGATTACAGGTGCATGCCGCCACNCCTAGCTA	300
Query	301	ATGTTTTTTGTATCTTGGTANANATGGNGTTTCACCTTGTTGCCCATGCCGCTCTTGAAC	360
Sbjct	301	ATGTTTTTTGTATCTTGGTANANATGGNGTTTCACCTTGTTGCCCATGCCGCTCTTGAAC	360
Query	361	TCCTTGGCCTCCCAAAGTGTTAGGATTACAGGCGTGAGCCACTGTGCCTGGCCCCAATTT	420
Sbjct	361	TCCTTGGCCTCCCAAAGTGTTAGGATTACAGGCGTGAGCCACTGTGCCTGGCCCCAATTT	420
Query	421	ANCACCTTACTGGGTGCTGAGGCTGTGAGCCATAGTAGAATGCATGTGATCCAGGGCCTT	480
Sbjct	421	ANCACCTTACTGGGTGCTGAGGCTGTGAGCCATAGTAGAATGCATGTGATCCAGGGCCTT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCTGAATTCATGGGCTAATAGGGAGCCTGAC	511
Sbjct	481	GCTGAATTCATGGGCTAATAGGGAGCCTGAC	511

Sequence 635 matched with Sequence 236

Query= Sequence ID - 635
Length=592

nt: 592

SEQ ID NO: 236

nt: 592

ALIGNMENTS

Identities = 592/592 (100%), Gaps = 0/592 (0%)

Query	1	TGAGCGTTGGGCTGTAGGTCGCTGTGCTGTGTGATCCCCAGAGCCATGCCCGAGATAGT	60
Sbjct	1	TGAGCGTTGGGCTGTAGGTCGCTGTGCTGTGTGATCCCCAGAGCCATGCCCGAGATAGT	60
Query	61	GGATACCTGTTTCGTTGGCCTCTCCGGCTTCCGTCTGCCGGACCAAGCACCTGCACCTGCG	120
Sbjct	61	GGATACCTGTTTCGTTGGCCTCTCCGGCTTCCGTCTGCCGGACCAAGCACCTGCACCTGCG	120
Query	121	CTGCAGCGTCGACTTTACTCGCCGGACGCTGACCGGGACTGCTGCTCTCACGGTCCAGTC	180
Sbjct	121	CTGCAGCGTCGACTTTACTCGCCGGACGCTGACCGGGACTGCTGCTCTCACGGTCCAGTC	180
Query	181	TCAGGAGGACAATCTGCGCAGCCTGGTTTTGGATACAAAGGACCTTACAATAGAAAAAGT	240
Sbjct	181	TCAGGAGGACAATCTGCGCAGCCTGGTTTTGGATACAAAGGACCTTACAATAGAAAAAGT	240
Query	241	AGTGATCAATGGACAAGAAGTCAAATATGCTCTTGGAGAAAGACAAAGTTACAAGGGATC	300
Sbjct	241	AGTGATCAATGGACAAGAAGTCAAATATGCTCTTGGAGAAAGACAAAGTTACAAGGGATC	300
Query	301	GCCAATGGAAATCTCTCTTCCTATCGCTTTGAGCAAAAATCAAGAAATTGTTATAGAAAT	360
Sbjct	301	GCCAATGGAAATCTCTCTTCCTATCGCTTTGAGCAAAAATCAAGAAATTGTTATAGAAAT	360
Query	361	TTCTTTTGAGACCTCTCCAAAATCTTCTGCTCTCCAGTGGCTCACTCCTGAACAGACTTC	420
Sbjct	361	TTCTTTTGAGACCTCTCCAAAATCTTCTGCTCTCCAGTGGCTCACTCCTGAACAGACTTC	420
Query	421	TGGGAAGGAACACCCATATCTCTTTAGTCAGTGCCAGGCCATCCACTGCAGAGCAATCCT	480
Sbjct	421	TGGGAAGGAACACCCATATCTCTTTAGTCAGTGCCAGGCCATCCACTGCAGAGCAATCCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TCCTTGTCAGGACACTCCTTCTGNGAAATTAACCTATACTGCAGAGGTGTCTGTCCCTAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TCCTTGTCAGGACACTCCTTCTGNGAAATTAACCTATACTGCAGAGGTGTCTGTCCCTAA  540

Query  541  AGAACTGGTGGCACTTATGAGTGCTATTCGTGATGGAGAAACACCTGACCCA  592
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AGAACTGGTGGCACTTATGAGTGCTATTCGTGATGGAGAAACACCTGACCCA  592
```

nt: 572

nt: 572

Identities = 572/572 (100%), Gaps = 0/572 (0%)

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PATENT SEQUENCE ALIGNMENT

```
Query 481 CTAACCTCAGTCCCTTTTTTGAGAGTGAATGGTGGAGGGTGGGAAAGGGACCCAAATTTG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 CTAACCTCAGTCCCTTTTTTGAGAGTGAATGGTGGAGGGTGGGAAAGGGACCCAAATTTG 540

Query 541 TAGATCTCTTTGTCTGGGGGAGGGGAANGATG 572
          ||||||||||||||||||||||||||||
Sbjct 541 TAGATCTCTTTGTCTGGGGGAGGGGAANGATG 572
```


Sequence 637 matched with Sequence 238

Query= Sequence ID - 637 nt: 482
Length=482

SEQ ID NO: 238 nt: 482

ALIGNMENTS

Identities = 482/482 (100%), Gaps = 0/482 (0%)

Query	1	TTAAACAGGCGCAGGGTAAAAATGAGAATGAATCTGAAAAAGAGAGTTGGTGTTTAA	60
Sbjct	1	TTAAACAGGCGCAGGGTAAAAATGAGAATGAATCTGAAAAAGAGAGTTGGTGTTTAA	60
Query	61	AGAGGATGGACAAGAGTATGCTCAGGTAATCAAAATGTTGGGAAATGGACGATTGGAAGC	120
Sbjct	61	AGAGGATGGACAAGAGTATGCTCAGGTAATCAAAATGTTGGGAAATGGACGATTGGAAGC	120
Query	121	ATTGTGTTTTGATGGTGTAAAGAGGTTATGCCATATCAGAGGGAAATTGAGAAAAAGGT	180
Sbjct	121	ATTGTGTTTTGATGGTGTAAAGAGGTTATGCCATATCAGAGGGAAATTGAGAAAAAGGT	180
Query	181	TTGGATAAATACATCAGACATTATATTGGTTGGTCTACGGGACTATCAGGATAACAAAGC	240
Sbjct	181	TTGGATAAATACATCAGACATTATATTGGTTGGTCTACGGGACTATCAGGATAACAAAGC	240
Query	241	TGATGTAATTTTAAAGTACAATGCAGATGAAGCTAGAAGCCTGAAGGCATATGGCGAGCT	300
Sbjct	241	TGATGTAATTTTAAAGTACAATGCAGATGAAGCTAGAAGCCTGAAGGCATATGGCGAGCT	300
Query	301	TCCAGAACATGCTAAAATCAATGAAACAGACACATTTGGTCCTGGAGATGATGATGAAAT	360
Sbjct	301	TCCAGAACATGCTAAAATCAATGAAACAGACACATTTGGTCCTGGAGATGATGATGAAAT	360
Query	361	CCAGTTTGACGATATTGGAGATGATGATGAAGACATTGATGATATCTAAATTGAACCAAG	420
Sbjct	361	CCAGTTTGACGATATTGGAGATGATGATGAAGACATTGATGATATCTAAATTGAACCAAG	420
Query	421	TGTTTTTACATGACAAGTTCTCTGAGGATGGTTCTACAGTTGGGATTTTGGCCATCATCA	480
Sbjct	421	TGTTTTTACATGACAAGTTCTCTGAGGATGGTTCTACAGTTGGGATTTTGGCCATCATCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AC	482
Sbjct	481	AC	482

Sequence 638 matched with Sequence 239

Query= Sequence ID - 638
Length=545

nt: 545

SEQ ID NO: 239

nt: 545

ALIGNMENTS

Identities = 545/545 (100%), Gaps = 0/545 (0%)

Query	1	TTTGAAGGCAAAGAGGGATTAATCTGTGCTGGCATCATGTAAGGAGACTTGATAGATAAG	60
Sbjct	1	TTTGAAGGCAAAGAGGGATTAATCTGTGCTGGCATCATGTAAGGAGACTTGATAGATAAG	60
Query	61	AAAAAGCTTTACCTAAGTTTTGAAGAATAGGTTTTTCATAATGGAAAAATTTAAGGGAAAA	120
Sbjct	61	AAAAAGCTTTACCTAAGTTTTGAAGAATAGGTTTTTCATAATGGAAAAATTTAAGGGAAAA	120
Query	121	ATCTCCAAAAAAGTGCTACTCAAGTTTTATCCATTTGTATTTCCAACACAGCCTAGGACA	180
Sbjct	121	ATCTCCAAAAAAGTGCTACTCAAGTTTTATCCATTTGTATTTCCAACACAGCCTAGGACA	180
Query	181	GTACCTGCACATAGTAGGTGATTAATAAAAAATTTAGAAAGCATTAACTAAAGAGGAAA	240
Sbjct	181	GTACCTGCACATAGTAGGTGATTAATAAAAAATTTAGAAAGCATTAACTAAAGAGGAAA	240
Query	241	AATAGCAATGGCAAGAAAACACATGTAGGGAACACATGTAGCCAAAAAATAATATATAAT	300
Sbjct	241	AATAGCAATGGCAAGAAAACACATGTAGGGAACACATGTAGCCAAAAAATAATATATAAT	300
Query	301	CAGAGAAATAATAGGACTTCTGGaaaaaaaGATGAGATCAGATTGGTTAGGATCTTTAC	360
Sbjct	301	CAGAGAAATAATAGGACTTCTGGAAAAAAAAAGATGAGATCAGATTGGTTAGGATCTTTAC	360
Query	361	TAACATGACAAGAGCATGAAttttttttCTGTAGATAATAAGTATGAAAGAATTTTAGCT	420
Sbjct	361	TAACATGACAAGAGCATGAATTTTTTTTCTGTAGATAATAAGTATGAAAGAATTTTAGCT	420
Query	421	TAAAAATTAGCATAATTTGGATCCACATATGCAAATCAATGAATGTAATTCATAATATAA	480
Sbjct	421	TAAAAATTAGCATAATTTGGATCCACATATGCAAATCAATGAATGTAATTCATAATATAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ACAGAACTAAACACAAAAACCACGTGATTATCTCAATAGACACAGAAAAGGCCTTCaaaa  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ACAGAACTAAACACAAAAACCACGTGATTATCTCAATAGACACAGAAAAGGCCTTCAAAA  540

Query  541  aaaTT  545
          |||||
Sbjct  541  AAATT  545
```

Sequence 639 matched with Sequence 240

Query= Sequence ID - 639
Length=624

nt: 624

SEQ ID NO: 240

nt: 624

ALIGNMENTS

Identities = 624/624 (100%), Gaps = 0/624 (0%)

Query	1	GACACACGAGCATATTTACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAA	60
Sbjct	1	GACACACGAGCATATTTACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAA	60
Query	61	GTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTC	120
Sbjct	61	GTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTC	120
Query	121	TGAGCCCTAGGATTCATCTTTCTTTTACCCGTAGGTGGCCTGACTGGCATTGTATTAGCA	180
Sbjct	121	TGAGCCCTAGGATTCATCTTTCTTTTACCCGTAGGTGGCCTGACTGGCATTGTATTAGCA	180
Query	181	AACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGTAGCCCACTTCCACTAT	240
Sbjct	181	AACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGTAGCCCACTTCCACTAT	240
Query	241	GTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTA	300
Sbjct	241	GTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTA	300
Query	301	TTCTCAGGCTACACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATC	360
Sbjct	301	TTCTCAGGCTACACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATC	360
Query	361	GGCGTAAATCTAACTTTCTTCCACAACACTTTCTCGGCCTATCCGGAATGCCCCGACGT	420
Sbjct	361	GGCGTAAATCTAACTTTCTTCCACAACACTTTCTCGGCCTATCCGGAATGCCCCGACGT	420
Query	421	TACTCGGACTACCCCGATGCATACACCACATGAAACATCCTATCATCTGTAGGCTCATTC	480
Sbjct	421	TACTCGGACTACCCCGATGCATACACCACATGAAACATCCTATCATCTGTAGGCTCATTC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATTTCTCTAACAGCAGTAATATTAATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAG  540
          |||
Sbjct  481  ATTTCTCTAACAGCAGTAATATTAATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAG  540

Query  541  CGAAAAGTCCTAATAGTAGAAGAACCCTCCATAAACCTGGAGTGACTATATGGATGCCCC  600
          |||
Sbjct  541  CGAAAAGTCCTAATAGTAGAAGAACCCTCCATAAACCTGGAGTGACTATATGGATGCCCC  600

Query  601  CCACCCTACCACACATTTCGAAGAA  624
          |||
Sbjct  601  CCACCCTACCACACATTTCGAAGAA  624
```

Sequence 641 matched with Sequence 241

Query= Sequence ID 641

Length=421

SEQ ID NO: 241

ALIGNMENTS

Identities = 421/421 (100%), Gaps = 0/421 (0%)

Query	1	CAAGATGACAAAGAAAAGAAGGAACAATGGTCGTGCCAAAAAGGGCCGCGCCACGTGCA	60
Sbjct	1	CAAGATGACAAAGAAAAGAAGGAACAATGGTCGTGCCAAAAAGGGCCGCGCCACGTGCA	60
Query	61	GCCTATTCGCTGCACTAACTGTGCCCGATGCGTGCCCAAGGACAAGGCCATTAAGAAATT	120
Sbjct	61	GCCTATTCGCTGCACTAACTGTGCCCGATGCGTGCCCAAGGACAAGGCCATTAAGAAATT	120
Query	121	CGTCATTCGAAACATAGTGGAGGCCGAGCAGTCAGGGACATTTCTGAAGCGAGCGTCTT	180
Sbjct	121	CGTCATTCGAAACATAGTGGAGGCCGAGCAGTCAGGGACATTTCTGAAGCGAGCGTCTT	180
Query	181	CGATGCCTATGTGCTTCCCAAGCTGTATGTGAAGCTACATTACTGTGTGAGTTGTGCAAT	240
Sbjct	181	CGATGCCTATGTGCTTCCCAAGCTGTATGTGAAGCTACATTACTGTGTGAGTTGTGCAAT	240
Query	241	TCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCGCAAGGACCGAACACCCCCACC	300
Sbjct	241	TCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCGCAAGGACCGAACACCCCCACC	300
Query	301	CCGATTTAGACCTGCGGGTGCTGCCCCACGTCCCCACCAAAGCCCATGTAAGGAGCTGA	360
Sbjct	301	CCGATTTAGACCTGCGGGTGCTGCCCCACGTCCCCACCAAAGCCCATGTAAGGAGCTGA	360
Query	361	GTTCTTAAAGACTGAAGACAGGCTATTCTCTGGAGAAAAATAAAATGGAAATTGTACTTA	420
Sbjct	361	GTTCTTAAAGACTGAAGACAGGCTATTCTCTGGAGAAAAATAAAATGGAAATTGTACTTA	420
Query	421	A	421
Sbjct	421	A	421

Sequence 642 matched with Sequence 242

Query= Sequence ID 642
Length=539

SEQ ID NO: 242

ALIGNMENTS

Identities = 539/539 (100%), Gaps = 0/539 (0%)

Query	1	TGCTTGGCCCTCTACCTCCTGCCCTCTTCCTGTTTCATCTCCCAACCACTGCACTCTTGAT	60
Sbjct	1	TGCTTGGCCCTCTACCTCCTGCCCTCTTCCTGTTTCATCTCCCAACCACTGCACTCTTGAT	60
Query	61	TTTTATACCACACAGAAGGTAAGAAAATTCTAGGAACCCTAAGGATCAATCCTCTCCATT	120
Sbjct	61	TTTTATACCACACAGAAGGTAAGAAAATTCTAGGAACCCTAAGGATCAATCCTCTCCATT	120
Query	121	TTCACTCAAATGCCTGGGGCCCAGCTCTGCAATGACTGACTCCAGGGCCTCTTTCCTCAC	180
Sbjct	121	TTCACTCAAATGCCTGGGGCCCAGCTCTGCAATGACTGACTCCAGGGCCTCTTTCCTCAC	180
Query	181	TGCCAGCATAGAAGTCAGGGGAGCCAGCTGGGCCCTGCGGTCAGGAAGGTTCTCATTTTT	240
Sbjct	181	TGCCAGCATAGAAGTCAGGGGAGCCAGCTGGGCCCTGCGGTCAGGAAGGTTCTCATTTTT	240
Query	241	GGAGCATTCCCTGAGCCCAGATCATAGGAGCAGCTGTCCCTGGTGGGACACAGGAGTCAT	300
Sbjct	241	GGAGCATTCCCTGAGCCCAGATCATAGGAGCAGCTGTCCCTGGTGGGACACAGGAGTCAT	300
Query	301	GACTCCTACCCTCCACCCTCCACACCCACCAGGCATTTAGCAGTCTGTCCTATGCAAGAC	360
Sbjct	301	GACTCCTACCCTCCACCCTCCACACCCACCAGGCATTTAGCAGTCTGTCCTATGCAAGAC	360
Query	361	AGATGAATTCTCAGCCAGGATACCTCAAGGCAGGCAAAGGTGAGTGGAGGGAAAATTAC	420
Sbjct	361	AGATGAATTCTCAGCCAGGATACCTCAAGGCAGGCAAAGGTGAGTGGAGGGAAAATTAC	420
Query	421	AAACATTCAGGGTGTGTGGTGTCTGGCATCACCATGGCCAAATCCAAGAGGTCTTCCTGGA	480
Sbjct	421	AAACATTCAGGGTGTGTGGTGTCTGGCATCACCATGGCCAAATCCAAGAGGTCTTCCTGGA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGAGGGCCCAA	CTGGAACCAA	AGAATGCTGTCAGCAGTTGGAATAGAGCTGTGAATT	539
Sbjct	481	AGAGGGCCCAA	CTGGAACCAA	AGAATGCTGTCAGCAGTTGGAATAGAGCTGTGAATT	539

Sequence 643 matched with Sequence 243

Query= Sequence ID 643
Length=397

SEQ ID NO: 243

ALIGNMENTS

Identities = 397/397 (100%), Gaps = 0/397 (0%)

Query	1	CTTTCCAAGAGGAATCCTCGGCAGATAAACTGGACTGTCCTCTACAGAAGGAAGCACAAA	60
Sbjct	1	CTTTCCAAGAGGAATCCTCGGCAGATAAACTGGACTGTCCTCTACAGAAGGAAGCACAAA	60
Query	61	AAGGGACAGTCGGAAGAAATTCAAAAGAAAAGAACCCGCCGAGCAGTCAAATTCAGAGG	120
Sbjct	61	AAGGGACAGTCGGAAGAAATTCAAAAGAAAAGAACCCGCCGAGCAGTCAAATTCAGAGG	120
Query	121	GCCATTACTGGTGCATCTCTTGCTGATATAATGGCCAAGAGGAATCAGAAACCTGAAGTT	180
Sbjct	121	GCCATTACTGGTGCATCTCTTGCTGATATAATGGCCAAGAGGAATCAGAAACCTGAAGTT	180
Query	181	AGAAAGGCTCAACGAGAACAAGCTATCAGGGCTGCTAAGGAAGCAAAAAAGGCTAAGCAA	240
Sbjct	181	AGAAAGGCTCAACGAGAACAAGCTATCAGGGCTGCTAAGGAAGCAAAAAAGGCTAAGCAA	240
Query	241	GCATCTAAAAAGACTGCAATGGCTGCTGCTAAGGCACCTACAAAGGCAGCACCTAAGCAA	300
Sbjct	241	GCATCTAAAAAGACTGCAATGGCTGCTGCTAAGGCACCTACAAAGGCAGCACCTAAGCAA	300
Query	301	AAGATTGTGAAGCCTGTGAAAGTTTCAGCTCCCCGAGTTGGTGGAAAACGCTAAACTGGC	360
Sbjct	301	AAGATTGTGAAGCCTGTGAAAGTTTCAGCTCCCCGAGTTGGTGGAAAACGCTAAACTGGC	360
Query	361	AGATTAGATTTTAAATAAAGATTGGATTATAACTCT	397
Sbjct	361	AGATTAGATTTTAAATAAAGATTGGATTATAACTCT	397

Sequence 644 matched with Sequence 244

Query= Sequence ID 644
Length=542

SEQ ID NO: 244

ALIGNMENTS

Identities = 542/542 (100%), Gaps = 0/542 (0%)

Query	1	CTTTGATAGAGAAGAAAATTCTCCTAGGATACAAGAGCCTCAACATTTTAAAGATTTTCT	60
Sbjct	1	CTTTGATAGAGAAGAAAATTCTCCTAGGATACAAGAGCCTCAACATTTTAAAGATTTTCT	60
Query	61	GCATCTCAAAAAGCGTAGGCTCCTTGCTGGGCAAGGTGAGCCTCTGTGAGTCCTCATAGGA	120
Sbjct	61	GCATCTCAAAAAGCGTAGGCTCCTTGCTGGGCAAGGTGAGCCTCTGTGAGTCCTCATAGGA	120
Query	121	CCGAGCAAATCTGATTCACCCCAGAAAATCCAATATCGAAGCTGAGCTTTGGCCTGAGCG	180
Sbjct	121	CCGAGCAAATCTGATTCACCCCAGAAAATCCAATATCGAAGCTGAGCTTTGGCCTGAGCG	180
Query	181	GGTTCCATTTCTCCTCCCCAGATCCTATTTAGGAAGTGTCTCCTGACAACCTCCAAAAGGTG	240
Sbjct	181	GGTTCCATTTCTCCTCCCCAGATCCTATTTAGGAAGTGTCTCCTGACAACCTCCAAAAGGTG	240
Query	241	CTAACATGCAACGTTCTGAAGGGTTATTGCTCAAAAACAAGATTTTCCTTGTGGTCAAGA	300
Sbjct	241	CTAACATGCAACGTTCTGAAGGGTTATTGCTCAAAAACAAGATTTTCCTTGTGGTCAAGA	300
Query	301	CTCTGCGAGCCTCGAACACGATGAATCCGCTCGAATGGGCTTGGGCTTTGCCCGGGTGGC	360
Sbjct	301	CTCTGCGAGCCTCGAACACGATGAATCCGCTCGAATGGGCTTGGGCTTTGCCCGGGTGGC	360
Query	361	GCACGCTCACACGCTGGAAGCACAGCTTTGACGATCTCCACACACGCACAGGCACACACG	420
Sbjct	361	GCACGCTCACACGCTGGAAGCACAGCTTTGACGATCTCCACACACGCACAGGCACACACG	420
Query	421	CCACAGATGATGCCGGCTCATTCTCAGGGGGTGTCTAAGTTCTGCTTTAAATATTTACCC	480
Sbjct	421	CCACAGATGATGCCGGCTCATTCTCAGGGGGTGTCTAAGTTCTGCTTTAAATATTTACCC	480

Sequence 645 matched with Sequence 245

Query= Sequence ID - 645
Length=649

nt: 649

SEQ ID NO: 245

nt: 649

ALIGNMENTS

Identities = 649/649 (100%), Gaps = 0/649 (0%)

Query	1	CTACAGCCTGGGCAGCGCGCTGCGCCCCAGCACCAGCCGCAGCCTCTACGCCTCGTCCCC	60
Sbjct	1	CTACAGCCTGGGCAGCGCGCTGCGCCCCAGCACCAGCCGCAGCCTCTACGCCTCGTCCCC	60
Query	61	GGGCGGCGTGTATGCCACGCGCTCCTCTGCCGTGCGCCTGCGGAGCAGCGTGCCCGGGGT	120
Sbjct	61	GGGCGGCGTGTATGCCACGCGCTCCTCTGCCGTGCGCCTGCGGAGCAGCGTGCCCGGGGT	120
Query	121	GCGGCTCCTGCAGGACTCGGTGGACTTCTCGCTGGCCGACGCCATCAACACCGAGTTCAA	180
Sbjct	121	GCGGCTCCTGCAGGACTCGGTGGACTTCTCGCTGGCCGACGCCATCAACACCGAGTTCAA	180
Query	181	GAACACCCGCACCAACGAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCAACTA	240
Sbjct	181	GAACACCCGCACCAACGAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCAACTA	240
Query	241	CATCGACAAGGTGCGCTTCCTGGAGCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCA	300
Sbjct	241	CATCGACAAGGTGCGCTTCCTGGAGCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCA	300
Query	301	GCTCAAGGGCCAAGGCAAGTCGCGCCTGGGGGACCTCTACGAGGAGGAGATGCGGGAGCT	360
Sbjct	301	GCTCAAGGGCCAAGGCAAGTCGCGCCTGGGGGACCTCTACGAGGAGGAGATGCGGGAGCT	360
Query	361	GCGCCGGCAGGTGGACCAGCTAACCAACGACAAAGCCGCGTCGAGGTGGAGCGCGACAA	420
Sbjct	361	GCGCCGGCAGGTGGACCAGCTAACCAACGACAAAGCCGCGTCGAGGTGGAGCGCGACAA	420
Query	421	CCTGGCCGAGGACATCATGCGCCTCCGGGAGAAATTGCAGGAGGAGATGCTTCAGAGAGA	480
Sbjct	421	CCTGGCCGAGGACATCATGCGCCTCCGGGAGAAATTGCAGGAGGAGATGCTTCAGAGAGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGAAGCCGAAAACACCCTGCAATCTTTCAGACAGGAAATCCAGGAGCTGCAGGCTCAGAT  540
          |||
Sbjct  481  GGAAGCCGAAAACACCCTGCAATCTTTCAGACAGGAAATCCAGGAGCTGCAGGCTCAGAT  540

Query  541  TCAGGAACAGCATGTCCAAATCGATGTGGATGTTTCCAAGCCTGACCTCACGGCTGCCTT  600
          |||
Sbjct  541  TCAGGAACAGCATGTCCAAATCGATGTGGATGTTTCCAAGCCTGACCTCACGGCTGCCTT  600

Query  601  GCGTGACGTACGTANCAATATGAAAGTGTGGCTGCCAAAAACCTTGCGAG  649
          |||
Sbjct  601  GCGTGACGTACGTANCAATATGAAAGTGTGGCTGCCAAAAACCTTGCGAG  649
```

Sequence 646 matched with Sequence 246

Query= Sequence ID - 646
Length=600

nt: 600

SEQ ID NO: 246

nt: 600

ALIGNMENTS

Identities = 600/600 (100%), Gaps = 0/600 (0%)

Query	1	GAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGGAG	60
Sbjct	1	GAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGGAG	60
Query	61	GCTATCCAGCGTACTCCAAAGATTGAGGTTTACTCACGTCATCCAGCAGAGAATGGAAAG	120
Sbjct	61	GCTATCCAGCGTACTCCAAAGATTGAGGTTTACTCACGTCATCCAGCAGAGAATGGAAAG	120
Query	121	TCAAATTCCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAAGTTGACTTA	180
Sbjct	121	TCAAATTCCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAAGTTGACTTA	180
Query	181	CTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTGAGACTTGTCTTTCAGCAAGGAC	240
Sbjct	181	CTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTGAGACTTGTCTTTCAGCAAGGAC	240
Query	241	TGGTCTTTCATCTCTTGTACTACACTGAATTCACCCCCACTGAAAAAGATGAGTATGCC	300
Sbjct	241	TGGTCTTTCATCTCTTGTACTACACTGAATTCACCCCCACTGAAAAAGATGAGTATGCC	300
Query	301	TGCCGTGTGAACCATGTGACTTTGTCACAGCCCAAGATAGTTAAGTGGGATCGAGACATG	360
Sbjct	301	TGCCGTGTGAACCATGTGACTTTGTCACAGCCCAAGATAGTTAAGTGGGATCGAGACATG	360
Query	361	TAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTCCAAATTCTG	420
Sbjct	361	TAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTCCAAATTCTG	420
Query	421	CTTGCTTGCTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACAAAATGTAGG	480
Sbjct	421	CTTGCTTGCTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACAAAATGTAGG	480

PATENT SEQUENCE ALIGNMENT

Query	481	GTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAGTGCTGTCTC	540
Sbjct	481	GTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAGTGCTGTCTC	540
Query	541	CATGTTTGATGTATCTGAGCAGGGTGCTCCACAGGTAGCTCTAGGAGGGCTGGCAACTTA	600
Sbjct	541	CATGTTTGATGTATCTGAGCAGGGTGCTCCACAGGTAGCTCTAGGAGGGCTGGCAACTTA	600

Sequence 647 matched with Sequence 247

Query= Sequence ID 647
Length=331

SEQ ID NO: 247

ALIGNMENTS

Identities = 331/331 (100%), Gaps = 0/331 (0%)

Query	1	CGAATGTGCAGGTTTGTACATAGGTATATATATGCCATGATGGAAATATTTAttttttt	60
Sbjct	1	CGAATGTGCAGGTTTGTACATAGGTATATATATGCCATGATGGAAATATTTATTTTTTT	60
Query	61	AAGCGTAATTTTGCCAAATAATAAAAAACAGAAGGAAATTGAGATTAGAGGGAGGTGTTTA	120
Sbjct	61	AAGCGTAATTTTGCCAAATAATAAAAAACAGAAGGAAATTGAGATTAGAGGGAGGTGTTTA	120
Query	121	AAGAGAGGTTATAGAGTAGAAGATTTGATGCTGGAGAGGTTAAGGTGCAATAAGAATTTA	180
Sbjct	121	AAGAGAGGTTATAGAGTAGAAGATTTGATGCTGGAGAGGTTAAGGTGCAATAAGAATTTA	180
Query	181	GGGAGAAATGTTGTTTCATTATTGGAGGGTAAATGATGTGGTGCCTGAGGTCTGTACGTTA	240
Sbjct	181	GGGAGAAATGTTGTTTCATTATTGGAGGGTAAATGATGTGGTGCCTGAGGTCTGTACGTTA	240
Query	241	CCTCTTAACAATTTCTGTCCTTCAGATGGAACTCTTTAACTTCTCGTAAAAGTCATATA	300
Sbjct	241	CCTCTTAACAATTTCTGTCCTTCAGATGGAACTCTTTAACTTCTCGTAAAAGTCATATA	300
Query	301	CCTATATAATAAAGCTACTGATTTCCAAAAA	331
Sbjct	301	CCTATATAATAAAGCTACTGATTTCCAAAAA	331

Sequence 648 matched with Sequence 248

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 648
Length=41

SEQ ID NO: 248	81.8	3e-22
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ALIGNMENTS

Identities = 41/41 (100%), Gaps = 0/41 (0%)

Query	1	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	41
Sbjct	1	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	41

Sequence 649 matched with Sequence 249

Query= Sequence ID - 649
Length=425

nt: 425

SEQ ID NO: 249

nt: 425

ALIGNMENTS

Identities = 425/425 (100%), Gaps = 0/425 (0%)

Query	1	CaaaaaaaaCGAAGAAAAGTGACGACAGTCTGAGGGACTTATGGGAGATCATCAAGTGAAC	60
Sbjct	1	CAAAAAAACGAAGAAAAGTGACGACAGTCTGAGGGACTTATGGGAGATCATCAAGTGAAC	60
Query	61	CACTATATGTGTAATGTAAGTCTTGGAATgagaagagagaaggagaaggaggagagagCT	120
Sbjct	61	CACTATATGTGTAATGTAAGTCTTGGAATGAGAAGAGAGAAGGAGAAGGAGGAGAGAGCT	120
Query	121	TATTTGTAGAAATAATGGCTGAAAACATCCCAAACCTTTCcttttttGAGGAAAGAAATA	180
Sbjct	121	TATTTGTAGAAATAATGGCTGAAAACATCCCAAACCTTTCCTTTTTTTGAGGAAAGAAATA	180
Query	181	GGCATACAAGTTCAAGAAACTCAAGGAACTCCAGAGAGGACAATTCTAAAGACACCCCCT	240
Sbjct	181	GGCATACAAGTTCAAGAAACTCAAGGAACTCCAGAGAGGACAATTCTAAAGACACCCCCT	240
Query	241	CTAACATACATTATAATCAAATTGTCAAAAAGTAAAATACAAAGAGAATCTTTTAAATTGA	300
Sbjct	241	CTAACATACATTATAATCAAATTGTCAAAAAGTAAAATACAAAGAGAATCTTTTAAATTGA	300
Query	301	CAAGAGAAAAGCAGCTGGTCACGTTCAAGGGAGTTCTATAAGAATTCAGCAGATTTCTC	360
Sbjct	301	CAAGAGAAAAGCAGCTGGTCACGTTCAAGGGAGTTCTATAAGAATTCAGCAGATTTCTC	360
Query	361	AGCAGAAACCTTGCAGGCCAACAGGCAGTGGGATGATACATTCAAAGTGCaaaaaaaaa	420
Sbjct	361	AGCAGAAACCTTGCAGGCCAACAGGCAGTGGGATGATACATTCAAAGTGCAAAAAAAAAA	420
Query	421	aaaaa 425	
Sbjct	421	AAAAA 425	

Sequence 650 matched with Sequence 250

Query= Sequence ID 650

Length=633

SEQ ID NO: 250

ALIGNMENTS

Identities = 633/633 (100%), Gaps = 0/633 (0%)

Query	1	CGAGAGTTTACCAGTNGCCTAATAATGCAATAAAAAATGCTTTGAGATAGCTAACNGCCC	60
Sbjct	1	CGAGAGTTTACCAGTNGCCTAATAATGCAATAAAAAATGCTTTGAGATAGCTAACNGCCC	60
Query	61	ATAAAACAAACTCAAATTGCTTATAAAGTTTCTTCCCATGTTCCCATTTGATGAAAAGTC	120
Sbjct	61	ATAAAACAAACTCAAATTGCTTATAAAGTTTCTTCCCATGTTCCCATTTGATGAAAAGTC	120
Query	121	TTACATCACATATAACTGGGAAGCAGGGTCCCTCCTCAATTTTCAGACATTTTGAAAGG	180
Sbjct	121	TTACATCACATATAACTGGGAAGCAGGGTCCCTCCTCAATTTTCAGACATTTTGAAAGG	180
Query	181	ATGACAGTTCTGTTTGTAGATGAGTAAACCTCTATATTCATAAGTTCTAAAATCCTTCA	240
Sbjct	181	ATGACAGTTCTGTTTGTAGATGAGTAAACCTCTATATTCATAAGTTCTAAAATCCTTCA	240
Query	241	TTATGAGGGATTCAAAGTATTTATAAAAAACACTGCCCTCTAAAAATTCCTCAGATCTGA	300
Sbjct	241	TTATGAGGGATTCAAAGTATTTATAAAAAACACTGCCCTCTAAAAATTCCTCAGATCTGA	300
Query	301	AGTATGGNCTTGGNCCTGAATATACAGTGTTATCCTATGTTTAAAAGGGTGATCCAGACA	360
Sbjct	301	AGTATGGNCTTGGNCCTGAATATACAGTGTTATCCTATGTTTAAAAGGGTGATCCAGACA	360
Query	361	TGAGACGCAACTAGTTGGTGCATAAGAAGGCCCACTTGGCTATTTTCATATCTACCTACA	420
Sbjct	361	TGAGACGCAACTAGTTGGTGCATAAGAAGGCCCACTTGGCTATTTTCATATCTACCTACA	420
Query	421	ATTGACCaaaaaaaTTTTTTAGGCCAGCAATTATTATTTAGCTTCGCTCTTTCTAGTGC	480
Sbjct	421	ATTGACCAAAAAAATTTTTTAGGCCAGCAATTATTATTTAGCTTCGCTCTTTCTAGTGC	480

Query	481	AAGAAACTGCAGGCTGGATCAGTAGTTCAACAGCTAAACAGTCATAAAATAGTCATTGGC	540
Sbjct	481	AAGAAACTGCAGGCTGGATCAGTAGTTCAACAGCTAAACAGTCATAAAATAGTCATTGGC	540
Query	541	ATGTTAAATTTCTTTCAATGCTTCAAAGATAAATTCCAATTCTATTTACTTATTCATTGN	600
Sbjct	541	ATGTTAAATTTCTTTCAATGCTTCAAAGATAAATTCCAATTCTATTTACTTATTCATTGN	600
Query	601	GACNGNATTACTAAACAGGTAAGGATGGGAATA	633
Sbjct	601	GACNGNATTACTAAACAGGTAAGGATGGGAATA	633

Sequence 651 matched with Sequence 251

Query= Sequence ID - 651
Length=251

nt: 251

SEQ ID NO: 251

nt: 251

ALIGNMENTS

Identities = 251/251 (100%), Gaps = 0/251 (0%)

Query	1	CTTTGGGAGGCCGAGGCGGGCGGATCACTTGAGGTCAGGGGTTGAGACCAGTCTGGCCA	60
Sbjct	1	CTTTGGGAGGCCGAGGCGGGCGGATCACTTGAGGTCAGGGGTTGAGACCAGTCTGGCCA	60
Query	61	ACATGGTGAAACCCCAACTCTACTAAAAATACAAAAGTTAGCCAAGTGTGGTGGCAAGTG	120
Sbjct	61	ACATGGTGAAACCCCAACTCTACTAAAAATACAAAAGTTAGCCAAGTGTGGTGGCAAGTG	120
Query	121	CCTGTAATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATCACTTTGAACCTGGGAGGCG	180
Sbjct	121	CCTGTAATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATCACTTTGAACCTGGGAGGCG	180
Query	181	GAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTTCAGCCTGGGCAACAGAGCAAGATT	240
Sbjct	181	GAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTTCAGCCTGGGCAACAGAGCAAGATT	240
Query	241	CCGTCCATCTC	251
Sbjct	241	CCGTCCATCTC	251

Sequence 652 matched with Sequence 252

Query= Sequence ID 652
Length=593

SEQ ID NO: 252

ALIGNMENTS

Identities = 593/593 (100%), Gaps = 0/593 (0%)

Query	1	CTTTCTTCAGCCTTGCAGACACCTAAACATCATGTAATTACCTAAGGAATTCCCAAGTGC	60
Sbjct	1	CTTTCTTCAGCCTTGCAGACACCTAAACATCATGTAATTACCTAAGGAATTCCCAAGTGC	60
Query	61	CTCTTCCAGGTTATACGTGTAAATAGCTGTTTTTATGCAAGATTAGTTAGATACTGCTCT	120
Sbjct	61	CTCTTCCAGGTTATACGTGTAAATAGCTGTTTTTATGCAAGATTAGTTAGATACTGCTCT	120
Query	121	TTACAGGATGAGTGGTGTCTTTGGCTgggggggNCTTAAATGTGTTTCTAATGTGTG	180
Sbjct	121	TTACAGGATGAGTGGTGTCTTTGGCTGGGGGGNCTTAAATGTGTTTCTAATGTGTG	180
Query	181	TGTCAAATAATTACCTGTAAACAGACTGCCAATCTGGCTGAAGCCAATGCTTCTGAAGA	240
Sbjct	181	TGTCAAATAATTACCTGTAAACAGACTGCCAATCTGGCTGAAGCCAATGCTTCTGAAGA	240
Query	241	AGATAAAATTAAAGCAATGATGTGCGCAATCTGGCCATGAATACGACCCAATCAATTACAT	300
Sbjct	241	AGATAAAATTAAAGCAATGATGTGCGCAATCTGGCCATGAATACGACCCAATCAATTACAT	300
Query	301	GAAGAAACCTCTAGGTCCACCACCTCCATCTTACACGTGTTTCCGTTGTGGTAAACCTGG	360
Sbjct	301	GAAGAAACCTCTAGGTCCACCACCTCCATCTTACACGTGTTTCCGTTGTGGTAAACCTGG	360
Query	361	ACATTATATTAAGAATTGCCCAACAAATGGGGATAAAAACTTTGAATCTGGTCCTAGGAT	420
Sbjct	361	ACATTATATTAAGAATTGCCCAACAAATGGGGATAAAAACTTTGAATCTGGTCCTAGGAT	420
Query	421	TAAAAAGAGCACTGGAATTCCCAGAAGTTTCATGATGGAAGTGAAAGATCCTAATATGAA	480
Sbjct	421	TAAAAAGAGCACTGGAATTCCCAGAAGTTTCATGATGGAAGTGAAAGATCCTAATATGAA	480

PATENT SEQUENCE ALIGNMENT

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Query  481  AGGTGCAATGCTTACCAACACTGGAAAATATGCAATCCAACCTATAGATGCAGAAGCATAT  540
          |||
Sbjct  481  AGGTGCAATGCTTACCAACACTGGAAAATATGCAATCCAACCTATAGATGCAGAAGCATAT  540

Query  541  GCAATTGGGAAGAAAGAGAAACCTCCTTNTTACCAGAGAGCCATCTTNTTCT  593
          |||
Sbjct  541  GCAATTGGGAAGAAAGAGAAACCTCCTTNTTACCAGAGAGCCATCTTNTTCT  593
```

Sequence 653 matched with Sequence 253

Query= Sequence ID 653
Length=211

SEQ ID NO: 253

ALIGNMENTS

Identities = 211/211 (100%), Gaps = 0/211 (0%)

Query	1	GTTGTGACTCGTTGGCATGTGATCTGAAGTTCCTGCCCTGCAGCTGACGAGCCAGTGTTT	60
Sbjct	1	GTTGTGACTCGTTGGCATGTGATCTGAAGTTCCTGCCCTGCAGCTGACGAGCCAGTGTTT	60
Query	61	CAATAATTAAAACAACTCAACTCACTGTCCTCCTGCCTTGAATTTGATCATTGCGCTTT	120
Sbjct	61	CAATAATTAAAACAACTCAACTCACTGTCCTCCTGCCTTGAATTTGATCATTGCGCTTT	120
Query	121	GCATGTATGTATCACAATACCACATGTACCCCATAAATATGTACAAAGATTATGTGTCAA	180
Sbjct	121	GCATGTATGTATCACAATACCACATGTACCCCATAAATATGTACAAAGATTATGTGTCAA	180
Query	181	TaaaaaacaaaaattaaaaTCCCAATTTTTA	211
Sbjct	181	TAAAAAACAAAAATTAAAATCCCAATTTTTA	211

Sequence 654 matched with Sequence 254

Query= Sequence ID 654
Length=247

SEQ ID NO: 254

ALIGNMENTS

Identities = 247/247 (100%), Gaps = 0/247 (0%)

Query	1	GTTGCTAGTAGCGGCAGGAAGATGTCAGGCTCACTTTCCTCTGATTCCCGAAATGGGGGG	60
Sbjct	1	GTTGCTAGTAGCGGCAGGAAGATGTCAGGCTCACTTTCCTCTGATTCCCGAAATGGGGGG	60
Query	61	AACCTCTAACCATAAAGGAATGGTAGAACAGTCCATTCTCGGATCAGAGAAAAATGCAG	120
Sbjct	61	AACCTCTAACCATAAAGGAATGGTAGAACAGTCCATTCTCGGATCAGAGAAAAATGCAG	120
Query	121	ACATGGTGTACCTGGAtttttttCTGCCCATGAATGTTGCCAGTCAGTACCTGTCCTCC	180
Sbjct	121	ACATGGTGTACCTGGATTTTTTTCTGCCCATGAATGTTGCCAGTCAGTACCTGTCCTCC	180
Query	181	TTGTTTCTCTATTTTTTGTTATGAATGTTGGGGTTACCACCTGCATTTAGGGGAAAATTG	240
Sbjct	181	TTGTTTCTCTATTTTTTGTTATGAATGTTGGGGTTACCACCTGCATTTAGGGGAAAATTG	240
Query	241	TGTTCTG	247
Sbjct	241	TGTTCTG	247

Sequence 655 matched with Sequence 255

Query= Sequence ID 655
Length=244

SEQ ID NO: 255

ALIGNMENTS

Identities = 244/244 (100%), Gaps = 0/244 (0%)

Query	1	GTCCCCGGGAATCGCGCCGCGTCGACGGTTTATTTTCAGTGCTTGAAGATACATTACACA	60
Sbjct	1	GTCCCCGGGAATCGCGCCGCGTCGACGGTTTATTTTCAGTGCTTGAAGATACATTACACA	60
Query	61	AATACTTGTTTGGGAAGACACCGTTTAATTTTAAGTTAACTTGCATGTTGTAAATGCGT	120
Sbjct	61	AATACTTGTTTGGGAAGACACCGTTTAATTTTAAGTTAACTTGCATGTTGTAAATGCGT	120
Query	121	TTTATGTTTAAATAAAGAGGAAAAATTTTTTGaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	180
Sbjct	121	TTTATGTTTAAATAAAGAGGAAAAATTTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	180
Query	181	aaaT	240
Sbjct	181	AAT	240
Query	241	TTTT 244	
Sbjct	241	TTTT 244	

Sequence 656 matched with Sequence 256

Query= Sequence ID 656

Length=433

SEQ ID NO: 256

ALIGNMENTS

Identities = 433/433 (100%), Gaps = 0/433 (0%)

Query	1	TAGAGGCCTGAATAGGTAGACAATGGCAGCAGCGTTTTTAATCACAGTCCTATTCATGCC	60
Sbjct	1	TAGAGGCCTGAATAGGTAGACAATGGCAGCAGCGTTTTTAATCACAGTCCTATTCATGCC	60
Query	61	CTAATTCGGGAGTGATGATTAAAGGACATTAGAGGGAGCACTTTGACATCTGATCCTTTG	120
Sbjct	61	CTAATTCGGGAGTGATGATTAAAGGACATTAGAGGGAGCACTTTGACATCTGATCCTTTG	120
Query	121	AACTGACGTCTGTGCAGGCTGCACTCCATAGAGCTCACTTGCCAAACTGATTCCTTAA	180
Sbjct	121	AACTGACGTCTGTGCAGGCTGCACTCCATAGAGCTCACTTGCCAAACTGATTCCTTAA	180
Query	181	ATAAAGTGCTGTGATTTCCAATGTAGGAAATATTACATTAGAGCCTATTGAAATGATTAG	240
Sbjct	181	ATAAAGTGCTGTGATTTCCAATGTAGGAAATATTACATTAGAGCCTATTGAAATGATTAG	240
Query	241	GAATTGAGGAGCTTTTCTTTAGGTGGGAATGTGGTGTATGCTGTATACTCACAAAAGTGA	300
Sbjct	241	GAATTGAGGAGCTTTTCTTTAGGTGGGAATGTGGTGTATGCTGTATACTCACAAAAGTGA	300
Query	301	GATCATTAATATTGCATGTACTACTTTGAATATCAGGGACCACAGAGAAATAGCATGAGA	360
Sbjct	301	GATCATTAATATTGCATGTACTACTTTGAATATCAGGGACCACAGAGAAATAGCATGAGA	360
Query	361	AACGCCTTCCTGCAGTCATGCACTTAAATGAATATGAACAAAAATGTGGAACCTCTGCTG	420
Sbjct	361	AACGCCTTCCTGCAGTCATGCACTTAAATGAATATGAACAAAAATGTGGAACCTCTGCTG	420
Query	421	TCATAGCTCTCCG	433
Sbjct	421	TCATAGCTCTCCG	433

Sequence 657 matched with Sequence 257

Query= Sequence ID 657
Length=380

SEQ ID NO: 257

ALIGNMENTS

Identities = 380/380 (100%), Gaps = 0/380 (0%)

Query	1	GGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGtttttttCTCT	60
Sbjct	1	GGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTTTTTCTCT	60
Query	61	TTGAAAGATAGAGATTAATACAACCTCTAAAAAATATAGTCAATAGGTTACTAAGATATT	120
Sbjct	61	TTGAAAGATAGAGATTAATACAACCTCTAAAAAATATAGTCAATAGGTTACTAAGATATT	120
Query	121	GCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAATATGAA	180
Sbjct	121	GCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAATATGAA	180
Query	181	GACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATGACGGAGGT	240
Sbjct	181	GACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATGACGGAGGT	240
Query	241	TGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAGAAAATTGAGAGAAAGGAC	300
Sbjct	241	TGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAGAAAATTGAGAGAAAGGAC	300
Query	301	TACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAAGGTGA	360
Sbjct	301	TACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAAGGTGA	360
Query	361	CTTAAACAGCTTAAAGTTTA	380
Sbjct	361	CTTAAACAGCTTAAAGTTTA	380

Sequence 658 matched with Sequence 258

Query= Sequence ID 658
Length=572

SEQ ID NO: 258

ALIGNMENTS

Identities = 572/572 (100%), Gaps = 0/572 (0%)

Query	1	GACCTTTGAGAAAATTAATTTAAATCCTAGAACTTTGGGTGAACCGAAGAAATTTATAAT	60
Sbjct	1	GACCTTTGAGAAAATTAATTTAAATCCTAGAACTTTGGGTGAACCGAAGAAATTTATAAT	60
Query	61	ATTTGTTTAGTTAATAACAGATAAAAAAGGAAAGATTCAAGCCTATTGGATGAGAATTTGT	120
Sbjct	61	ATTTGTTTAGTTAATAACAGATAAAAAAGGAAAGATTCAAGCCTATTGGATGAGAATTTGT	120
Query	121	ACATTATTTTAGAGCTAATAATAATGGTTTTTCAGTTTAGTGAGGATTTAAAAAATGTTTT	180
Sbjct	121	ACATTATTTTAGAGCTAATAATAATGGTTTTTCAGTTTAGTGAGGATTTAAAAAATGTTTT	180
Query	181	TGAATCAAACttttttCCTTTATAATCCTTTTAACTAACTCAGGAAATAAGGTATTATG	240
Sbjct	181	TGAATCAAACCTTTTTTCTTTATAATCCTTTTAACTAACTCAGGAAATAAGGTATTATG	240
Query	241	AAATCCACACACTGTTACCTCCTTAAAGTATGAGGATACTTCCCACTGTTTGGTCCACTA	300
Sbjct	241	AAATCCACACACTGTTACCTCCTTAAAGTATGAGGATACTTCCCACTGTTTGGTCCACTA	300
Query	301	GTGGCTGATTATTTTGTGGATTATTTGTAATTTCTTTTAAATCCTCCTTAAAGA	360
Sbjct	301	GTGGCTGATTATTTTGTGGATTATTTGTAATTTCTTTTAAATCCTCCTTAAAGA	360
Query	361	GCATGGCATTGAGTCACAGACCTATATTTGAATCCTGTCATTTACTAGCGTTTGGACC	420
Sbjct	361	GCATGGCATTGAGTCACAGACCTATATTTGAATCCTGTCATTTACTAGCGTTTGGACC	420
Query	421	TTGAACAATTATGCTCAGAGTCTCAGTTTTTCTTGTAAGTGATGATGATACTACTTAA	480
Sbjct	421	TTGAACAATTATGCTCAGAGTCTCAGTTTTTCTTGTAAGTGATGATGATACTACTTAA	480

PATENT SEQUENCE ALIGNMENT

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Query  481  CTCACAGGGTTGTAGTGAAGATCAAATGAGATCATGTCTGTANAACACCCTGCCCGGCAC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTCACAGGGTTGTAGTGAAGATCAAATGAGATCATGTCTGTANAACACCCTGCCCGGCAC  540

Query  541  TCAATAAGTATTAATAGGAACCCATATACCTC  572
          ||||||||||||||||||||||||
Sbjct  541  TCAATAAGTATTAATAGGAACCCATATACCTC  572
```

Sequence 660 matched with Sequence 259

Query= Sequence ID 660
Length=477

SEQ ID NO: 259

ALIGNMENTS

Identities = 477/477 (100%), Gaps = 0/477 (0%)

Query	1	TGttttttatTTTTAAAAGGTATAAACACCaaaaaaaTTAACATTGTATGAAGATGG	60
Sbjct	1	TGTTTTTATTTTTAAAAGGTATAAACACCAAAAAAAAATTAACATTGTATGAAGATGG	60
Query	61	AAAATAAGAAGATGCACTTTCTGTAACCTTGTCTAAGGATTTAAATTACTAACTTATGAA	120
Sbjct	61	AAAATAAGAAGATGCACTTTCTGTAACCTTGTCTAAGGATTTAAATTACTAACTTATGAA	120
Query	121	CTCCAATTTGAATTGAACTTAACTATCGGCTTTCTTACTGGTAAAATTATATGGTTTATT	180
Sbjct	121	CTCCAATTTGAATTGAACTTAACTATCGGCTTTCTTACTGGTAAAATTATATGGTTTATT	180
Query	181	TTAAATGCGTACATATTGACCAATGGCCTCTGAAAAAGCACATTTTAGATACTGAAATTG	240
Sbjct	181	TTAAATGCGTACATATTGACCAATGGCCTCTGAAAAAGCACATTTTAGATACTGAAATTG	240
Query	241	AAGGAAAGAAAATGCATCTTCAAACATTTTTTGGAAATCTCACCACATATACtttgttana	300
Sbjct	241	AAGGAAAGAAAATGCATCTTCAAACATTTTTTGGAAATCTCACCACATATACTTTGTANA	300
Query	301	tttgtgtattgtaggggtgtttgttttgatttttgattgtatatgaacttttttAAAT	360
Sbjct	301	TTTGTGTATTGTAGGGTGTGTTTGTATTTTGTATTGTATATGAACTTTTTTTAAAT	360
Query	361	GTGACAGTTAAACACATCTTTAAAAGCATAGTCACAGACAAAAGCATACAGTATAAAAAT	420
Sbjct	361	GTGACAGTTAAACACATCTTTAAAAGCATAGTCACAGACAAAAGCATACAGTATAAAAAT	420
Query	421	TTCCTTGAAAACCTCCTACAATATTATATTTGGAGGCAGCTTCAGACTGTTTTATTGG	477
Sbjct	421	TTCCTTGAAAACCTCCTACAATATTATATTTGGAGGCAGCTTCAGACTGTTTTATTGG	477

Sequence 661 matched with Sequence 260

Query= Sequence ID 661
Length=256

SEQ ID NO: 260

ALIGNMENTS

Identities = 253/253 (100%), Gaps = 0/253 (0%)

Query	1	CTCTGGCACACATTAGTTCCTCTTATATTACATTGATATAAGCAAGTCATATGGATTTAT	60
Sbjct	1	CTCTGGCACACATTAGTTCCTCTTATATTACATTGATATAAGCAAGTCATATGGATTTAT	60
Query	61	CTGAGTGTAAGGAGAGCTGGAAAAAATAGTTTCTAGCAGGTCAGCCACCTCCCAGTGAGG	120
Sbjct	61	CTGAGTGTAAGGAGAGCTGGAAAAAATAGTTTCTAGCAGGTCAGCCACCTCCCAGTGAGG	120
Query	121	GCTGCATACCATAGAAAGGGGAGAATGAATTTTGGGAAAACAGGTAATTATCTCTGTCACA	180
Sbjct	121	GCTGCATACCATAGAAAGGGGAGAATGAATTTTGGGAAAACAGGTAATTATCTCTGTCACA	180
Query	181	GAAGGGGATGAAAAGTATGGTAGTTACNCAAGTTANACATCTGTATGGAAAATACCACTT	240
Sbjct	181	GAAGGGGATGAAAAGTATGGTAGTTACNCAAGTTANACATCTGTATGGAAAATACCACTT	240
Query	241	GGTTCTACAAATG	253
Sbjct	241	GGTTCTACAAATG	253

Sequence 663 matched with Sequence 261

Query= Sequence ID - 663
Length=627

nt: 627

SEQ ID NO: 261

nt: 627

ALIGNMENTS

Identities = 627/627 (100%), Gaps = 0/627 (0%)

Query	1	GCCTCCCGGGTTCAGGGATTTCTCCTGCCTCAGCCTCCTGAGTGGCTGCATTGCAGGCAC	60
Sbjct	1	GCCTCCCGGGTTCAGGGATTTCTCCTGCCTCAGCCTCCTGAGTGGCTGCATTGCAGGCAC	60
Query	61	CTGCCACCACGCCTTGCAAATTTTGTGTTTTAGTGGAGATGGGGTTTTGCCATGTTGG	120
Sbjct	61	CTGCCACCACGCCTTGCAAATTTTGTGTTTTAGTGGAGATGGGGTTTTGCCATGTTGG	120
Query	121	CCAGGCTGGTCTCGGACTCCTGACCTCAGGTGATCCGCCCGCCTCAGCCTCCAGAGGGC	180
Sbjct	121	CCAGGCTGGTCTCGGACTCCTGACCTCAGGTGATCCGCCCGCCTCAGCCTCCAGAGGGC	180
Query	181	TGGGATTACAGGCGTGAGCCACTGTGCCTGGCCCCAAGTTTTGCATCTTTAATGCCCTC	240
Sbjct	181	TGGGATTACAGGCGTGAGCCACTGTGCCTGGCCCCAAGTTTTGCATCTTTAATGCCCTC	240
Query	241	TGAACAAATACATAGAGAAAACCTCTCAGAACAAATTAACCTGCAGAGCAACAGTGTCTC	300
Sbjct	241	TGAACAAATACATAGAGAAAACCTCTCAGAACAAATTAACCTGCAGAGCAACAGTGTCTC	300
Query	301	CCATGTCTTAGGTTTCAAGTTTGCCTCTAAAATTCTAATCCATATTTTCTACTTCTCAG	360
Sbjct	301	CCATGTCTTAGGTTTCAAGTTTGCCTCTAAAATTCTAATCCATATTTTCTACTTCTCAG	360
Query	361	ATAATTTATGTGTGTGTACTCTTCCTAGACGTACAAGAGACTTTTTAATGCTAAATATTT	420
Sbjct	361	ATAATTTATGTGTGTGTACTCTTCCTAGACGTACAAGAGACTTTTTAATGCTAAATATTT	420
Query	421	GTCAGTGCTTAACAAAAACTCAATTTACATTACTCATattgtttttgttttaattgaat	480
Sbjct	421	GTCAGTGCTTAACAAAAACTCAATTTACATTACTCATATTGTTTTGTTTTAATTGAAT	480

PATENT SEQUENCE ALIGNMENT

Query	481	gtgaattaaatTTTTattagttatttgatttggaatggtatgtATGCCATTAACACTATT	540
Sbjct	481	GTGAATTAAATTTTTATTAGTTATTTGATTTGGAATGTTATGTATGCCATTAACACTATT	540
Query	541	AGGGGAATCTCTAGCATTCTGTATTTTAAAGAATTTGATTCTTTTGTANATTCTGCCT	600
Sbjct	541	AGGGGAATCTCTAGCATTCTGTATTTTAAAGAATTTGATTCTTTTGTANATTCTGCCT	600
Query	601	GTGTGGCATTTTAAACATGTGTGACAT	627
Sbjct	601	GTGTGGCATTTTAAACATGTGTGACAT	627

Sequence 665 matched with Sequence 262

Query= Sequence ID - 665
Length=345

nt: 345

SEQ ID NO: 262

nt: 345

ALIGNMENTS

Identities = 345/345 (100%), Gaps = 0/345 (0%)

Query	1	ACCGGCGACATGGCCAAACGTACCAAGAAAGTCGGGATCGTCGGTAAATACGGGACCCGC	60
Sbjct	1	ACCGGCGACATGGCCAAACGTACCAAGAAAGTCGGGATCGTCGGTAAATACGGGACCCGC	60
Query	61	TATGGGGCCTCCCTCCGAAAAATGGTGAAGAAAATTGAAATCAGCCAGCACGCCAAGTAC	120
Sbjct	61	TATGGGGCCTCCCTCCGAAAAATGGTGAAGAAAATTGAAATCAGCCAGCACGCCAAGTAC	120
Query	121	ACTTGCTCTTTCTGTGGCAAAACCAAGATGAAGAGACGAGCTGTGGGGATCTGGCACTGT	180
Sbjct	121	ACTTGCTCTTTCTGTGTGGCAAAACCAAGATGAAGAGACGAGCTGTGGGGATCTGGCACTGT	180
Query	181	GGTTCCTGCATGAAGACAGTGGCTGGCGGTGCCTGGACGTACAATACCACTTCCGCTGTC	240
Sbjct	181	GGTTCCTGCATGAAGACAGTGGCTGGCGGTGCCTGGACGTACAATACCACTTCCGCTGTC	240
Query	241	ACGGTAAAGTCCGCCATCAGAAGACTGAAGGAGTTGAAAGACCAGTAGACGCTCCTCTAC	300
Sbjct	241	ACGGTAAAGTCCGCCATCAGAAGACTGAAGGAGTTGAAAGACCAGTAGACGCTCCTCTAC	300
Query	301	TCTTTGAGACATCACTGGCCTATAATAAATGGGTTAATTTATGTA	345
Sbjct	301	TCTTTGAGACATCACTGGCCTATAATAAATGGGTTAATTTATGTA	345

Sequence 666 matched with Sequence 263

Query= Sequence ID - 666
Length=252

nt: 252

SEQ ID NO: 263

nt: 252

ALIGNMENTS

Identities = 252/252 (100%), Gaps = 0/252 (0%)

Query	1	ATAATTCAGAACTTCTTCATATGCTCGAGTCTCCAGAGTCACTCCGTTCTAAGGTTGATG	60
Sbjct	1	ATAATTCAGAACTTCTTCATATGCTCGAGTCTCCAGAGTCACTCCGTTCTAAGGTTGATG	60
Query	61	AAGCTGTAGCTGTACTACAAGCCCACCAAGCTAAAGAGGCTGCCAGAAAGCAGTTAACA	120
Sbjct	61	AAGCTGTAGCTGTACTACAAGCCCACCAAGCTAAAGAGGCTGCCAGAAAGCAGTTAACA	120
Query	121	GTGCCACCGGTGTTCCAAGTGTAAATTTGATCAGGGACCATGAAAAGAACTTGTGCT	180
Sbjct	121	GTGCCACCGGTGTTCCAAGTGTAAATTTGATCAGGGACCATGAAAAGAACTTGTGCT	180
Query	181	TCACCGAAGaaaaatatctaatacatcgaaaaacttaaatattatggaaaaaaaaacattgc	240
Sbjct	181	TCACCGAAGAAAAATATCTAAACATCGAAAAACTTAAATATTATGGAAAAAAAACATTGC	240
Query	241	aaaatataaaaT	252
Sbjct	241	AAAATATAAAAT	252

Sequence 669 matched with Sequence 264

Query= Sequence ID 669
Length=294

SEQ ID NO: 264

ALIGNMENTS

Identities = 294/294 (100%), Gaps = 0/294 (0%)

Query	1	TTACTTTTAACCAGNGAAATTGACCTGCCCGTGAANAGGCGGGCNTGACACAGCAAGACG	60
Sbjct	1	TTACTTTTAACCAGNGAAATTGACCTGCCCGTGAANAGGCGGGCNTGACACAGCAAGACG	60
Query	61	AGAAGACCCTATGGAGCTTTAATTTATTAATGCAAACGGTACCTAACAAACCCACAGGTC	120
Sbjct	61	AGAAGACCCTATGGAGCTTTAATTTATTAATGCAAACGGTACCTAACAAACCCACAGGTC	120
Query	121	CTAAACTACCAAACCTGCATTAAAAATTCGGTTGGGGCGACCTCGGAGCAGAACCCAAC	180
Sbjct	121	CTAAACTACCAAACCTGCATTAAAAATTCGGTTGGGGCGACCTCGGAGCAGAACCCAAC	180
Query	181	CTCCGAGCAGTACATGCTAAGACTTCACCAGTCAAAGCGAACTACTATACTCAATTGATC	240
Sbjct	181	CTCCGAGCAGTACATGCTAAGACTTCACCAGTCAAAGCGAACTACTATACTCAATTGATC	240
Query	241	CAATAACTTGACCAACGGAACAAGTTACCCTAGGGATAACAGCGCAATCCTATT	294
Sbjct	241	CAATAACTTGACCAACGGAACAAGTTACCCTAGGGATAACAGCGCAATCCTATT	294

Sequence 670 matched with Sequence 265

Query= Sequence ID 670
Length=370

SEQ ID NO: 265

ALIGNMENTS

Identities = 370/370 (100%), Gaps = 0/370 (0%)

Query	1	GGCTGATTCCTGAGCTATAAAAGCATAATTGCTTTATATTTTGGATCATTTTTTACTGGG	60
Sbjct	1	GGCTGATTCCTGAGCTATAAAAGCATAATTGCTTTATATTTTGGATCATTTTTTACTGGG	60
Query	61	GGCGGACTTggggggggTTGCATACAAAGATAACATATATATCCAACTTTCTGAAATGAA	120
Sbjct	61	GGCGGACTTGGGGGGGGTTGCATACAAAGATAACATATATATCCAACTTTCTGAAATGAA	120
Query	121	ATGTTTTTAGATTACTTTTTCAACTGTAAATAATGTACATTTAATGTCACAAGaaaaaaa	180
Sbjct	121	ATGTTTTTAGATTACTTTTTCAACTGTAAATAATGTACATTTAATGTCACAAGAAAAAAAA	180
Query	181	TGTCTTCTGCAAATTTTCTAGTATAACAGAAATTTTGTAGATGaaaaaaaTCATTATGT	240
Sbjct	181	TGTCTTCTGCAAATTTTCTAGTATAACAGAAATTTTGTAGATGAAAAAATCATTATGT	240
Query	241	TTAGAGGTCTAATGCTATGTTTTCATATTACAGAGTGAATTTGTATTTAAACAAAAATTT	300
Sbjct	241	TTAGAGGTCTAATGCTATGTTTTCATATTACAGAGTGAATTTGTATTTAAACAAAAATTT	300
Query	301	AAATTTTGGAATCCTCTAAACATTTTGTATCTTTAATTGGTTTATTATTAAATAAATCA	360
Sbjct	301	AAATTTTGGAATCCTCTAAACATTTTGTATCTTTAATTGGTTTATTATTAAATAAATCA	360
Query	361	TATAAAAATT 370	
Sbjct	361	TATAAAAATT 370	

Sequence 671 matched with Sequence 266

Query= Sequence ID 671
Length=353

SEQ ID NO: 266

ALIGNMENTS

Identities = 353/353 (100%), Gaps = 0/353 (0%)

Query	1	CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCAGGCC	60
Sbjct	1	CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCAGGCC	60
Query	61	TCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGCTCTGTCTT	120
Sbjct	61	TCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGCTCTGTCTT	120
Query	121	TAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTTACCTGAAAGAAACT	180
Sbjct	121	TAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTTACCTGAAAGAAACT	180
Query	181	ACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTATTTGAGAACCATTCTAC	240
Sbjct	181	ACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTATTTGAGAACCATTCTAC	240
Query	241	CTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACAGTACATCCACCCTAACTCTA	300
Sbjct	241	CTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACAGTACATCCACCCTAACTCTA	300
Query	301	TAAATGTTGATGGTAATACAGCATTATCTATCACCAATAACCCTTCAGCACTA	353
Sbjct	301	TAAATGTTGATGGTAATACAGCATTATCTATCACCAATAACCCTTCAGCACTA	353

Sequence 672 matched with Sequence 267

Query= Sequence ID 672

Length=433

SEQ ID NO: 267

ALIGNMENTS

Identities = 433/433 (100%), Gaps = 0/433 (0%)

Query	1	CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCAGGCC	60
Sbjct	1	CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCAGGCC	60
Query	61	TCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGCTCTGTCTT	120
Sbjct	61	TCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGCTCTGTCTT	120
Query	121	TAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTTACCTGAAAGAAACT	180
Sbjct	121	TAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTTACCTGAAAGAAACT	180
Query	181	ACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTATTTCAANAACCATTCTAC	240
Sbjct	181	ACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTATTTCAANAACCATTCTAC	240
Query	241	CTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACAGTACATCCACCCTAACTCTA	300
Sbjct	241	CTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACAGTACATCCACCCTAACTCTA	300
Query	301	TAAATGTTGATGGTAATACAGCATTATCTATCACCAATAACCCTTCAGCACTAGATCCCT	360
Sbjct	301	TAAATGTTGATGGTAATACAGCATTATCTATCACCAATAACCCTTCAGCACTAGATCCCT	360
Query	361	ATCAGTCCAATGGAAATGTTGGATTANAACCAGGCATTGTTTCAATANACTCTCGCTCTG	420
Sbjct	361	ATCAGTCCAATGGAAATGTTGGATTANAACCAGGCATTGTTTCAATANACTCTCGCTCTG	420
Query	421	TGAACACACATGG	433
Sbjct	421	TGAACACACATGG	433

Sequence 673 matched with Sequence 268

Query= Sequence ID 673
Length=683

SEQ ID NO: 268

ALIGNMENTS

Identities = 127/127 (100%), Gaps = 0/127 (0%)

Query	548	aaaaaaTTTTTNCTCCCCNCCCTTTTCTTCCTGCCGGCCCCAATTTAAGCCCNNGGCGC	607
Sbjct	548	AAAAAATTTTTNCTCCCCNCCCTTTTCTTCCTGCCGGCCCCAATTTAAGCCCNNGGCGC	607
Query	608	TTGGGGCAAATCCCCCTTTAGNgggggggTTTanaaaaaCCNGGGGCGGGNTTTAAAAC	667
Sbjct	608	TTGGGGCAAATCCCCCTTTAGNGGGGGGGTTTANAAAAACCNGGGGCGGGNTTTAAAAC	667
Query	668	CNCGGGG	674
Sbjct	668	CNCGGGG	674

Sequence 674 matched with Sequence 269

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 674
Length=49

SEQ ID NO: 269 97.6 8e-27

ALIGNMENTS

Identities = 49/49 (100%), Gaps = 0/49 (0%)

Query	1	ACCTCTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATG	49
Sbjct	1	ACCTCTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATG	49

Sequence 675 matched with Sequence 270

Query= Sequence ID - 675
Length=591

nt: 591

SEQ ID NO: 270

nt: 591

ALIGNMENTS

Identities = 591/591 (100%), Gaps = 0/591 (0%)

Query	1	GTATAGAAAATAATGTCCCCAGNGCATAGAAAAAATGAGTCTCTGGGCCAGTGAATACAA	60
Sbjct	1	GTATAGAAAATAATGTCCCCAGNGCATAGAAAAAATGAGTCTCTGGGCCAGTGAATACAA	60
Query	61	AACATCATGTCGAGAATCATTGGAAGATATACAGAGTTCGTATTTTCAGCTTTGTTTATCC	120
Sbjct	61	AACATCATGTCGAGAATCATTGGAAGATATACAGAGTTCGTATTTTCAGCTTTGTTTATCC	120
Query	121	TTCCTGTTAAGAGCCTCTGAGTTTTTAGTTTTAAAAGGATGAAAAGCTTATGCAACATGC	180
Sbjct	121	TTCCTGTTAAGAGCCTCTGAGTTTTTAGTTTTAAAAGGATGAAAAGCTTATGCAACATGC	180
Query	181	TCAGCAGGAGCTTCATCAACGATATATGTCAGATCTAAAGGTATATTTTCATTCTGTAAT	240
Sbjct	181	TCAGCAGGAGCTTCATCAACGATATATGTCAGATCTAAAGGTATATTTTCATTCTGTAAT	240
Query	241	TATGTTACATAAAAGCAATGTAAATCAGAATAAATATGTTAGACCAGAATAAAATTAATT	300
Sbjct	241	TATGTTACATAAAAGCAATGTAAATCAGAATAAATATGTTAGACCAGAATAAAATTAATT	300
Query	301	ATATTCTGGTCTTCAAAGGACACACAGAACAGATATCAGCAGAATCACTTAATACTTCAT	360
Sbjct	301	ATATTCTGGTCTTCAAAGGACACACAGAACAGATATCAGCAGAATCACTTAATACTTCAT	360
Query	361	AGAACAAAAATCACTCAAAACCTGTTTATAACCAAAGAATTCATGAAAAAGAAAGCCTTT	420
Sbjct	361	AGAACAAAAATCACTCAAAACCTGTTTATAACCAAAGAATTCATGAAAAAGAAAGCCTTT	420
Query	421	GCCATTTGTCTTAGAAAGTTATTTTTTaaaaaaaaaTCATACTTACTATTAGTATCTATG	480
Sbjct	421	GCCATTTGTCTTAGAAAGTTATTTTTTAAAAAAAAAATCATACTTACTATTAGTATCTATG	480

PATENT SEQUENCE ALIGNMENT

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Query  481  GAAGTATATGTAACAATTTTTATGTAAAGGTCATCTTTCTGTGATAGTAAAAAATATGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAAGTATATGTAACAATTTTTATGTAAAGGTCATCTTTCTGTGATAGTAAAAAATATGT  540

Query  541  CTTTACTAAGTTGAAATGAATACTTTCTGNCTTTGCTAATGGATAGTTATT  591
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CTTTACTAAGTTGAAATGAATACTTTCTGNCTTTGCTAATGGATAGTTATT  591
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Sequence 676 matched with Sequence 271

Query= Sequence ID 676

Length=329

SEQ ID NO: 271

ALIGNMENTS

Identities = 329/329 (100%), Gaps = 0/329 (0%)

Query	1	CTCAATTCTACTAAAAAGCCCCCAAGAAAAGCGAATGAGAAAACAGAGTCATCCTCTGC	60
Sbjct	1	CTCAATTCTACTAAAAAGCCCCCAAGAAAAGCGAATGAGAAAACAGAGTCATCCTCTGC	60
Query	61	ACAGCAAGTAGCAGTGTACGCCTTAGCGCTTCCAGCTCCAGCTCAGATTCCAGCTCCTC	120
Sbjct	61	ACAGCAAGTAGCAGTGTACGCCTTAGCGCTTCCAGCTCCAGCTCAGATTCCAGCTCCTC	120
Query	121	CTCTTCCTCGTCGTCGTCTTCAGACACCAGTGATTTCAGACTCAGGCTAAGGGGTCAGGCC	180
Sbjct	121	CTCTTCCTCGTCGTCGTCTTCAGACACCAGTGATTTCAGACTCAGGCTAAGGGGTCAGGCC	180
Query	181	AGATGGGGCAGGAAGGCTNCGCAGGACCGGACCCCTAGACCACCCTGCCCCACCTGCCCC	240
Sbjct	181	AGATGGGGCAGGAAGGCTNCGCAGGACCGGACCCCTAGACCACCCTGCCCCACCTGCCCC	240
Query	241	TTCCCCCTTTGCTGTGACACTTCTTCATCTCAccccccctgccccctCTAGGAGAGCT	300
Sbjct	241	TTCCCCCTTTGCTGTGACACTTCTTCATCTCACCCCCCCTGCCCCCTCTAGGAGAGCT	300
Query	301	GGCTCTGCAGTGGGGGAGGGATGCAGGGA	329
Sbjct	301	GGCTCTGCAGTGGGGGAGGGATGCAGGGA	329

Sequence 679 matched with Sequence 272

Query= Sequence ID 679
Length=688

SEQ ID NO: 272

ALIGNMENTS

Identities = 682/682 (100%), Gaps = 0/682 (0%)

Query	7	TTTCCTNTCGNAAANCGCGCCTTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACaaa	66
Sbjct	7	TTTCCTNTCGNAAANCGCGCCTTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACAAA	66
Query	67	aaaaaaaaaaaaaaaaaaaaaaaaaTNTAGACTCGANCAAGCTTATGCANGCNTGCGG	126
Sbjct	67	AAAAAAAAAAAAAAAAAAAAAAAAAANTNTAGACTCGANCAAGCTTATGCANGCNTGCGG	126
Query	127	CCGCAATTCGAGCTCGGCCGACTTGGCCAATTCGCCCTATAGNGAGTCGTATTACAATTC	186
Sbjct	127	CCGCAATTCGAGCTCGGCCGACTTGGCCAATTCGCCCTATAGNGAGTCGTATTACAATTC	186
Query	187	ACTGGCCGTCGTTTTACAACGTCGNGACTGGGAAAACCCTGGCGTTACCCA ACTTAATCG	246
Sbjct	187	ACTGGCCGTCGTTTTACAACGTCGNGACTGGGAAAACCCTGGCGTTACCCA ACTTAATCG	246
Query	247	CCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATANCGAANAGGCCCGCACC GATCG	306
Sbjct	247	CCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATANCGAANAGGCCCGCACC GATCG	306
Query	307	CCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAANGGAAATTGTAAGCGTTAATATTTTG	366
Sbjct	307	CCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAANGGAAATTGTAAGCGTTAATATTTTG	366
Query	367	TTAAAATTCGCGTTAAATTTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATC	426
Sbjct	367	TTAAAATTCGCGTTAAATTTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATC	426
Query	427	GGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGNGTTGTTCCAGTT	486
Sbjct	427	GGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGNGTTGTTCCAGTT	486

PATENT SEQUENCE ALIGNMENT

Query	487	TGGAACAANAGTCCACTNTTAAAGAACGNGGACTCCAACGTCAAAGGGCGAAAAACCGTC	546
Sbjct	487	TGGAACAANAGTCCACTNTTAAAGAACGNGGACTCCAACGTCAAAGGGCGAAAAACCGTC	546
Query	547	TATCAGGGCGATGGCCCACTACGTGAACCATCNCCTAATCAAGTTTTTTGGGGTCGAGG	606
Sbjct	547	TATCAGGGCGATGGCCCACTACGTGAACCATCNCCTAATCAAGTTTTTTGGGGTCGAGG	606
Query	607	NGCCGTAAAGCACTAAATCGGAACCTAAAGGGAGCCCCGATTTAAAGCTTGACGGGGA	666
Sbjct	607	NGCCGTAAAGCACTAAATCGGAACCTAAAGGGAGCCCCGATTTAAAGCTTGACGGGGA	666
Query	667	AAGCCCGGCGAACGTGGCGAAA	688
Sbjct	667	AAGCCCGGCGAACGTGGCGAAA	688

Sequence 682 matched with Sequence 273

Query= Sequence ID 682

Length=271

SEQ ID NO: 273

ALIGNMENTS

Identities = 271/271 (100%), Gaps = 0/271 (0%)

Query	1	CACCTGCAGTCCAAGTACATCGGCACGGGCCACGCCGACACCACCAAGTGGGAGTGGCTG	60
Sbjct	1	CACCTGCAGTCCAAGTACATCGGCACGGGCCACGCCGACACCACCAAGTGGGAGTGGCTG	60
Query	61	GTGAACCAACACCGCGACTCGTACTGCTCCTACATGGGCCACTTCGACCTTCTCAACTAC	120
Sbjct	61	GTGAACCAACACCGCGACTCGTACTGCTCCTACATGGGCCACTTCGACCTTCTCAACTAC	120
Query	121	TTCGCCATTGCGGAGAATGAGAGCAAAGCGCGAGTCCGCTTCAACTTGATGGAAAAGATG	180
Sbjct	121	TTCGCCATTGCGGAGAATGAGAGCAAAGCGCGAGTCCGCTTCAACTTGATGGAAAAGATG	180
Query	181	CTTCAGCCTTGTGGACCGCCAGCCGACAAGCCCGAGGAAAAC TGAACTTTGCTTAACNA	240
Sbjct	181	CTTCAGCCTTGTGGACCGCCAGCCGACAAGCCCGAGGAAAAC TGAACTTTGCTTAACNA	240
Query	241	CCGAATGGNGGGGANCTTTTCCAACGNTTTT	271
Sbjct	241	CCGAATGGNGGGGANCTTTTCCAACGNTTTT	271

Sequence 683 matched with Sequence 274

Query= Sequence ID 683
Length=213

SEQ ID NO: 274

ALIGNMENTS

Identities = 213/213 (100%), Gaps = 0/213 (0%)

Query	1	TTGGTTTCATACTGNTGGGGNTTGAATGNTCCCTNCAACACTNATGTTGANACTTAATCC	60
Sbjct	1	TTGGTTTCATACTGNTGGGGNTTGAATGNTCCCTNCAACACTNATGTTGANACTTAATCC	60
Query	61	CTAATGNGGCAATACTGAAAGGTGGGGCCTTTGAGATGTGATTGGATCGTAAGGCTGTGC	120
Sbjct	61	CTAATGNGGCAATACTGAAAGGTGGGGCCTTTGAGATGTGATTGGATCGTAAGGCTGTGC	120
Query	121	CTTCATTCATGGGTTAATGGATTAATGGGTTATCACAGGAATGGGACTGGTGGCTTTATA	180
Sbjct	121	CTTCATTCATGGGTTAATGGATTAATGGGTTATCACAGGAATGGGACTGGTGGCTTTATA	180
Query	181	AGAAGAGGAAAAGAGAACTGAGCTTGCATGCCC	213
Sbjct	181	AGAAGAGGAAAAGAGAACTGAGCTTGCATGCCC	213

Sequence 684 matched with Sequence 275

Query= Sequence ID - 684
Length=545

nt: 545

SEQ ID NO: 275

nt: 545

ALIGNMENTS

Identities = 545/545 (100%), Gaps = 0/545 (0%)

Query	1	GTGGAAGNGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGATGCC	60
Sbjct	1	GTGGAAGNGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGATGCC	60
Query	61	CANGGAAGACAGGGCGACCTGGAAGTCCAACCTACTTCCTTAAGATCATCCAACCTATTGGA	120
Sbjct	61	CANGGAAGACAGGGCGACCTGGAAGTCCAACCTACTTCCTTAAGATCATCCAACCTATTGGA	120
Query	121	TGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCA	180
Sbjct	121	TGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCA	180
Query	181	GATCCGCATGTCCCTTCNCGGGAAGGCTGTGGTGCTGATGGGCAAGAACACCATGATGCG	240
Sbjct	181	GATCCGCATGTCCCTTCNCGGGAAGGCTGTGGTGCTGATGGGCAAGAACACCATGATGCG	240
Query	241	CAAGGCCATCCGAGGGCACCTGGAAAAACAACCCAGCTCTGGAGAAACTGCTGCCTCATAT	300
Sbjct	241	CAAGGCCATCCGAGGGCACCTGGAAAAACAACCCAGCTCTGGAGAAACTGCTGCCTCATAT	300
Query	301	CCGGGGGAATGTGGGCTTTGTGTTACCAAGGAGGACCTCACTGANATCAGGGACATGTT	360
Sbjct	301	CCGGGGGAATGTGGGCTTTGTGTTACCAAGGAGGACCTCACTGANATCAGGGACATGTT	360
Query	361	GCTGGCCAATAAGGTGCCAGCTGCTGCCCCTGCTGGTGCCATTGCCCCATGTGAAGTCAC	420
Sbjct	361	GCTGGCCAATAAGGTGCCAGCTGCTGCCCCTGCTGGTGCCATTGCCCCATGTGAAGTCAC	420
Query	421	TGTGCCAGCCCAGAACACTGGTCTCGGGCCCGATAAGACCTCCTTTTTCCAGGCTTTAGG	480
Sbjct	421	TGTGCCAGCCCAGAACACTGGTCTCGGGCCCGATAAGACCTCCTTTTTCCAGGCTTTAGG	480

PATENT SEQUENCE ALIGNMENT

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Query  481  TATCACCCTAAAATCTCCAGGGGCACCATTGAAATCCTGAGTGATGTGCACTGATCAAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TATCACCCTAAAATCTCCAGGGGCACCATTGAAATCCTGAGTGATGTGCACTGATCAAG  540

Query  541  ACTGG  545
          ||||
Sbjct  541  ACTGG  545
```

Sequence 685 matched with Sequence 276

Query= Sequence ID 685

Length=260

SEQ ID NO: 276

ALIGNMENTS

Identities = 260/260 (100%), Gaps = 0/260 (0%)

Query	1	GGAAAGGGCCATTTTATTGCCTAAAACACCTGGNTTTTNAGGTAACAGTTCCAACATGT	60
Sbjct	1	GGAAAGGGCCATTTTATTGCCTAAAACACCTGGNTTTTNAGGTAACAGTTCCAACATGT	60
Query	61	CCTTTTTTGAATAGCTGTTCTAATTATTATATATTCAGCTGATTAATAGGAGTACTTGAT	120
Sbjct	61	CCTTTTTTGAATAGCTGTTCTAATTATTATATATTCAGCTGATTAATAGGAGTACTTGAT	120
Query	121	AGGTGGACTGTGTCAGGTAGCCTCAGGCAATCCTACTTCAACAAGCTGTCAGGGAGCCAT	180
Sbjct	121	AGGTGGACTGTGTCAGGTAGCCTCAGGCAATCCTACTTCAACAAGCTGTCAGGGAGCCAT	180
Query	181	GCCATGCTTCTTTATGACATAGGTGAATTTGATAGGCTCACTAGCAGAACATGGGATCAC	240
Sbjct	181	GCCATGCTTCTTTATGACATAGGTGAATTTGATAGGCTCACTAGCAGAACATGGGATCAC	240
Query	241	AAGGTGGAACCNTTCCNTTT	260
Sbjct	241	AAGGTGGAACCNTTCCNTTT	260

Sequence 686 matched with Sequence 277

Query= Sequence ID 686
Length=603

SEQ ID NO: 277

ALIGNMENTS

Identities = 28/28 (100%), Gaps = 0/28 (0%)

Query	40	GACCCCTTCCTTACACCTTATACAAAAA	67
Sbjct	1	GACCCCTTCCTTACACCTTATACAAAAA	28

Sequence 687 matched with Sequence 278

Query= Sequence ID - 687
Length=268

nt: 268

SEQ ID NO: 278

nt: 268

ALIGNMENTS

Identities = 268/268 (100%), Gaps = 0/268 (0%)

Query	1	TTTATGTGTTTTTGCTTGGGGGGCGCTGGGCCTAGCCCAGAGTAGTGCTTGCTCCCCCTG	60
Sbjct	1	TTTATGTGTTTTTGCTTGGGGGGCGCTGGGCCTAGCCCAGAGTAGTGCTTGCTCCCCCTG	60
Query	61	CCTTGTTCCCAACCAGGGAGGCAGCAGACTCAGGCCCTCCATGGTCCTCTTTGTCATTTTGT	120
Sbjct	61	CCTTGTTCCCAACCAGGGAGGCAGCAGACTCAGGCCCTCCATGGTCCTCTTTGTCATTTTGT	120
Query	121	TGACATGCATTCCTCCTTTTGTTCATCTTGTTGGGGGGAGGGGATTAACCAAAGGCCACCC	180
Sbjct	121	TGACATGCATTCCTCCTTTTGTTCATCTTGTTGGGGGGAGGGGATTAACCAAAGGCCACCC	180
Query	181	TGACTTTGTTTTTGTGGACACACAATAAAAAGCCCCGTTTATTTGTaaaaaaaaaaaaaaaaa	240
Sbjct	181	TGACTTTGTTTTTGTGGACACACAATAAAAAGCCCCGTTTATTTGTAAAAAAAAAAAAAAAAA	240
Query	241	aaaaaaaaaaaaaaaaaaaaaaaaaaaaa	268
Sbjct	241	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	268

Sequence 688 matched with Sequence 279

Query= Sequence ID - 688
Length=569

nt: 569

SEQ ID NO: 279

nt: 569

ALIGNMENTS

Identities = 569/569 (100%), Gaps = 0/569 (0%)

Query	1	CTTTAGCCAGCCTGATCAGaaaaaaCAAAAGAAGAGGAAAGACGTAGATTACCAACATC	60
Sbjct	1	CTTTAGCCAGCCTGATCAGAAAAAAACAAAAGAAGAGGAAAGACGTAGATTACCAACATC	60
Query	61	AAGAATGTGAGTTATGATATCACTACAGACTCTCCAGGTATTTAAAAGCATAATTAGAGAA	120
Sbjct	61	AAGAATGTGAGTTATGATATCACTACAGACTCTCCAGGTATTTAAAAGCATAATTAGAGAA	120
Query	121	TGATATGAGCAGCTATATGCAAATAAGTTCAACATTGGACAAATGGACAAATTTCTTGAA	180
Sbjct	121	TGATATGAGCAGCTATATGCAAATAAGTTCAACATTGGACAAATGGACAAATTTCTTGAA	180
Query	181	AGATAAATTATGAAATTTTCATTCTGAAAGAACTACATGACCTTAATTGTCTTACATCTAT	240
Sbjct	181	AGATAAATTATGAAATTTTCATTCTGAAAGAACTACATGACCTTAATTGTCTTACATCTAT	240
Query	241	TAAATAAGTGGAAATTGTAGTTTAGAAACTTTCCCACAAAGAAAACTCTAGGCCCAGATG	300
Sbjct	241	TAAATAAGTGGAAATTGTAGTTTAGAAACTTTCCCACAAAGAAAACTCTAGGCCCAGATG	300
Query	301	GCATCAAAAATAATATTCAGATGAATGAAATGGAGAAAGGATAGCCTTTTCAACAAATGGT	360
Sbjct	301	GCATCAAAAATAATATTCAGATGAATGAAATGGAGAAAGGATAGCCTTTTCAACAAATGGT	360
Query	361	GGTGAACAATTGGATTTCCATATGCaaaaaaTAGAGATGGACGCAGAGGTGTGTGCTT	420
Sbjct	361	GGTGAACAATTGGATTTCCATATGCAAAAAAATAGAGATGGACGCAGAGGTGTGTGCTT	420
Query	421	AGGAGGCTGAGGTGAGAGGATTGTTTGAGGCCAGCCTGGGCAACATAGCAAGACCCATT	480
Sbjct	421	AGGAGGCTGAGGTGAGAGGATTGTTTGAGGCCAGCCTGGGCAACATAGCAAGACCCATT	480

PATENT SEQUENCE ALIGNMENT

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Query  481  TCAAAAACAAAAATAAAGAACTTGTAGCCTTACCTTGTGCCATATTATGAAAATGTATCA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TCAAAAACAAAAATAAAGAACTTGTAGCCTTACCTTGTGCCATATTATGAAAATGTATCA  540

Query  541  TAGGCTTAAATGTGAAACGTAAAACAAAA  569
          ||||||||||||||||||||||||
Sbjct  541  TAGGCTTAAATGTGAAACGTAAAACAAAA  569
```

Sequence 689 matched with Sequence 280

Query= Sequence ID 689

Length=492

SEQ ID NO: 280

ALIGNMENTS

Identities = 492/492 (100%), Gaps = 0/492 (0%)

Query	1	CGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGttttttt	60
Sbjct	1	CGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTTTTT	60
Query	61	CTCTTTGAAAGATAGAGATTAATACAACACTTTAAAAATATAGTCAATAGGTTACTAAG	120
Sbjct	61	CTCTTTGAAAGATAGAGATTAATACAACACTTTAAAAATATAGTCAATAGGTTACTAAG	120
Query	121	ATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAAT	180
Sbjct	121	ATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAAT	180
Query	181	ATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAAGGTTTCTAAAACATGACG	240
Sbjct	181	ATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAAGGTTTCTAAAACATGACG	240
Query	241	GAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAATGTATTTAAAAGAAAATTGAGAGAA	300
Sbjct	241	GAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAATGTATTTAAAAGAAAATTGAGAGAA	300
Query	301	AGGACTACAGAGCCCCGAATTAATACTAATAGAAAGGCAATGCTTTTAGATTAAAATGAA	360
Sbjct	301	AGGACTACAGAGCCCCGAATTAATACTAATAGAAAGGCAATGCTTTTAGATTAAAATGAA	360
Query	361	GGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTGAAG	420
Sbjct	361	GGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTGAAG	420
Query	421	GCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGACGC	480
Sbjct	421	GCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGACGC	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGGGAGAATTGC	492
Sbjct	481	AGGGAGAATTGC	492

Sequence 690 matched with Sequence 281

Query= Sequence ID 690

Length=355

SEQ ID NO: 281

ALIGNMENTS

Identities = 355/355 (100%), Gaps = 0/355 (0%)

Query	1	CGAAAAGCAAATATAACTTGCCACTAACCAAGATCACCTCTGCAAAAAGAAATGAAAACA	60
Sbjct	1	CGAAAAGCAAATATAACTTGCCACTAACCAAGATCACCTCTGCAAAAAGAAATGAAAACA	60
Query	61	ACTTTTGGCAGGATTCTGTTTCATCTGACAGAATTCAGAAGCAGGaaaaaaGCCTTTTA	120
Sbjct	61	ACTTTTGGCAGGATTCTGTTTCATCTGACAGAATTCAGAAGCAGGAAAAAAGCCTTTTA	120
Query	121	AAAATACCGAGAACATTAAAAATTCGCATTTGAAGAAATCAGCATTTCTAACTGAAGTGA	180
Sbjct	121	AAAATACCGAGAACATTAAAAATTCGCATTTGAAGAAATCAGCATTTCTAACTGAAGTGA	180
Query	181	GCCAAAAGGAAAATTATGCTGGGGCAAAGTTTAGTGATCCACCTTCTCCTAGTGTTCTTC	240
Sbjct	181	GCCAAAAGGAAAATTATGCTGGGGCAAAGTTTAGTGATCCACCTTCTCCTAGTGTTCTTC	240
Query	241	CAAAGCCTCCTAGTCACTGGATGGGAAGCACTGTTGAAAATTCCAACCAAAACAGGGAGC	300
Sbjct	241	CAAAGCCTCCTAGTCACTGGATGGGAAGCACTGTTGAAAATTCCAACCAAAACAGGGAGC	300
Query	301	TGATGGCAGTACACTTAAAAACGCTCCTCAAAGTTCAAACCTTAGATTTTCAGATTT	355
Sbjct	301	TGATGGCAGTACACTTAAAAACGCTCCTCAAAGTTCAAACCTTAGATTTTCAGATTT	355

Sequence 691 matched with Sequence 282

Query= Sequence ID 691

Length=619

SEQ ID NO: 282

ALIGNMENTS

Identities = 619/619 (100%), Gaps = 0/619 (0%)

Query	1	CCGGTCTCTACACAATATATAGAAATCTGGGCATGGTGGTGCCTGGCTGTAGTCTCAGCT	60
Sbjct	1	CCGGTCTCTACACAATATATAGAAATCTGGGCATGGTGGTGCCTGGCTGTAGTCTCAGCT	60
Query	61	ACCTAGTTGGGTGAGGTGGGAGAGTCGCTTGAGTCCTGGAGGTTGAGGCTGTAGTGAGCC	120
Sbjct	61	ACCTAGTTGGGTGAGGTGGGAGAGTCGCTTGAGTCCTGGAGGTTGAGGCTGTAGTGAGCC	120
Query	121	AGGGCTGCACCACTGCATTCCAGCCTGGGTAACAGAGTGAGACCCTGTCTCaaaaagaaa	180
Sbjct	121	AGGGCTGCACCACTGCATTCCAGCCTGGGTAACAGAGTGAGACCCTGTCTCAAAAAGAAA	180
Query	181	aaaaaaaaTTGCTAATTTTAAACAAATCACAAAACCTGACTCAGGCAAGTTGTCTGACTCAA	240
Sbjct	181	AAAAAAAAATTGCTAATTTTAAACAAATCACAAAACCTGACTCAGGCAAGTTGTCTGACTCAA	240
Query	241	AAGCCCTTGAAAAACCATCAAAGACAGTAGAATGTAACTGGTCATTTACGTAAAATAGT	300
Sbjct	241	AAGCCCTTGAAAAACCATCAAAGACAGTAGAATGTAACTGGTCATTTACGTAAAATAGT	300
Query	301	GTTTCATTAAATTTTTGGTTTCATTTAGGATAATCATTTTAAATGAGACTGTATTTGAGACT	360
Sbjct	301	GTTTCATTAAATTTTTGGTTTCATTTAGGATAATCATTTTAAATGAGACTGTATTTGAGACT	360
Query	361	GtatacacatacatatacatggtttacacacatacatagtaaatatatgtacatTCTATCT	420
Sbjct	361	GTATACACATACATATACATGTTTACACACATATACGTACAATATATGTACATTCTATCT	420
Query	421	AAAAGATCATACATGTGTGTACATATATGTTTTTAAAAGTCAAACCTGACATATTAATGGA	480
Sbjct	421	AAAAGATCATACATGTGTGTACATATATGTTTTTAAAAGTCAAACCTGACATATTAATGGA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AACAGTGCTTACATCTCTGGTAGTGATTTTCTATTAGCAGCAGCCCTACATATGCTGCGT	540
Sbjct	481	AACAGTGCTTACATCTCTGGTAGTGATTTTCTATTAGCAGCAGCCCTACATATGCTGCGT	540
Query	541	CTCTGAACAGCATGTCAGTGCCATGACTGTCTAAACATGCAAATATGACTGACAGACTCT	600
Sbjct	541	CTCTGAACAGCATGTCAGTGCCATGACTGTCTAAACATGCAAATATGACTGACAGACTCT	600
Query	601	TGAGACAGCTTTCACCTTG	619
Sbjct	601	TGAGACAGCTTTCACCTTG	619

Sequence 692 matched with Sequence 283

Query= Sequence ID 692

Length=328

SEQ ID NO: 283

ALIGNMENTS

Identities = 328/328 (100%), Gaps = 0/328 (0%)

Query	1	AATTCGNGGCCGCGTCNNCCTANGAGGCACCAGGAAATCCCGCGGGGTGGCCCATGCAGA	60
Sbjct	1	AATTCGNGGCCGCGTCNNCCTANGAGGCACCAGGAAATCCCGCGGGGTGGCCCATGCAGA	60
Query	61	CCAGGCGCACGTGGCTCATGGGGCANAATTGCCAAGGACAGCTCACGACAGTGCCACCTT	120
Sbjct	61	CCAGGCGCACGTGGCTCATGGGGCANAATTGCCAAGGACAGCTCACGACAGTGCCACCTT	120
Query	121	CTCACCATTCCAGCCAAGGAGAGATGTGACGTTGGAAGTCTCTGGCACTTCTGTCAAGC	180
Sbjct	121	CTCACCATTCCAGCCAAGGAGAGATGTGACGTTGGAAGTCTCTGGCACTTCTGTCAAGC	180
Query	181	CTCCCCGCCCCAATTGCCTTGAGATCTCTGCTCTTTGTCAGAGATTGCAAAGACTCAC	240
Sbjct	181	CTCCCCGCCCCAATTGCCTTGAGATCTCTGCTCTTTGTCAGAGATTGCAAAGACTCAC	240
Query	241	GTTTTTGTGTTTTCTCATCATTCCATTGTGATACTAAGAACTAAGAAGCTTAATGAAA	300
Sbjct	241	GTTTTTGTGTTTTCTCATCATTCCATTGTGATACTAAGAACTAAGAAGCTTAATGAAA	300
Query	301	AGAAATAAAATGCCTATGTTGTTGTTCT	328
Sbjct	301	AGAAATAAAATGCCTATGTTGTTGTTCT	328

Sequence 693 matched with Sequence 284

Query= Sequence ID 693

Length=563

SEQ ID NO: 284

ALIGNMENTS

Identities = 563/563 (100%), Gaps = 0/563 (0%)

Query	1	CTAGAACCCATGACTCCTAGGTCTTATACTGCAACCACAGTATCAGCAAATAATCTTTCA	60
Sbjct	1	CTAGAACCCATGACTCCTAGGTCTTATACTGCAACCACAGTATCAGCAAATAATCTTTCA	60
Query	61	TAAGGGGATTATTCTCTGATTAACAGGAAATACAGGAATTTAATTTGTGAACACGCTAGG	120
Sbjct	61	TAAGGGGATTATTCTCTGATTAACAGGAAATACAGGAATTTAATTTGTGAACACGCTAGG	120
Query	121	TAGAAGCAGAAACCCAAATCCAAATCCAAATTTAAACATTTAAATTCATTCTATAACTA	180
Sbjct	121	TAGAAGCAGAAACCCAAATCCAAATCCAAATTTAAACATTTAAATTCATTCTATAACTA	180
Query	181	AGATCTAACAGTCATTTTCTTCCCAGTAAGAAATAACCAAAGCATGCTAAAAATCACTGG	240
Sbjct	181	AGATCTAACAGTCATTTTCTTCCCAGTAAGAAATAACCAAAGCATGCTAAAAATCACTGG	240
Query	241	ACTAAATTGGTGTCAAAACTGCCACATTGCCAGGCATgggggggTCATACTTGTAATCCC	300
Sbjct	241	ACTAAATTGGTGTCAAAACTGCCACATTGCCAGGCATGGGGGGGTCATACTTGTAATCCC	300
Query	301	AGCACTTTGGGAGGCCGAGGTGGGAAAATTGCTTGAGGCCAGGAGTTCGAAACCAGCCTG	360
Sbjct	301	AGCACTTTGGGAGGCCGAGGTGGGAAAATTGCTTGAGGCCAGGAGTTCGAAACCAGCCTG	360
Query	361	GGCAACACAGTGAGACCCCATCTCCACaaaaaaaaaattaaaaacaaaacaaaaCAT	420
Sbjct	361	GGCAACACAGTGAGACCCCATCTCCACAAAAAAAAAAAAATTAAAAACAAAACAAAACAT	420
Query	421	TAGCTGGGCATGGTGGTACACGCCTGTAGTCCCAGCTACTCAGGAGCCTGAAGTGAGAGG	480
Sbjct	421	TAGCTGGGCATGGTGGTACACGCCTGTAGTCCCAGCTACTCAGGAGCCTGAAGTGAGAGG	480

PATENT SEQUENCE ALIGNMENT

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Query  481  ATCACTGAAGCCCAGGAGGTAGAGCTATGACTGTAGTGAGCTATGACTGTGCCACTACAC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATCACTGAAGCCCAGGAGGTAGAGCTATGACTGTAGTGAGCTATGACTGTGCCACTACAC  540

Query  541  TCCACCTGGGTGACAGGGGACTC  563
          ||||||||||||||||
Sbjct  541  TCCACCTGGGTGACAGGGGACTC  563
```

Sequence 694 matched with Sequence 285

Query= Sequence ID 694
Length=257

SEQ ID NO: 285

ALIGNMENTS

Identities = 257/257 (100%), Gaps = 0/257 (0%)

Query	1	CGACTTCCATTTGTATTAATGGAATACTAAGTCCCTCTGTGATTTCTGAACCAAGCTATT	60
Sbjct	1	CGACTTCCATTTGTATTAATGGAATACTAAGTCCCTCTGTGATTTCTGAACCAAGCTATT	60
Query	61	CCTAGGCCTGAGTTTTATTTTGTGACACAGAAATAAATTANAAGGCCAAGCGTGGTGGC	120
Sbjct	61	CCTAGGCCTGAGTTTTATTTTGTGACACAGAAATAAATTANAAGGCCAAGCGTGGTGGC	120
Query	121	ATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCAGGAGTTCAAGGC	180
Sbjct	121	ATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCAGGAGTTCAAGGC	180
Query	181	TGCAGCAAGCTTTGATTGCGCCACTGCACTCCAGCCTTGGCGACAGACTAAGACGCTGTC	240
Sbjct	181	TGCAGCAAGCTTTGATTGCGCCACTGCACTCCAGCCTTGGCGACAGACTAAGACGCTGTC	240
Query	241	TCaaaaaaaaacaaaaa	257
Sbjct	241	TCAAAAAAAAAACAAAAA	257

Sequence 696 matched with Sequence 286

Query= Sequence ID 696

Length=602

SEQ ID NO: 286

ALIGNMENTS

Identities = 602/602 (100%), Gaps = 0/602 (0%)

Query	1	GGTTATCAATGAGATTAAGAGACAACTAGAGTaaaaacaaaagaaaagaaaangaa	60
Sbjct	1	GGTTATCAATGAGATTAAGAGACAACTAGAGTAAAAACAAAAGAAAAGAAAANGAA	60
Query	61	aaCAACAGAAGCTCTATTAAGTACCTCTAACCAATACAACAGGTAACTGATGTTCTCC	120
Sbjct	61	AACAACAGAAGCTCTATTAAGTACCTCTAACCAATACAACAGGTAACTGATGTTCTCC	120
Query	121	ATTCTGTATATAAAAAATCCCAGTGGACACCCACAACACAGGCTTCAGGCTTGTAGGACAC	180
Sbjct	121	ATTCTGTATATAAAAAATCCCAGTGGACACCCACAACACAGGCTTCAGGCTTGTAGGACAC	180
Query	181	TTTCTAGTTCATCTGAGCACTTTTGTCTCAGCAGTTGAGCTGTATACTTAGCAACATTT	240
Sbjct	181	TTTCTAGTTCATCTGAGCACTTTTGTCTCAGCAGTTGAGCTGTATACTTAGCAACATTT	240
Query	241	GGTGCTTCCAAACCCATTTGTGCCTGTAGCACTTACTATTGAAATACATAATTTAATTAA	300
Sbjct	241	GGTGCTTCCAAACCCATTTGTGCCTGTAGCACTTACTATTGAAATACATAATTTAATTAA	300
Query	301	ATATTATATAAAGGAATGGAATACGAGTTGGACAAGAAAAAGAGTTAAATCTGAAGGTTA	360
Sbjct	301	ATATTATATAAAGGAATGGAATACGAGTTGGACAAGAAAAAGAGTTAAATCTGAAGGTTA	360
Query	361	GGTAAAAAGAGCAACTTCTTTTCTCTGTTTTGCAGGTTGGCAAAATCATTTAAAAACAAT	420
Sbjct	361	GGTAAAAAGAGCAACTTCTTTTCTCTGTTTTGCAGGTTGGCAAAATCATTTAAAAACAAT	420
Query	421	TGGAAGTATTATATGTTCTGCATTAAGTTGTCATTTTACTTAAAAACTAGGCATCAAAGA	480
Sbjct	421	TGGAAGTATTATATGTTCTGCATTAAGTTGTCATTTTACTTAAAAACTAGGCATCAAAGA	480

Query	481	TGATGCATAATAAAATTTAGTGTATGCAAGAATGACTGCTTGGGACCTCAATATATGAATT	540
Sbjct	481	TGATGCATAATAAAATTTAGTGTATGCAAGAATGACTGCTTGGGACCTCAATATATGAATT	540
Query	541	CTTAATCCAAGGAAAGTCCTTGGCCTTACATTTAAAAGTCGGCAAATAAGTGTACGTTCA	600
Sbjct	541	CTTAATCCAAGGAAAGTCCTTGGCCTTACATTTAAAAGTCGGCAAATAAGTGTACGTTCA	600
Query	601	TT	602
Sbjct	601	TT	602

Sequence 697 matched with Sequence 287

Query= Sequence ID 697

Length=306

SEQ ID NO: 287

ALIGNMENTS

Identities = 306/306 (100%), Gaps = 0/306 (0%)

Query	1	GAACATTTAAAAATAATGCAAATAAGGCTGGGCGTGGGGGCTCACACCTGTAATCCCAGC	60
Sbjct	1	GAACATTTAAAAATAATGCAAATAAGGCTGGGCGTGGGGGCTCACACCTGTAATCCCAGC	60
Query	61	ACTTTGGGAGGCCGAGGCAGGCAGATCACGAGGTCAGGAGATTGAGACCATCCTGGCTAA	120
Sbjct	61	ACTTTGGGAGGCCGAGGCAGGCAGATCACGAGGTCAGGAGATTGAGACCATCCTGGCTAA	120
Query	121	CACAGTGAAACCCTGTCTCTACTTaaaaataaaaaaTTAGCCAGGCGTGGTGGTGGGC	180
Sbjct	121	CACAGTGAAACCCTGTCTCTACTTAAAAAATAAAAAAATTAGCCAGGCGTGGTGGTGGGC	180
Query	181	GCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGGCG	240
Sbjct	181	GCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGGCG	240
Query	241	GAGCTTGCANTGAGCTGAGATCGTGCCACTGCACTCCAGCCTGAGCGACAGAGCGAGACT	300
Sbjct	241	GAGCTTGCANTGAGCTGAGATCGTGCCACTGCACTCCAGCCTGAGCGACAGAGCGAGACT	300
Query	301	CTGTCT 306	
Sbjct	301	CTGTCT 306	

Sequence 698 matched with Sequence 288

Query= Sequence ID 698
Length=419

SEQ ID NO: 288

ALIGNMENTS

Identities = 419/419 (100%), Gaps = 0/419 (0%)

Query	1	TCATTAGAATCCAAGCTTTGAAAATTTCTGATTAATGCTCATGTATTCTTTATCTTTGT	60
Sbjct	1	TCATTAGAATCCAAGCTTTGAAAATTTCTGATTAATGCTCATGTATTCTTTATCTTTGT	60
Query	61	TTTTCCTTGTGAAGAAAGACTTTACCACTGTCTGAGTGATGATGCTGTTGATAAGGATG	120
Sbjct	61	TTTTCCTTGTGAAGAAAGACTTTACCACTGTCTGAGTGATGATGCTGTTGATAAGGATG	120
Query	121	ATGTCGATGACTACTATATTGCATCTCTCAGGAACAGCTGATGGGAAGGGAGGGGCTGCT	180
Sbjct	121	ATGTCGATGACTACTATATTGCATCTCTCAGGAACAGCTGATGGGAAGGGAGGGGCTGCT	180
Query	181	GAGTTCCTTGTTCCTAGCTAGCAGCACGCTCCTCANAGAGGGGGCCGAGTTACAGACAGC	240
Sbjct	181	GAGTTCCTTGTTCCTAGCTAGCAGCACGCTCCTCANAGAGGGGGCCGAGTTACAGACAGC	240
Query	241	AGCCGCATTCTCATGCAAAATTAGTTTTAAACTGCTAGTGTGGGCATCGGTACCTTTTGC	300
Sbjct	241	AGCCGCATTCTCATGCAAAATTAGTTTTAAACTGCTAGTGTGGGCATCGGTACCTTTTGC	300
Query	301	CTGGGTGATACCGAAGAATTGTTGAGGATTTAGTATGCTCCGTAGAGACAGTTCAGCCAG	360
Sbjct	301	CTGGGTGATACCGAAGAATTGTTGAGGATTTAGTATGCTCCGTAGAGACAGTTCAGCCAG	360
Query	361	TCATTTCTGCATTGGAGAGACTTCTCATACTTTCTTTGAAGACTCATAGAAAGCTGGAT	419
Sbjct	361	TCATTTCTGCATTGGAGAGACTTCTCATACTTTCTTTGAAGACTCATAGAAAGCTGGAT	419

Sequence 699 matched with Sequence 289

Query= Sequence ID 699

Length=626

SEQ ID NO: 289

ALIGNMENTS

Identities = 626/626 (100%), Gaps = 0/626 (0%)

Query	1	ATTAAGGTTTGTNCCCAACAAGAATAGATGTAATTAGaaaaanTGNCTTCCTTACCTAT	60
Sbjct	1	ATTAAGGTTTGTNCCCAACAAGAATAGATGTAATTAGAAAAAANTGNCTTCCTTACCTAT	60
Query	61	TGCCTCTGATNTTTACTTGCTTAAAttttttttATTGNAAATCCAGAAAAAGNGGATTTA	120
Sbjct	61	TGCCTCTGATNTTTACTTGCTTAAATTTTTTTTATTGNAAATCCAGAAAAAGNGGATTTA	120
Query	121	GAGAACAACACTAACTCCACCTAATCTATGACAganatgtacaananagtacctgtgaa	180
Sbjct	121	GAGAACAACACTAACTCCACCTAATCTATGACAGANATGTACAANANAGTACCTGTGAA	180
Query	181	aaatgtgaaagnatntgaaaaatgtAACCTTTGGCAGCCTGAGCATAGTCAACCAGAAAA	240
Sbjct	181	AAATGTGAAAGNATNTGAAAAATGTAACTTTGGCAGCCTGAGCATAGTCAACCAGAAAA	240
Query	241	ACTATCTGAATTAAATAATTGGTCCATAGGTACTATTTTATTTGGTCCATAAGGATTAt	300
Sbjct	241	ACTATCTGAATTAAATAATTGGTCCATAGGTACTATTTTATTTGGTCCATAAGGATTAT	300
Query	301	tttttcaacttttttttCAAGTGTATTATTATGTCATTTCCACGTAGGTTACTGATACC	360
Sbjct	301	TTTTTCAACTTTTTTTTCAAGTGTATTATTATGTCATTTCCACGTAGGTTACTGATACC	360
Query	361	TGAAGACTTTTNCACCTTTAACCTTNCTCGTTGAGGAGCTTTGTANTCTAATAAAAGAG	420
Sbjct	361	TGAAGACTTTTNCACCTTTAACCTTNCTCGTTGAGGAGCTTTGTANTCTAATAAAAGAG	420
Query	421	AAATATAAGTAAATGTTAGATATATGGGNGGATAATGGTAACTATGTGCTTAAAGAGGTA	480
Sbjct	421	AAATATAAGTAAATGTTAGATATATGGGNGGATAATGGTAACTATGTGCTTAAAGAGGTA	480

PATENT SEQUENCE ALIGNMENT

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Query  481  TAAAAGAAGGGTAGGGAGCAGATAAGACAAAGGAAGGGCTATATTATAANGAAGAATATT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TAAAAGAAGGGTAGGGAGCAGATAAGACAAAGGAAGGGCTATATTATAANGAAGAATATT  540

Query  541  CCAAGTAGGGAAGAGAAAAAGATATGTTATCCATATAATATTTTATGTGCAGTAGAGAAC  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CCAAGTAGGGAAGAGAAAAAGATATGTTATCCATATAATATTTTATGTGCAGTAGAGAAC  600

Query  601  ATGTTCTATAGAANAGACAGAAGATG  626
          |||||||||||||||||||
Sbjct  601  ATGTTCTATAGAANAGACAGAAGATG  626
```

Sequence 700 matched with Sequence 290

Query= Sequence ID 700

Length=623

SEQ ID NO: 290

ALIGNMENTS

Identities = 623/623 (100%), Gaps = 0/623 (0%)

Query	1	CTTGAGCCCAGGAATTCCAGCCTGGGCAATATAGTAAGACTCCGTCTCTACAAAAGATAC	60
Sbjct	1	CTTGAGCCCAGGAATTCCAGCCTGGGCAATATAGTAAGACTCCGTCTCTACAAAAGATAC	60
Query	61	AAAAATTAGCCAGATGTGGTGGTGCCTGTAGTTCCAGATACTGGAAAGACTGAGGC	120
Sbjct	61	AAAAATTAGCCAGATGTGGTGGTGCCTGTAGTTCCAGATACTGGAAAGACTGAGGC	120
Query	121	AGGAGGATTGCTTGAGCATGGGAAGTTGAGGCTGCAATGAGCTGTGATTACGCCACTACA	180
Sbjct	121	AGGAGGATTGCTTGAGCATGGGAAGTTGAGGCTGCAATGAGCTGTGATTACGCCACTACA	180
Query	181	CTCCAGCCTGGGCAACAGAGTAAGATCTTGTCTCaaaaaaaaaattgaattcagctaaaa	240
Sbjct	181	CTCCAGCCTGGGCAACAGAGTAAGATCTTGTCTCAAAAAAAAAAATTGAATTCAGCTAAAA	240
Query	241	ataataaaaattttaaaataatttttaaaaaGCCCTCAACAGCTTTGTTTTTCTCTCCTTGC	300
Sbjct	241	ATAATAAAATTTTAAAATAATTTTAAAAAGCCCTCAACAGCTTTGTTTTTCTCTCCTTGC	300
Query	301	CAGCTTCTCTGCAGCCTATAGCCTGCAGGCTGGCTGCTGCGAGCCAGGACAAGCGGTGGG	360
Sbjct	301	CAGCTTCTCTGCAGCCTATAGCCTGCAGGCTGGCTGCTGCGAGCCAGGACAAGCGGTGGG	360
Query	361	AAATGCAATCACAGCGTGAAATCTCTGTGTTTCAGAGACACGCAGGAAGCAGGTGAACCAT	420
Sbjct	361	AAATGCAATCACAGCGTGAAATCTCTGTGTTTCAGAGACACGCAGGAAGCAGGTGAACCAT	420
Query	421	GAAGGGCCAACACATGCCCCCAGTTAGCAGGGTGTAGAGACCGGGGCAGGGCTTTCTTCT	480
Sbjct	421	GAAGGGCCAACACATGCCCCCAGTTAGCAGGGTGTAGAGACCGGGGCAGGGCTTTCTTCT	480

Sequence 701 matched with Sequence 291

Query= Sequence ID - 701
Length=579

nt: 579

SEQ ID NO: 291

nt: 579

ALIGNMENTS

Identities = 579/579 (100%), Gaps = 0/579 (0%)

Query	1	CTTTGGAGCTTCTGTCTGTGCTGTGGACCTCAATGCAGATGGCTTCTCAGATCTGCTCGT	60
Sbjct	1	CTTTGGAGCTTCTGTCTGTGCTGTGGACCTCAATGCAGATGGCTTCTCAGATCTGCTCGT	60
Query	61	GGGAGCACCCATGCAGAGCACCATCAGAGAGGAAGGAAGAGTGTTTGTGTACATCAACTC	120
Sbjct	61	GGGAGCACCCATGCAGAGCACCATCAGAGAGGAAGGAAGAGTGTTTGTGTACATCAACTC	120
Query	121	TGGCTCGGGAGCAGTAATGAATGCAATGGAAACAAACCTCGTTGGAAGTGACAAATATGC	180
Sbjct	121	TGGCTCGGGAGCAGTAATGAATGCAATGGAAACAAACCTCGTTGGAAGTGACAAATATGC	180
Query	181	TGCAAGATTTGGGGAATCTATAGTTAATCTTGGCGACATTGACAATGATGGCTTTGAAGG	240
Sbjct	181	TGCAAGATTTGGGGAATCTATAGTTAATCTTGGCGACATTGACAATGATGGCTTTGAAGG	240
Query	241	TAATTAATAATTATCAAATTGGTGCTTGATTTCTGCTTTTAAATGGTTTATGGAAGAAAA	300
Sbjct	241	TAATTAATAATTATCAAATTGGTGCTTGATTTCTGCTTTTAAATGGTTTATGGAAGAAAA	300
Query	301	TATGATTAAAGTTTTGTATTGTTTTCTTCCTATAGAAGATGGAGCCAGAATGGCATGCT	360
Sbjct	301	TATGATTAAAGTTTTGTATTGTTTTCTTCCTATAGAAGATGGAGCCAGAATGGCATGCT	360
Query	361	AAGTTTTTTCTTTTCTTTAGTGTTATATATGACTTCTCCTCAATTGTCACCCATTGATCT	420
Sbjct	361	AAGTTTTTTCTTTTCTTTAGTGTTATATATGACTTCTCCTCAATTGTCACCCATTGATCT	420
Query	421	TTACCACTGTTAATAATGGATGATATTCAAAATACCTTATTTTCAGTGATTCTAAGGCACC	480
Sbjct	421	TTACCACTGTTAATAATGGATGATATTCAAAATACCTTATTTTCAGTGATTCTAAGGCACC	480

PATENT SEQUENCE ALIGNMENT

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Query  481  ATTGATTAGAAACTGCATTATTATTTATGTGTCCCTAAAAGCTACCTATTAAGCTGTTAC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATTGATTAGAAACTGCATTATTATTTATGTGTCCCTAAAAGCTACCTATTAAGCTGTTAC  540

Query  541  ACCCACCATTTTCTGTTAAGAAAATCCTGATTTCAGAA  579
          ||||||||||||||||||||||||||||||||
Sbjct  541  ACCCACCATTTTCTGTTAAGAAAATCCTGATTTCAGAA  579
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Length=709

Identities = 705/705 (100%), Gaps = 0/705 (0%)

Query	5	TCCTCTCGGAACGCGCCTTNTGTAGCCAGGTGCTACCAGACCNAATACACGGTTGTTCCA 	64
Sbjct	5	TCCTCTCGGAACGCGCCTTNTGTAGCCAGGTGCTACCAGACCNAATACACGGTTGTTCCA 	64
Query	65	GCTTGCGCATTACCGATGGCGTAGATATCCGGATCGGAAGTCTGGCAGGAATCATTAAT 	124
Sbjct	65	GCTTGCGCATTACCGATGGCGTAGATATCCGGATCGGAAGTCTGGCAGGAATCATTAAT 	124
Query	125	GACAATACCCCCACGCGGAGCAACGTCCAGACCACACTGGGTTGCCAGCTTATCGCGCGG 	184
Sbjct	125	GACAATACCCCCACGCGGAGCAACGTCCAGACCACACTGGGTTGCCAGCTTATCGCGCGG 	184
Query	185	ACGGATACCGGTAGAGAAGACGATAAAGTCGACTTCCAGTTCGCTGCCGTCGGCAAAACG 	244
Sbjct	185	ACGGATACCGGTAGAGAAGACGATAAAGTCGACTTCCAGTTCGCTGCCGTCGGCAAAACG 	244
Query	245	CATGGTTTTACGCGCTTCAACACCTTCCTGCACAATCTCAAGGGTGTTTTTGCTGGTGTG 	304
Sbjct	245	CATGGTTTTACGCGCTTCAACACCTTCCTGCACAATCTCAAGGGTGTTTTTGCTGGTGTG 	304
Query	305	AACGCGCACGCCCATACTTTCGATTTTGCGACGCAGCTGCTCGCCGCCCATCTGATCAAG 	364
Sbjct	305	AACGCGCACGCCCATACTTTCGATTTTGCGACGCAGCTGCTCGCCGCCCATCTGATCAAG 	364
Query	365	CTGTTCTGCCATCAGCATAGGGGCAAATTCGATAACGTGGGTTTCAATACCTAAGTTTTT 	424
Sbjct	365	CTGTTCTGCCATCAGCATAGGGGCAAATTCGATAACGTGGGTTTCAATACCTAAGTTTTT 	424
Query	425	CAGCGCGCCTGCGGCTTCCAGACCTAACAGGCCGCAATTCGAGCTCGGCCGACTTGGCCA 	484
Sbjct	425	CAGCGCGCCTGCGGCTTCCAGACCTAACAGGCCGCAATTCGAGCTCGGCCGACTTGGCCA 	484

Query	485	ATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACT	544
Sbjct	485	ATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACT	544
Query	545	GGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCT	604
Sbjct	545	GGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCT	604
Query	605	GGCGTAATAGCGAAAGAGGCCCGCACCCGATCGCCCTTTC AACAGTTGCGCACCTGAAT	664
Sbjct	605	GGCGTAATAGCGAAAGAGGCCCGCACCCGATCGCCCTTTC AACAGTTGCGCACCTGAAT	664
Query	665	GGCGAATGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGT	709
Sbjct	665	GGCGAATGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGT	709

Sequence 703 matched with Sequence 293

Query= Sequence ID 703

Length=471

SEQ ID NO: 293

ALIGNMENTS

Identities = 471/471 (100%), Gaps = 0/471 (0%)

Query	1	CTGCGCAGACCAGACTTCGCTCGTACTCGTGCGCCTCGCTTCGCTTTTCCTCCGCAACCA	60
Sbjct	1	CTGCGCAGACCAGACTTCGCTCGTACTCGTGCGCCTCGCTTCGCTTTTCCTCCGCAACCA	60
Query	61	TGTCTGACAAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAAACTGAAGAAGA	120
Sbjct	61	TGTCTGACAAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAAACTGAAGAAGA	120
Query	121	CAGAGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAACGATTGAACAGGAGAAGCAAG	180
Sbjct	121	CAGAGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAACGATTGAACAGGAGAAGCAAG	180
Query	181	CAGGCGAATCGTAATGAGGCGTGCGCCGCCAATATGCACTGTACATTCCACAAGCATTGC	240
Sbjct	181	CAGGCGAATCGTAATGAGGCGTGCGCCGCCAATATGCACTGTACATTCCACAAGCATTGC	240
Query	241	CTTCTTATTTTACTTCTTTTAGCTGTTTAACTTTGTAAGATGCAAAGAGGTTGGATCAAG	300
Sbjct	241	CTTCTTATTTTACTTCTTTTAGCTGTTTAACTTTGTAAGATGCAAAGAGGTTGGATCAAG	300
Query	301	TTTAAATGACTGTGCTGCCCCTTTCACATCAAAGAACTACTGACAACGAAGGCCGCGCCT	360
Sbjct	301	TTTAAATGACTGTGCTGCCCCTTTCACATCAAAGAACTACTGACAACGAAGGCCGCGCCT	360
Query	361	GCCTTTCCCATCTGTCTATCTATCTGGCTGGCAGGGAAGGAAAGAACTTGCATGTTGGTG	420
Sbjct	361	GCCTTTCCCATCTGTCTATCTATCTGGCTGGCAGGGAAGGAAAGAACTTGCATGTTGGTG	420
Query	421	AAGGAAGAAGTGGGGTGAAGAAGTGGGGTGGGACGACAGTGAAATCTAA	471
Sbjct	421	AAGGAAGAAGTGGGGTGAAGAAGTGGGGTGGGACGACAGTGAAATCTAA	471

Sequence 704 matched with Sequence 294

Query= Sequence ID 704
Length=495

SEQ ID NO: 294

ALIGNMENTS

Identities = 495/495 (100%), Gaps = 0/495 (0%)

Query	1	CTTGTATTCAAGAACTACTGTAATGCATTAGTGGTCTGGCTTCATTTTGTATGATGCCAG	60
Sbjct	1	CTTGTATTCAAGAACTACTGTAATGCATTAGTGGTCTGGCTTCATTTTGTATGATGCCAG	60
Query	61	ATCCTTAATTTACCCAGCACAATCATTTTCAGTAGTTTCCTATGGCTCCTGCAAAAATGCA	120
Sbjct	61	ATCCTTAATTTACCCAGCACAATCATTTTCAGTAGTTTCCTATGGCTCCTGCAAAAATGCA	120
Query	121	AACAGAAACCACCACAGGAACAGCCCCTTGCTGCCTCCTGTTGCTGAGGTAGTAGTCGCT	180
Sbjct	121	AACAGAAACCACCACAGGAACAGCCCCTTGCTGCCTCCTGTTGCTGAGGTAGTAGTCGCT	180
Query	181	AAAGAAAATTGAAGGCTCCTTACAATCTATATTTGAAAAGTAGAACTTCTGTAGAAACAC	240
Sbjct	181	AAAGAAAATTGAAGGCTCCTTACAATCTATATTTGAAAAGTAGAACTTCTGTAGAAACAC	240
Query	241	ACAGATCCCGATCTTAGAAGTTGTACAGGACAATCTGGTAAAAGTACATAATTGTGATT	300
Sbjct	241	ACAGATCCCGATCTTAGAAGTTGTACAGGACAATCTGGTAAAAGTACATAATTGTGATT	300
Query	301	TATTAACATGAATTAAAATGCCCAACCAGTGCTTCAGTGTGACAGTATATTTAAAATAAA	360
Sbjct	301	TATTAACATGAATTAAAATGCCCAACCAGTGCTTCAGTGTGACAGTATATTTAAAATAAA	360
Query	361	AAAGAAATTAAGGTCATATACTGTACTACTTTACAAAGATCCACAGTTTGGCAAAAGA	420
Sbjct	361	AAAGAAATTAAGGTCATATACTGTACTACTTTACAAAGATCCACAGTTTGGCAAAAGA	420
Query	421	CTTGTCATATGTACAATGCTATATATCAAATGAGAAAAGCTGTAAGCAATTATATACGCA	480
Sbjct	421	CTTGTCATATGTACAATGCTATATATCAAATGAGAAAAGCTGTAAGCAATTATATACGCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AAAGAAATGGCAGTA	495
Sbjct	481	AAAGAAATGGCAGTA	495

Sequence 705 matched with Sequence 295

Query= Sequence ID 705
Length=531

SEQ ID NO: 295

ALIGNMENTS

Identities = 531/531 (100%), Gaps = 0/531 (0%)

Query	1	TTCCAGTCCTTTCATTTAGTATAAAAGAAATACTGAACAAGCCAGTGGGATGGAATTGAA	60
Sbjct	1	TTCCAGTCCTTTCATTTAGTATAAAAGAAATACTGAACAAGCCAGTGGGATGGAATTGAA	60
Query	61	AGAACTAATCATGAGGACTCTGTCCTGACACAGGTCCTCAAAGCTAGCAGAGATACGCAG	120
Sbjct	61	AGAACTAATCATGAGGACTCTGTCCTGACACAGGTCCTCAAAGCTAGCAGAGATACGCAG	120
Query	121	ACATTGTGGCATCTGGGTAGAAGAATACTGTATTgtgtgtgcagtgcacagtgtgtggtg	180
Sbjct	121	ACATTGTGGCATCTGGGTAGAAGAATACTGTATTGTGTGTGCAGTGCACAGTGTGTGGTG	180
Query	181	tgtgCACACTCATTCCCTTCTGCTCTTGGGCACAGGCAGTGGGTGTAGAGGTAACCAGTAG	240
Sbjct	181	TGTGCACACTCATTCCCTTCTGCTCTTGGGCACAGGCAGTGGGTGTAGAGGTAACCAGTAG	240
Query	241	CTTTGAGAAGCTACATGTAGCTCACCAGTGGTTTTCTCTAAGGAATCACAAAGGTAAACT	300
Sbjct	241	CTTTGAGAAGCTACATGTAGCTCACCAGTGGTTTTCTCTAAGGAATCACAAAGGTAAACT	300
Query	301	ACCCAACCACATGCCACGTAATATTTTCAGCCATTCAGAGGAAACTGTTTTCTCTTTATTT	360
Sbjct	301	ACCCAACCACATGCCACGTAATATTTTCAGCCATTCAGAGGAAACTGTTTTCTCTTTATTT	360
Query	361	GCTTATATGTTAATATGGTTTTTAAATTGGTAACTTTTATATAGTATGGTAACAGTATGT	420
Sbjct	361	GCTTATATGTTAATATGGTTTTTAAATTGGTAACTTTTATATAGTATGGTAACAGTATGT	420
Query	421	TAATACACACATACATATGCACACATGCTTTGGGTCCTTCCATAATACTTTTATATTTGT	480
Sbjct	421	TAATACACACATACATATGCACACATGCTTTGGGTCCTTCCATAATACTTTTATATTTGT	480

PATENT SEQUENCE ALIGNMENT

Query	481	AAATCAATGTTTTTGGAGCAATCCCAAGTTTAAGGGAAATATTTTTGTAAA	531
Sbjct	481	AAATCAATGTTTTTGGAGCAATCCCAAGTTTAAGGGAAATATTTTTGTAAA	531

Sequence 706 matched with Sequence 296

Query= Sequence ID - 706
Length=496

nt: 496

SEQ ID NO: 296

nt: 496

ALIGNMENTS

Identities = 496/496 (100%), Gaps = 0/496 (0%)

Query	1	CAACCCTCTCTCCTCAGCGCTTCTTCTTTCTTGGTTTGATCCTGACTGCTGTCATGGCGT	60
Sbjct	1	CAACCCTCTCTCCTCAGCGCTTCTTCTTTCTTGGTTTGATCCTGACTGCTGTCATGGCGT	60
Query	61	GCCCTCTGGAGAAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAGTACTCGGGCAAAG	120
Sbjct	61	GCCCTCTGGAGAAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAGTACTCGGGCAAAG	120
Query	121	AGGGTGACAAGTTCAAGCTCAACAAGTCAGAACTAAAGGAGCTGCTGACCCGGGAGCTGC	180
Sbjct	121	AGGGTGACAAGTTCAAGCTCAACAAGTCAGAACTAAAGGAGCTGCTGACCCGGGAGCTGC	180
Query	181	CCAGCTTCTTGGGGAAAAGGACAGATGAAGCTGCTTTCCAGAAGCTGATGAGCAACTTGG	240
Sbjct	181	CCAGCTTCTTGGGGAAAAGGACAGATGAAGCTGCTTTCCAGAAGCTGATGAGCAACTTGG	240
Query	241	ACAGCAACAGGGACAACGAGGTGGACTTCCAAGAGTACTGTGTCTTCCTGTCCTGCATCG	300
Sbjct	241	ACAGCAACAGGGACAACGAGGTGGACTTCCAAGAGTACTGTGTCTTCCTGTCCTGCATCG	300
Query	301	CCATGATGTGTAACGAATTCTTTGAAGGCTTCCCAGATAAGCAGCCCAGGAAGAAATGAA	360
Sbjct	301	CCATGATGTGTAACGAATTCTTTGAAGGCTTCCCAGATAAGCAGCCCAGGAAGAAATGAA	360
Query	361	AACTCCTCTGATGTGGTTGGGGGTCTGCCAGCTGGGGCCCTCCCTGTCGCCAGTGGGCA	420
Sbjct	361	AACTCCTCTGATGTGGTTGGGGGTCTGCCAGCTGGGGCCCTCCCTGTCGCCAGTGGGCA	420
Query	421	CtttttttttttCCACCCTGGCTCCTTCAACACGTGCTTGATGCTGAGCAAAGTTCAATAA	480
Sbjct	421	CTTTTTTTTTTCCACCCTGGCTCCTTCAACACGTGCTTGATGCTGAGCAAAGTTCAATAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGATTTTGGGAAGTTT	496
Sbjct	481	AGATTTTGGGAAGTTT	496

Sequence 707 matched with Sequence 297

Query= Sequence ID - 707
Length=397

nt: 397

SEQ ID NO: 297

nt: 397

ALIGNMENTS

Identities = 397/397 (100%), Gaps = 0/397 (0%)

Query	1	CGGATGTGGTGGCAGGCGCCTCTAGTCCCAGCTACTCGGCAGGCTGAGGTAGGAGAATGG	60
Sbjct	1	CGGATGTGGTGGCAGGCGCCTCTAGTCCCAGCTACTCGGCAGGCTGAGGTAGGAGAATGG	60
Query	61	CTTGAACCCAGGAGGTGGAGCTGACAGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTG	120
Sbjct	61	CTTGAACCCAGGAGGTGGAGCTGACAGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTG	120
Query	121	GGCGGCAGAGCGAGACTCCATCTCaaaaaaaaaaaaaaaaaaaaaTAGACTTTGAGACCAG	180
Sbjct	121	GGCGGCAGAGCGAGACTCCATCTCAAAAAAAAAAAAAAAAAAAAAATAGACTTTGAGACCAG	180
Query	181	CCTGACCAACATAGTGAAACCCGTCACTACTAAAAATACAAAAATTACCCGGGCGTG	240
Sbjct	181	CCTGACCAACATAGTGAAACCCGTCACTACTAAAAATACAAAAATTACCCGGGCGTG	240
Query	241	ACGGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGACAGGAGAATCACTTGAACCAGG	300
Sbjct	241	ACGGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGACAGGAGAATCACTTGAACCAGG	300
Query	301	GAGGCGGAGGTTGTAGTGAAGTGAATCGTGCCCTGCACTCCAGCCTGGGTAACAAGAG	360
Sbjct	301	GAGGCGGAGGTTGTAGTGAAGTGAATCGTGCCCTGCACTCCAGCCTGGGTAACAAGAG	360
Query	361	CGAAACTCCGTCTCaaaaataaataaataaataaaat	397
Sbjct	361	CGAAACTCCGTCTCAAAAATAAATAAATAAATAAAAT	397

Sequence 708 matched with Sequence 298

Query= Sequence ID - 708 nt: 293
Length=293

SEQ ID NO: 298 nt: 293

ALIGNMENTS

Identities = 293/293 (100%), Gaps = 0/293 (0%)

Query	1	CCAGCTTTTATGGTGTTTAATCTAATACTTAAGCTGCAGTCCCAAAATTAGGGGTCC	60
Sbjct	1	CCAGCTTTTATGGTGTTTAATCTAATACTTAAGCTGCAGTCCCAAAATTAGGGGTCC	60
Query	61	TTCAGTCTTGGAGACTATAAGGGAGCCTCTGCACCCAGGGAAAATGTTACCCTTTACAGG	120
Sbjct	61	TTCAGTCTTGGAGACTATAAGGGAGCCTCTGCACCCAGGGAAAATGTTACCCTTTACAGG	120
Query	121	GGGGAAGGGTAAACCAGTAGGGAATACAGTACAATCCCAACCCTACTGGGAGGGCGGGA	180
Sbjct	121	GGGGAAGGGTAAACCAGTAGGGAATACAGTACAATCCCAACCCTACTGGGAGGGCGGGA	180
Query	181	GGGAGGTGTTGCCGTCCTGTATTAAGTCGATGTTGGGAAACGTTTAAACATCTGGAGCC	240
Sbjct	181	GGGAGGTGTTGCCGTCCTGTATTAAGTCGATGTTGGGAAACGTTTAAACATCTGGAGCC	240
Query	241	TTTGTGGGTGGAAATATGTCTCCAGTTACAACCTCCGCAGTGGATGTGAAGAAG	293
Sbjct	241	TTTGTGGGTGGAAATATGTCTCCAGTTACAACCTCCGCAGTGGATGTGAAGAAG	293

Sequence 709 matched with Sequence 299

Query= Sequence ID 709

Length=452

SEQ ID NO: 299

ALIGNMENTS

Identities = 452/452 (100%), Gaps = 0/452 (0%)

Query	1	GGAAGCTACAATGATTTTGGGAATTACAACAATCAGTCTTCAAATTTTGGACCCATGAAG	60
Sbjct	1	GGAAGCTACAATGATTTTGGGAATTACAACAATCAGTCTTCAAATTTTGGACCCATGAAG	60
Query	61	GGAGGAAATTTTGGAGGCAGAAGCTCTGGCCCCTATGGCGGTGGAGGCCAATACTTTGCA	120
Sbjct	61	GGAGGAAATTTTGGAGGCAGAAGCTCTGGCCCCTATGGCGGTGGAGGCCAATACTTTGCA	120
Query	121	AAACCACGAAACCAAGGTGGCTATGGCGGTTCCAGCAGCAGCAGTAGCTATGGCAGTGGC	180
Sbjct	121	AAACCACGAAACCAAGGTGGCTATGGCGGTTCCAGCAGCAGCAGTAGCTATGGCAGTGGC	180
Query	181	AGAAGATTTTAATTAGGAAACAAAGCTTANCAGGAGAGGAGAGCCAGAGAAGTGACAGGG	240
Sbjct	181	AGAAGATTTTAATTAGGAAACAAAGCTTANCAGGAGAGGAGAGCCAGAGAAGTGACAGGG	240
Query	241	AAGCTACAGGTTACAACAGATTTGTGAACTCAGCCAAGCACAGTGGTGGCAGGGCCTAGC	300
Sbjct	241	AAGCTACAGGTTACAACAGATTTGTGAACTCAGCCAAGCACAGTGGTGGCAGGGCCTAGC	300
Query	301	TGCTACAAAGAAGACATGTTTTAGACAAATACTCATGTGTATGGGCAAAAAACTCGAGGA	360
Sbjct	301	TGCTACAAAGAAGACATGTTTTAGACAAATACTCATGTGTATGGGCAAAAAACTCGAGGA	360
Query	361	CTGTATTTGTGACTAATTGTATAACAGGTTATTTTAGTTTCTGTTCTGTGGAAAGTGTA	420
Sbjct	361	CTGTATTTGTGACTAATTGTATAACAGGTTATTTTAGTTTCTGTTCTGTGGAAAGTGTA	420
Query	421	AGCATTCCAACAAAGGGGTTTTAATGTANATT	452
Sbjct	421	AGCATTCCAACAAAGGGGTTTTAATGTANATT	452

Sequence 710 matched with Sequence 300

Query= Sequence ID 710

Length=480

SEQ ID NO: 300

ALIGNMENTS

Identities = 480/480 (100%), Gaps = 0/480 (0%)

Query	1	TGGATTCCCGTCGTAACCTAAAGGGAAACTTTCACAATGTCCGGAGCCCTTGATGTCCTG	60
Sbjct	1	TGGATTCCCGTCGTAACCTAAAGGGAAACTTTCACAATGTCCGGAGCCCTTGATGTCCTG	60
Query	61	CAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACTTAGGTGGCACC	120
Sbjct	61	CAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACTTAGGTGGCACC	120
Query	121	AATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATC	180
Sbjct	121	AATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATC	180
Query	181	ATAAATCTCAAGAGGACCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCAATTGTTGCCATT	240
Sbjct	181	ATAAATCTCAAGAGGACCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCAATTGTTGCCATT	240
Query	241	GAAAACCCTGCTGATGTCAGTGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTG	300
Sbjct	241	GAAAACCCTGCTGATGTCAGTGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTG	300
Query	301	AAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCTGGCCGCTTCACTCCTGGAACCTTC	360
Sbjct	301	AAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCTGGCCGCTTCACTCCTGGAACCTTC	360
Query	361	ACTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTGGTTACTGACCCAGG	420
Sbjct	361	ACTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTGGTTACTGACCCAGG	420
Query	421	GCTGACCACCAGCCTCTCACGGAGGCATCTTATGTTAACCTACCTACCATTGCCCTGTGT	480
Sbjct	421	GCTGACCACCAGCCTCTCACGGAGGCATCTTATGTTAACCTACCTACCATTGCCCTGTGT	480

Sequence 711 matched with Sequence 301

Query= Sequence ID - 711 nt: 498
Length=498

SEQ ID NO: 301 nt: 498

ALIGNMENTS

Identities = 498/498 (100%), Gaps = 0/498 (0%)

Query	1	GTGGTACATATACACAAAGGAAAAC	TATGTAGCCATTAAAAGAAAAGGAACTCCTATCAT	60
Sbjct	1	GTGGTACATATACACAAAGGAAAAC	TATGTAGCCATTAAAAGAAAAGGAACTCCTATCAT	60
Query	61	TTGTAACAACATAAATAAATCTGGAGGAGATTAGGCTAAGGTGAAATAAGCCAGGCACAA	120	
Sbjct	61	TTGTAACAACATAAATAAATCTGGAGGAGATTAGGCTAAGGTGAAATAAGCCAGGCACAA	120	
Query	121	AAAGACAAC	TACCATATGATCTTACTTATACGTGTGTGGAATCTAAAAAGGTGGAATTTA	180
Sbjct	121	AAAGACAAC	TACCATATGATCTTACTTATACGTGTGTGGAATCTAAAAAGGTGGAATTTA	180
Query	181	CAGAAGCAGAGAGTAGAATGGTGATTACCAGAGGCTGGGGAGTGAGGGCAGGAGGTTGGA	240	
Sbjct	181	CAGAAGCAGAGAGTAGAATGGTGATTACCAGAGGCTGGGGAGTGAGGGCAGGAGGTTGGA	240	
Query	241	GAAATGTTGGTCAAAGGATACAAAGTTTCAGTTATACAGGATGAATAAGTTCAAGAGATC	300	
Sbjct	241	GAAATGTTGGTCAAAGGATACAAAGTTTCAGTTATACAGGATGAATAAGTTCAAGAGATC	300	
Query	301	TATTGTACAACGTGGTGGCTATAGTTGATAACAATGTATTGTGTTCTTGAAAAATGCTGA	360	
Sbjct	301	TATTGTACAACGTGGTGGCTATAGTTGATAACAATGTATTGTGTTCTTGAAAAATGCTGA	360	
Query	361	GAGAGTAGATTTTAAGTGTTCTCACCACAAAACATAAGTATGTGAGGTAATGCATGTGTT	420	
Sbjct	361	GAGAGTAGATTTTAAGTGTTCTCACCACAAAACATAAGTATGTGAGGTAATGCATGTGTT	420	
Query	421	AATTANCTTAATTTAGACATTTTATAATGTATTATACATATTTCAAAACCACGTTGTACA	480	
Sbjct	421	AATTANCTTAATTTAGACATTTTATAATGTATTATACATATTTCAAAACCACGTTGTACA	480	

PATENT SEQUENCE ALIGNMENT

Query	481	TGAGAAAGATACACAATT	498
Sbjct	481	TGAGAAAGATACACAATT	498

Sequence 713 matched with Sequence 302

Query= Sequence ID 713

Length=474

SEQ ID NO: 302

ALIGNMENTS

Identities = 474/474 (100%), Gaps = 0/474 (0%)

Query	1	GCCCAGTCGACCCATGTTCTCCTTTCTACACCAGCATTAGACGCTGTCTTCACAGATTTG	60
Sbjct	1	GCCCAGTCGACCCATGTTCTCCTTTCTACACCAGCATTAGACGCTGTCTTCACAGATTTG	60
Query	61	GAAATCCTGGCTGCCATTTTTGCAGCTGCCATCCATGACGTTGATCATCCTGGAGTCTCC	120
Sbjct	61	GAAATCCTGGCTGCCATTTTTGCAGCTGCCATCCATGACGTTGATCATCCTGGAGTCTCC	120
Query	121	AATCAGTTTCTCATCAACACAAATTCAGAACTTGCTTTGATGTATAATGATGAATCTGTG	180
Sbjct	121	AATCAGTTTCTCATCAACACAAATTCAGAACTTGCTTTGATGTATAATGATGAATCTGTG	180
Query	181	TTGGAATAATCATCACCTTGCTGTGGGTTTCAAAGTCTGCAAGAAGAACTGTGACATC	240
Sbjct	181	TTGGAATAATCATCACCTTGCTGTGGGTTTCAAAGTCTGCAAGAAGAACTGTGACATC	240
Query	241	TTCATGAATCTCACCAAGAAGCAGCGTCAGACACTCAGGAAGATGGTTATTGACATGGTG	300
Sbjct	241	TTCATGAATCTCACCAAGAAGCAGCGTCAGACACTCAGGAAGATGGTTATTGACATGGTG	300
Query	301	TTAGCAACTGATATGTCTAAACATATGAGCCTGCTGGCAGACCTGAAGACAATGGTAGAA	360
Sbjct	301	TTAGCAACTGATATGTCTAAACATATGAGCCTGCTGGCAGACCTGAAGACAATGGTAGAA	360
Query	361	ACGAAGAAAGTTACAAGTTCAGGCGTTCTTCTCCTAGACAACCTATACCCGATCGCATTCA	420
Sbjct	361	ACGAAGAAAGTTACAAGTTCAGGCGTTCTTCTCCTAGACAACCTATACCCGATCGCATTCA	420
Query	421	GGTCCTTCGCAACATGGTCACTGTGCAGACCTGAGCAACCCACCAAGTCCTTG	474
Sbjct	421	GGTCCTTCGCAACATGGTCACTGTGCAGACCTGAGCAACCCACCAAGTCCTTG	474

Sequence 714 matched with Sequence 303

Query= Sequence ID 714

Length=535

SEQ ID NO: 303

ALIGNMENTS

Identities = 535/535 (100%), Gaps = 0/535 (0%)

Query	1	CTGTAACAGAGATTCCTTTTTTCAATAATCTTAATTCAAAGCATTATTAGACTTGAAAG	60
Sbjct	1	CTGTAACAGAGATTCCTTTTTTCAATAATCTTAATTCAAAGCATTATTAGACTTGAAAG	60
Query	61	GGTTTGATAATCTCCCAGTCCTTAGTAAAGATTGAGAGAGGCTGGAGCAGTTTTTCAGTTT	120
Sbjct	61	GGTTTGATAATCTCCCAGTCCTTAGTAAAGATTGAGAGAGGCTGGAGCAGTTTTTCAGTTT	120
Query	121	TAAATGAGTCTGCAGTTAATATCAAATGTGAGTTTGGGACTGCCTGGCAACATTTATATT	180
Sbjct	121	TAAATGAGTCTGCAGTTAATATCAAATGTGAGTTTGGGACTGCCTGGCAACATTTATATT	180
Query	181	TCTTATTCAGAACCCTTGATGAGACTATTTTAAACATACTAGTCTGCTGATAGAAAGCA	240
Sbjct	181	TCTTATTCAGAACCCTTGATGAGACTATTTTAAACATACTAGTCTGCTGATAGAAAGCA	240
Query	241	CTATACATCCTATTGTTTCTTTCTTTCCAAAATCAGCCTTCTGTCTGTAACAAAAATGTA	300
Sbjct	241	CTATACATCCTATTGTTTCTTTCTTTCCAAAATCAGCCTTCTGTCTGTAACAAAAATGTA	300
Query	301	CTTTATAGAGATGGAGGAAAAGGTCTAATACTACATAGCCTTAAGTGTTTCTGTCATTGT	360
Sbjct	301	CTTTATAGAGATGGAGGAAAAGGTCTAATACTACATAGCCTTAAGTGTTTCTGTCATTGT	360
Query	361	TCAAGTGTATTTTCTGTAACAGAAACATATTTGGAATGTTTTCTTTTCCCCTTATAAAT	420
Sbjct	361	TCAAGTGTATTTTCTGTAACAGAAACATATTTGGAATGTTTTCTTTTCCCCTTATAAAT	420
Query	421	TGTAATTCCTGAAATACTGCTGCTTTAAAAAGTCCCACTGTCAGATTATATTATCTAACA	480
Sbjct	421	TGTAATTCCTGAAATACTGCTGCTTTAAAAAGTCCCACTGTCAGATTATATTATCTAACA	480

PATENT SEQUENCE ALIGNMENT

Query	481	ATTGAATATTGNAAATATACTTGGCTTACCTCTCAATAAAAGGGTCTTTTCTATT	535
Sbjct	481	ATTGAATATTGNAAATATACTTGGCTTACCTCTCAATAAAAGGGTCTTTTCTATT	535

Sequence 717 matched with Sequence 304

Query= Sequence ID 717
Length=464

SEQ ID NO: 304

ALIGNMENTS

Identities = 464/464 (100%), Gaps = 0/464 (0%)

Query	1	TCCACCCACCTTGACCTCCCAAAGTGCTGGGATTATAGGCGTGAGCCACCTCGCCCAGCC	60
Sbjct	1	TCCACCCACCTTGACCTCCCAAAGTGCTGGGATTATAGGCGTGAGCCACCTCGCCCAGCC	60
Query	61	CGATACTAGGACTTATGCAGAAAAAACCTTGACATGGAGGAAAGTAAGATCTAAATAAAT	120
Sbjct	61	CGATACTAGGACTTATGCAGAAAAAACCTTGACATGGAGGAAAGTAAGATCTAAATAAAT	120
Query	121	ACTGTATTCATAGATTTAAAGACTCAGCATAATAAATATACCATTTCTCCCCAGATTGAT	180
Sbjct	121	ACTGTATTCATAGATTTAAAGACTCAGCATAATAAATATACCATTTCTCCCCAGATTGAT	180
Query	181	GTACAGATTTAACACAATTCCTATCAAGATCCCAGCAAGATTTTGTAGATATGTAAAAG	240
Sbjct	181	GTACAGATTTAACACAATTCCTATCAAGATCCCAGCAAGATTTTGTAGATATGTAAAAG	240
Query	241	ATTATTCAAAAATGTAAAAGGAAGGACAAAGGACTAGAATAGATAAAACAAAATGGAGAA	300
Sbjct	241	ATTATTCAAAAATGTAAAAGGAAGGACAAAGGACTAGAATAGATAAAACAAAATGGAGAA	300
Query	301	AGATTTAATAGGAATCACTGTAAGTATTTAAGACATACAGAACAATAATAGAACTGC	360
Sbjct	301	AGATTTAATAGGAATCACTGTAAGTATTTAAGACATACAGAACAATAATAGAACTGC	360
Query	361	TTGTATTAGTCCATTTTCACGCTGCTGATAAAGACATACCTGAGATTGGCAATTACAAAG	420
Sbjct	361	TTGTATTAGTCCATTTTCACGCTGCTGATAAAGACATACCTGAGATTGGCAATTACAAAG	420
Query	421	GAAAGANGTTTATTGGCTTACAGTTCCCATGGCTGGGGAGGCCT	464
Sbjct	421	GAAAGANGTTTATTGGCTTACAGTTCCCATGGCTGGGGAGGCCT	464

Sequence 718 matched with Sequence 305

Query= Sequence ID 718
Length=588

SEQ ID NO: 305

ALIGNMENTS

Identities = 588/588 (100%), Gaps = 0/588 (0%)

Query	1	CTCCTCTGGGTTGAAACCCGGGCGCCGCCAAGATGCCGGCTTACCACTCTTCTCTCATGG	60
Sbjct	1	CTCCTCTGGGTTGAAACCCGGGCGCCGCCAAGATGCCGGCTTACCACTCTTCTCTCATGG	60
Query	61	ATCCTGATACCAAACCTCATCGGAAACATGGCACTGTTGCCTATCAGAAGTCAATTCAAAG	120
Sbjct	61	ATCCTGATACCAAACCTCATCGGAAACATGGCACTGTTGCCTATCAGAAGTCAATTCAAAG	120
Query	121	GACCTGCCCCCAGAGAGACAAAAGATACAGATATTGTGGATGAAGCCATCTATTACTTCA	180
Sbjct	121	GACCTGCCCCCAGAGAGACAAAAGATACAGATATTGTGGATGAAGCCATCTATTACTTCA	180
Query	181	AGGCCAATGTCTTCTTCAAAAACCTATGAAATTAAGAATGAAGCTGATAGGACCTTGATAT	240
Sbjct	181	AGGCCAATGTCTTCTTCAAAAACCTATGAAATTAAGAATGAAGCTGATAGGACCTTGATAT	240
Query	241	ATATAACTCTCTACATTTCTGAATGTCTGAAGAACTGCAAAAGTGCAATTCCAAAAGCC	300
Sbjct	241	ATATAACTCTCTACATTTCTGAATGTCTGAAGAACTGCAAAAGTGCAATTCCAAAAGCC	300
Query	301	AAGGTGAGAAAAGAAATGTATACGCTGGGAATCACTAATTTTCCCATTCCTGGAGAGCCTG	360
Sbjct	301	AAGGTGAGAAAAGAAATGTATACGCTGGGAATCACTAATTTTCCCATTCCTGGAGAGCCTG	360
Query	361	GTTTTCCACTTAACGCAATTTATGCCAAACCTGCAACAAACAGGAAGATGAAGTGATGA	420
Sbjct	361	GTTTTCCACTTAACGCAATTTATGCCAAACCTGCAACAAACAGGAAGATGAAGTGATGA	420
Query	421	GAGCCTATTTACAACAGCTAAGGCAAGAGACTGGACTGAGACTTTGTGAGAAAAGTTTTTC	480
Sbjct	421	GAGCCTATTTACAACAGCTAAGGCAAGAGACTGGACTGAGACTTTGTGAGAAAAGTTTTTC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GACCCTCAGAAATGATAAACCCAGCAAGTGGNGGGCTTGCTTTGTGAAGAGACAGTTCATG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GACCCTCAGAAATGATAAACCCAGCAAGTGGNGGGCTTGCTTTGTGAAGAGACAGTTCATG  540

Query  541  AACAAANAGTCTTTCAGGACCTGGACAGTGAAGGGAGCCCGGGCAGCCA  588
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AACAAANAGTCTTTCAGGACCTGGACAGTGAAGGGAGCCCGGGCAGCCA  588
```

Sequence 719 matched with Sequence 306

Query= Sequence ID 719

Length=492

SEQ ID NO: 306

ALIGNMENTS

Identities = 489/489 (100%), Gaps = 0/489 (0%)

Query	4	GGCCGCGTNAACTTTTGATCGTCAGCTGGGGCTGGCAGGCACCTAAATGGGAAGGGTGAT	63
Sbjct	4	GGCCGCGTNAACTTTTGATCGTCAGCTGGGGCTGGCAGGCACCTAAATGGGAAGGGTGAT	63
Query	64	AGCAGTGTGTTGGGGGAGTTTAGGGAACGGTCCTCTACCGATAGAGGCAGCANCTCATT	123
Sbjct	64	AGCAGTGTGTTGGGGGAGTTTAGGGAACGGTCCTCTACCGATAGAGGCAGCANCTCATT	123
Query	124	GGAATTTCCCTCCTGAAGTTGTCTTGCCCCTTGAATCCTGCAGGAAGGCTGGCAAATGGCC	183
Sbjct	124	GGAATTTCCCTCCTGAAGTTGTCTTGCCCCTTGAATCCTGCAGGAAGGCTGGCAAATGGCC	183
Query	184	ATTTCCCTTCCACTTGAATAGAGACCCATAACTCAAGTATCTGCCCTTAAGACACCACAG	243
Sbjct	184	ATTTCCCTTCCACTTGAATAGAGACCCATAACTCAAGTATCTGCCCTTAAGACACCACAG	243
Query	244	GACTGTTCTTCGCGGGCCCTGCCCCTGGATTTGGGAGAGGCAGTCCANCTCACCCAACTA	303
Sbjct	244	GACTGTTCTTCGCGGGCCCTGCCCCTGGATTTGGGAGAGGCAGTCCANCTCACCCAACTA	303
Query	304	GGCTCTGCANGGGGACCANGAGGGATGGGTTGTGTCCACAGGACCAGCCAGACTGATGAG	363
Sbjct	304	GGCTCTGCANGGGGACCANGAGGGATGGGTTGTGTCCACAGGACCAGCCAGACTGATGAG	363
Query	364	GGATGCGGCAAGCATATTCTCACCACCTTCTTTACGTTTACAACANACCAGCNTTCCCT	423
Sbjct	364	GGATGCGGCAAGCATATTCTCACCACCTTCTTTACGTTTACAACANACCAGCNTTCCCT	423
Query	424	GTGTGGCAGGGGTTACATTGGTCACCGAGGACCTANAATCATGGAGTGCTCTGGGGATCC	483
Sbjct	424	GTGTGGCAGGGGTTACATTGGTCACCGAGGACCTANAATCATGGAGTGCTCTGGGGATCC	483

PATENT SEQUENCE ALIGNMENT

Query	484	GGGCTTGGA	492
Sbjct	484	GGGCTTGGA	492

Sequence 720 matched with Sequence 307

Query= Sequence ID 720
Length=430

SEQ ID NO: 307

ALIGNMENTS

Identities = 430/430 (100%), Gaps = 0/430 (0%)

Query	1	TCAGTGGTTGAATTTTGTCTGACACTTTCTCTGCATCAATTGGTATGACCATGTGA	60
Sbjct	1	TCAGTGGTTGAATTTTGTCTGACACTTTCTCTGCATCAATTGGTATGACCATGTGA	60
Query	61	tttCTGTAGCCTGTTAATATGGTTAATTTTCAAATATTGAGCTGATTAATTTTCAAATAT	120
Sbjct	61	TTTCTGTAGCCTGTTAATATGGTTAATTTTCAAATATTGAGCTGATTAATTTTCAAATAT	120
Query	121	TGAGCTCTCCTTGCATCTCTGGAATAAGTACCACTTGGTCGTGGTATATATTTCTTTTAA	180
Sbjct	121	TGAGCTCTCCTTGCATCTCTGGAATAAGTACCACTTGGTCGTGGTATATATTTCTTTTAA	180
Query	181	TATATTGCTGAATTCTGTTTGATCATGTTTCTTAAAGACTTTCGTGTCTGTTTTTCATGA	240
Sbjct	181	TATATTGCTGAATTCTGTTTGATCATGTTTCTTAAAGACTTTCGTGTCTGTTTTTCATGA	240
Query	241	TAGATACTGGTCTATAGTTTTGTTGTAATATCTTGGTTTGATTTTGATATCAGGATAATG	300
Sbjct	241	TAGATACTGGTCTATAGTTTTGTTGTAATATCTTGGTTTGATTTTGATATCAGGATAATG	300
Query	301	CTACCTTAATAGAATGAATTGGAGCCAAGTATGGTGGCAAATGCCTATAGTCCTAGCTAC	360
Sbjct	301	CTACCTTAATAGAATGAATTGGAGCCAAGTATGGTGGCAAATGCCTATAGTCCTAGCTAC	360
Query	361	TCAGGAGGCTGAGGTGGTGGGGACTGCTTGACCCANGAGTTCAAATCTAGCTTGGGCAAT	420
Sbjct	361	TCAGGAGGCTGAGGTGGTGGGGACTGCTTGACCCANGAGTTCAAATCTAGCTTGGGCAAT	420
Query	421	GTAGCAAGAC	430
Sbjct	421	GTAGCAAGAC	430

Sequence 721 matched with Sequence 308

Query= Sequence ID 721
Length=574

SEQ ID NO: 308

ALIGNMENTS

Identities = 574/574 (100%), Gaps = 0/574 (0%)

Query	1	TAGAAGGAATGACTATTCATGTCCAAAGTGAATGGTTTTGTGCAGTGAACAACACATGGC	60
Sbjct	1	TAGAAGGAATGACTATTCATGTCCAAAGTGAATGGTTTTGTGCAGTGAACAACACATGGC	60
Query	61	GAGGTACTAACTGAGAACTTTTTTCATGCTTTATGCCTACCTCTTGTAGTTGTTGCAGAG	120
Sbjct	61	GAGGTACTAACTGAGAACTTTTTTCATGCTTTATGCCTACCTCTTGTAGTTGTTGCAGAG	120
Query	121	CAAATATAAATTGTAATAAGATAGCTAGGCCTTGCAGAAACAAACAGAAAAACTTaaaaa	180
Sbjct	121	CAAATATAAATTGTAATAAGATAGCTAGGCCTTGCAGAAACAAACAGAAAAACTTAAAAA	180
Query	181	aaaaTGATATAAGAGCTGGAGTCTAGTATTTATATGAATCTGTGAGAGATAAatTTTTtG	240
Sbjct	181	AAAATGATATAAGAGCTGGAGTCTAGTATTTATATGAATCTGTGAGAGATAATTTTTTTTG	240
Query	241	GTCTCACTGCAATGAACCAAAAGCGGCTGAGTTTGGTTTTTAATTGTAGCCATGTATTGA	300
Sbjct	241	GTCTCACTGCAATGAACCAAAAGCGGCTGAGTTTGGTTTTTAATTGTAGCCATGTATTGA	300
Query	301	AGGCATCTTTTTGACCAACTCTTGTTGGTTCTGTCTTGAACCATTGTTAATCACTGTGCT	360
Sbjct	301	AGGCATCTTTTTGACCAACTCTTGTTGGTTCTGTCTTGAACCATTGTTAATCACTGTGCT	360
Query	361	GTAATTAGTATAGCTAAATCTTTTCCTTCCTTGCTCCTCCCCAGCCCACCCGCTTCC	420
Sbjct	361	GTAATTAGTATAGCTAAATCTTTTCCTTCCTTGCTCCTCCCCAGCCCACCCGCTTCC	420
Query	421	CTTAACATTTTTTCAgggggggTTGGGAGTGTTTTCATTTTAATGTGAGTGGATGTTTTG	480
Sbjct	421	CTTAACATTTTTTCAGGGGGGTTGGGAGTGTTTTCATTTTAATGTGAGTGGATGTTTTG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATAGTTGTAAGGAAAAAATGCATTTTCAGACACATTTTCACACATGAGCTATTTTCTTACAC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATAGTTGTAAGGAAAAAATGCATTTTCAGACACATTTTCACACATGAGCTATTTTCTTACAC  540

Query  541  AGTATGTCTTATTGGTAATAAGAATGTAATTCAT  574
          ||||||||||||||||||||||||||||
Sbjct  541  AGTATGTCTTATTGGTAATAAGAATGTAATTCAT  574
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Sequence 722 matched with Sequence 309

Query= Sequence ID 722
Length=327

SEQ ID NO: 309

ALIGNMENTS

Identities = 325/325 (100%), Gaps = 0/325 (0%)

Query	3	TTCCNTAAGAATACAAAAAATTAGCTGGGCGTGGTGGCAGGCGCCTGTAATCCCATCTAC	62
Sbjct	3	TTCCNTAAGAATACAAAAAATTAGCTGGGCGTGGTGGCAGGCGCCTGTAATCCCATCTAC	62
Query	63	TCAGGAAGCTGAGGCTGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCAGA	122
Sbjct	63	TCAGGAAGCTGAGGCTGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCAGA	122
Query	123	GATCACGCCACTGCAGTCCAGCCTGGGCAACAGTGCGAGACTCTGTCTCaaaaaaaaaT	182
Sbjct	123	GATCACGCCACTGCAGTCCAGCCTGGGCAACAGTGCGAGACTCTGTCTCAAAAAAAAAAAT	182
Query	183	AAATAAATTACCTGGGTGTGGCAGCGCGTGCCTGTAATCCCAGCTACCCAGGAGGCTGAG	242
Sbjct	183	AAATAAATTACCTGGGTGTGGCAGCGCGTGCCTGTAATCCCAGCTACCCAGGAGGCTGAG	242
Query	243	GCAAGAGAACTGCTTGAACCCAGGAGGCAGAGGTTGCATGGAGCTGAGATGGCGCCACTG	302
Sbjct	243	GCAAGAGAACTGCTTGAACCCAGGAGGCAGAGGTTGCATGGAGCTGAGATGGCGCCACTG	302
Query	303	CACTCCAGTCTGGTGACAGAGTGAG	327
Sbjct	303	CACTCCAGTCTGGTGACAGAGTGAG	327

Sequence 724 matched with Sequence 310

Query= Sequence ID 724
Length=273

SEQ ID NO: 310

ALIGNMENTS

Identities = 272/272 (100%), Gaps = 0/272 (0%)

Query	1	CTCTCTACTAAAAATACAAAAATTAGCTGGGCACGGNGGTGCATGCCTGTAAACCCAGCT	60
Sbjct	1	CTCTCTACTAAAAATACAAAAATTAGCTGGGCACGGNGGTGCATGCCTGTAAACCCAGCT	60
Query	61	ACCAGGTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCAGGGAGTCGGAGGTTGCG	120
Sbjct	61	ACCAGGTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCAGGGAGTCGGAGGTTGCG	120
Query	121	GCGAGCTGAGATCATGCCACTGCACTGCGGCCTGGAGACAAGAGCAAGACTCCGTCTCaa	180
Sbjct	121	GCGAGCTGAGATCATGCCACTGCACTGCGGCCTGGAGACAAGAGCAAGACTCCGTCTCAA	180
Query	181	aaaaaaaaaaaaaaaaaaaaaaaaaGACNTCACCTAATTGCAGNGNGNGGACCTTATTT	240
Sbjct	181	AAAAAAAAAAAAAAAAAAAAAAAAAAGACNTCACCTAATTGCAGNGNGNGGACCTTATTT	240
Query	241	GGCTNTTAATTCAAACCTATTA AAAAATGTGAAC	272
Sbjct	241	GGCTNTTAATTCAAACCTATTA AAAAATGTGAAC	272

Sequence 726 matched with Sequence 311

Query= Sequence ID - 726
Length=260

nt: 260

SEQ ID NO: 311

nt: 260

ALIGNMENTS

Identities = 260/260 (100%), Gaps = 0/260 (0%)

Query	1	CGGGGTCTGTACCGGGCTGGCCTGTGCCTATCACCTCTTATGCACACCTCCCACCCCCTG	60
Sbjct	1	CGGGGTCTGTACCGGGCTGGCCTGTGCCTATCACCTCTTATGCACACCTCCCACCCCCTG	60
Query	61	TATTCCCACCCCTGGACTGGTGGCCCCTGCCTTGGGGAAGGTCTCCCCATGTGCCTGCAC	120
Sbjct	61	TATTCCCACCCCTGGACTGGTGGCCCCTGCCTTGGGGAAGGTCTCCCCATGTGCCTGCAC	120
Query	121	CAGGAGACAGACAGAGAAGGCAGCAGGCGGCCTTTGTTGCTCAGCAAGGGGCTCTGCCCT	180
Sbjct	121	CAGGAGACAGACAGAGAAGGCAGCAGGCGGCCTTTGTTGCTCAGCAAGGGGCTCTGCCCT	180
Query	181	CCCTCCTTCCTTCTTGCTTCTCATAGCCCCGGTGTGCGGTGCATACACCCCCACCTCCTG	240
Sbjct	181	CCCTCCTTCCTTCTTGCTTCTCATAGCCCCGGTGTGCGGTGCATACACCCCCACCTCCTG	240
Query	241	CAATAAAATAGTAGCATCGG	260
Sbjct	241	CAATAAAATAGTAGCATCGG	260

Sequence 727 matched with Sequence 312

Query= Sequence ID 727
Length=538

SEQ ID NO: 312

ALIGNMENTS

Identities = 538/538 (100%), Gaps = 0/538 (0%)

Query	1	CTGAGTNTAGAAATGATGCCATTAATACTGATTGCAAAAACATTACAACCTCAGTACTGCA	60
Sbjct	1	CTGAGTNTAGAAATGATGCCATTAATACTGATTGCAAAAACATTACAACCTCAGTACTGCA	60
Query	61	GCTTTCATTCAAATAGGTTATATGTATAAACTGAGTTCAACAATATTGTATTTGAGATGG	120
Sbjct	61	GCTTTCATTCAAATAGGTTATATGTATAAACTGAGTTCAACAATATTGTATTTGAGATGG	120
Query	121	TAAAGTTAAAGAAATGCAATAATGTAAATAATACTTAAGAAAATAAGATCTCAGGAAACT	180
Sbjct	121	TAAAGTTAAAGAAATGCAATAATGTAAATAATACTTAAGAAAATAAGATCTCAGGAAACT	180
Query	181	GTATATACTCTGTACTTTTATGCAACTTTATCAGATCATTTTCAGTATATGCATCAAGGAT	240
Sbjct	181	GTATATACTCTGTACTTTTATGCAACTTTATCAGATCATTTTCAGTATATGCATCAAGGAT	240
Query	241	ATAGTGTATATGACATGAACTTTGAGTGCAAAAACCTGTACTATGTACCTTTTGTTTATTT	300
Sbjct	241	ATAGTGTATATGACATGAACTTTGAGTGCAAAAACCTGTACTATGTACCTTTTGTTTATTT	300
Query	301	TGCTGTCAACATCTAAATAAAGGtttttttgtttgttttttgtttttttaattgttttgt	360
Sbjct	301	TGCTGTCAACATCTAAATAAAGGTTTTTTTGTGTTGTTTTTGTGTTTTTAATTGTTTTGT	360
Query	361	tttaaagattgttttaattaattaataaaataattgttttaattaacaattgtttaatt	420
Sbjct	361	TTTAAAGATTGTTTTAATTAATTAATAAAATTAATTGTTTTAATTAACAATTGTTTAATT	420
Query	421	gttttaaaGTCGCCAGGCTGAGGCAGGTGAATCACAAGCTTAGGAGTTGGAGGCTAGCCT	480
Sbjct	421	GTTTTAAAGTCGCCAGGCTGAGGCAGGTGAATCACAAGCTTAGGAGTTGGAGGCTAGCCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCCAACATGGTGAAACCCCGTCTCTACTAAAAATACaaaaaaaTTAACTGGGTGTGGG	538
Sbjct	481	GCCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAAATTAACTGGGTGTGGG	538

Sequence 728 matched with Sequence 313

Query= Sequence ID 728

Length=629

SEQ ID NO: 313

ALIGNMENTS

Identities = 629/629 (100%), Gaps = 0/629 (0%)

Query	1	CCCATCTGCACCAGTACACAGGCAGGCATTATCATTCTTCACCTACTTTTAAATAGTGG	60
Sbjct	1	CCCATCTGCACCAGTACACAGGCAGGCATTATCATTCTTCACCTACTTTTAAATAGTGG	60
Query	61	CAACTTGGGATTCATTCTGGTGATTCTGAACCTTGCCTCATAGCTTAAAGTATAAAAAAG	120
Sbjct	61	CAACTTGGGATTCATTCTGGTGATTCTGAACCTTGCCTCATAGCTTAAAGTATAAAAAAG	120
Query	121	ATTCAAGAGCAGTGAGGTTTGTTCCTTCCAGTGAATGGTGGACTGAGTGGTGGGAGGTGG	180
Sbjct	121	ATTCAAGAGCAGTGAGGTTTGTTCCTTCCAGTGAATGGTGGACTGAGTGGTGGGAGGTGG	180
Query	181	AGGGCTAACAAGAGGAAAGAACTACATTCTTCAGAATACAGTGATGAAAATTCATTTTGA	240
Sbjct	181	AGGGCTAACAAGAGGAAAGAACTACATTCTTCAGAATACAGTGATGAAAATTCATTTTGA	240
Query	241	AACTCAAATATTTTCATTTTGGATATTCTCCTGTTTTTATTAAACCAGTGATTACACCTG	300
Sbjct	241	AACTCAAATATTTTCATTTTGGATATTCTCCTGTTTTTATTAAACCAGTGATTACACCTG	300
Query	301	GCCATCCCTCTAAATGTTCTAGGAAGGCATGTCTATTGTGATTTTGATGAAGACAGAATT	360
Sbjct	301	GCCATCCCTCTAAATGTTCTAGGAAGGCATGTCTATTGTGATTTTGATGAAGACAGAATT	360
Query	361	ATTTTCTCTGTAGAAACACAGATACCACTTTATCAGGGGAAGTTAGTCAAATGAAATGG	420
Sbjct	361	ATTTTCTCTGTAGAAACACAGATACCACTTTATCAGGGGAAGTTAGTCAAATGAAATGG	420
Query	421	AAATTGGTAAATGGACAAAAGCTAGCTAGTAAAAAGGACGACCCAGCAACATGCTTTAAC	480
Sbjct	421	AAATTGGTAAATGGACAAAAGCTAGCTAGTAAAAAGGACGACCCAGCAACATGCTTTAAC	480

PATENT SEQUENCE ALIGNMENT

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Query  481  CCCATTGTATGTTTGTGGAAAGAGCATAGTTTAACATCTTGAGAAATTGGGACATAAAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CCCATTGTATGTTTGTGGAAAGAGCATAGTTTAACATCTTGAGAAATTGGGACATAAAA  540

Query  541  GTTTTCATNGGTAGACAGTTCATGGCAGTATATGAATTGACATAATGGAAATAATCTGAT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GTTTTCATNGGTAGACAGTTCATGGCAGTATATGAATTGACATAATGGAAATAATCTGAT  600

Query  601  TTTATTTTACAACTAACATCCTTTCCCC  629
          ||||||||||||||||||||
Sbjct  601  TTTATTTTACAACTAACATCCTTTCCCC  629
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Sequence 736 matched with Sequence 314

Query= Sequence ID - 736
Length=641

nt: 641

SEQ ID NO: 314

nt: 641

ALIGNMENTS

Identities = 641/641 (100%), Gaps = 0/641 (0%)

Query	1	GGAATTCCAAGTGCTTGGGGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAGTACT	60
Sbjct	1	GGAATTCCAAGTGCTTGGGGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAGTACT	60
Query	61	TGAGTGTGCAGCTGCATGAGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGAAGCTATAC	120
Sbjct	61	TGAGTGTGCAGCTGCATGAGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGAAGCTATAC	120
Query	121	CAGTAGGACAAGGCAGGAAAATACTACACTTTCAGGATCAAGCCCCTCTGACTCTCATTT	180
Sbjct	121	CAGTAGGACAAGGCAGGAAAATACTACACTTTCAGGATCAAGCCCCTCTGACTCTCATTT	180
Query	181	GGAAACTGGATGTTTGCTAAGCACCTGCTTCTTAAGGATGCCGAGGGATTTAATGATACT	240
Sbjct	181	GGAAACTGGATGTTTGCTAAGCACCTGCTTCTTAAGGATGCCGAGGGATTTAATGATACT	240
Query	241	CCCAGAAACCTGGAGAGATTAATGGGGCCTATGGAGAAGTGCTCTGAACTCAGTGTTGGG	300
Sbjct	241	CCCAGAAACCTGGAGAGATTAATGGGGCCTATGGAGAAGTGCTCTGAACTCAGTGTTGGG	300
Query	301	ACTTGAATAAAATTAACCATTGTCATGTTTTTCAGAACAATAAGCTGTTTTATATTTTCAT	360
Sbjct	301	ACTTGAATAAAATTAACCATTGTCATGTTTTTCAGAACAATAAGCTGTTTTATATTTTCAT	360
Query	361	GTGCATGAAAGCCCTAGAACTAAGTTGTGTTATTTCCAGAAATGAAATAGATCCCACAGT	420
Sbjct	361	GTGCATGAAAGCCCTAGAACTAAGTTGTGTTATTTCCAGAAATGAAATAGATCCCACAGT	420
Query	421	TAGATGATGTGGCCATTAGGAAGTACCAAATTTATAAAAATCACTGGAGGTCTGTCTGAG	480
Sbjct	421	TAGATGATGTGGCCATTAGGAAGTACCAAATTTATAAAAATCACTGGAGGTCTGTCTGAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CAGTACCTAATAAAATATAGTATACTGAAAGTGAACAGATACTTTGTCTCTTTCTTTGGC	540
Sbjct	481	CAGTACCTAATAAAATATAGTATACTGAAAGTGAACAGATACTTTGTCTCTTTCTTTGGC	540
Query	541	TGCTTGATCTTTATCTGTGTCTGCCGTACAGTGCACCCTTAAAGTATTCTACACCAGTGC	600
Sbjct	541	TGCTTGATCTTTATCTGTGTCTGCCGTACAGTGCACCCTTAAAGTATTCTACACCAGTGC	600
Query	601	TTCTCAAACCTGGAAATGTGCATGTAAGTCACCCANGGGTCT	641
Sbjct	601	TTCTCAAACCTGGAAATGTGCATGTAAGTCACCCANGGGTCT	641

Sequence 739 matched with Sequence 315

Query= Sequence ID 739
Length=645

SEQ ID NO: 315

ALIGNMENTS

Identities = 645/645 (100%), Gaps = 0/645 (0%)

Query	1	TGCATGCCCATAGTCCCAGCTATTTGGGAGGCTGAGGCAGGAAAATCGCTTGAACCCGGG	60
Sbjct	1	TGCATGCCCATAGTCCCAGCTATTTGGGAGGCTGAGGCAGGAAAATCGCTTGAACCCGGG	60
Query	61	AGCCAGAGGTTGCAGTGAGCCGAGATCGCACTCCAGCTTGGCGACAGAACAAGACTCTGT	120
Sbjct	61	AGCCAGAGGTTGCAGTGAGCCGAGATCGCACTCCAGCTTGGCGACAGAACAAGACTCTGT	120
Query	121	CTCaaaaaaaaaaaaaaaaaGAAATCTTGGGATCCTGAACCCCTTACTCGAAGGGCTAAGG	180
Sbjct	121	CTCAAAAAAAAAAAAAAAAAAAGAAATCTTGGGATCCTGAACCCCTTACTCGAAGGGCTAAGG	180
Query	181	TAGCATCTCAGCATGTCTTATTCGAGACTTCGTANAACCAGACCTGCTGTTTGTAGATGT	240
Sbjct	181	TAGCATCTCAGCATGTCTTATTCGAGACTTCGTANAACCAGACCTGCTGTTTGTAGATGT	240
Query	241	TAATTAATCAAACCTTTCTCTACTCATTCTGGACCAGTTAAGGTTTCTCCTTCTCCGTA	300
Sbjct	241	TAATTAATCAAACCTTTCTCTACTCATTCTGGACCAGTTAAGGTTTCTCCTTCTCCGTA	300
Query	301	TGAGTTTTGATTTTCGTCCTCCTTGGTTGGAGATCACACTTTGGTCTGCTGCTAAGTTGG	360
Sbjct	301	TGAGTTTTGATTTTCGTCCTCCTTGGTTGGAGATCACACTTTGGTCTGCTGCTAAGTTGG	360
Query	361	ATGCCTCCCACTGTCTTTCCCTAAGTCTAGGGCTTCANACCCCAGTGTGGGGAGAGGGAC	420
Sbjct	361	ATGCCTCCCACTGTCTTTCCCTAAGTCTAGGGCTTCANACCCCAGTGTGGGGAGAGGGAC	420
Query	421	TTTCGTTTCCTGCCCCCTACCCACATCAGACACAGGCAGGCAAGAATAAGATGGCCAAAAG	480
Sbjct	421	TTTCGTTTCCTGCCCCCTACCCACATCAGACACAGGCAGGCAAGAATAAGATGGCCAAAAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCCGATGAACTTCTTGACCTAGCCTGGGACATTACCTGTTACTAGGTGGACTTCACTGCC	540
Sbjct	481	GCCGATGAACTTCTTGACCTAGCCTGGGACATTACCTGTTACTAGGTGGACTTCACTGCC	540
Query	541	TGTGAATGGAAGCTGAAGGGCTGtttttttGGTTTGTATTTGGACAGGCCAGGCTTANAG	600
Sbjct	541	TGTGAATGGAAGCTGAAGGGCTGTTTTTTTGGTTTGTATTTGGACAGGCCAGGCTTANAG	600
Query	601	AGGGAGAGAACTGGGCTACTCTTCAGCAGTGATCTTTAAAATGCC	645
Sbjct	601	AGGGAGAGAACTGGGCTACTCTTCAGCAGTGATCTTTAAAATGCC	645

Sequence 747 matched with Sequence 316

Query= Sequence ID 747
Length=542

SEQ ID NO: 316

ALIGNMENTS

Identities = 542/542 (100%), Gaps = 0/542 (0%)

Query	1	CAGAGTGCAAGACGATGACTTGCAAAATGTCGCAGCTGGAACGCAACATAGAGACCATCA	60
Sbjct	1	CAGAGTGCAAGACGATGACTTGCAAAATGTCGCAGCTGGAACGCAACATAGAGACCATCA	60
Query	61	TCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAACCAGGGGG	120
Sbjct	61	TCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAACCAGGGGG	120
Query	121	AATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGGAGAATAAGAATG	180
Sbjct	121	AATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGGAGAATAAGAATG	180
Query	181	AAAAGGTCATAGAACACATCATGGAGGACCTGGACACAAATGCAGACAAGCAGCTGAGCT	240
Sbjct	181	AAAAGGTCATAGAACACATCATGGAGGACCTGGACACAAATGCAGACAAGCAGCTGAGCT	240
Query	241	TCGAGGAGTTCATCATGCTGATGGCGAGGCTAACCTGGGCCTCCACGAGAAGATGCACG	300
Sbjct	241	TCGAGGAGTTCATCATGCTGATGGCGAGGCTAACCTGGGCCTCCACGAGAAGATGCACG	300
Query	301	AGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAGGCCTCGGGGAGGGCACCCCCTAAG	360
Sbjct	301	AGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAGGCCTCGGGGAGGGCACCCCCTAAG	360
Query	361	ACCACAGTGGCCAAGATCACAGTGGCCACGGCCACGGCCACAGTCATGGTGGCCACGGCC	420
Sbjct	361	ACCACAGTGGCCAAGATCACAGTGGCCACGGCCACGGCCACAGTCATGGTGGCCACGGCC	420
Query	421	ACAGCCACTAATCAGGAGGCCAGGCCACCCTGCCTCTACCCAACCAGGGCCCCGGGGCCT	480
Sbjct	421	ACAGCCACTAATCAGGAGGCCAGGCCACCCTGCCTCTACCCAACCAGGGCCCCGGGGCCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GTTATGTCAAAC	GTCTTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAAGTCTCTTTCC	540
Sbjct	481	GTTATGTCAAAC	GTCTTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAAGTCTCTTTCC	540
Query	541	TC	542	
Sbjct	541	TC	542	

Sequence 757 matched with Sequence 317

Query= Sequence ID - 757
Length=583

nt: 583

SEQ ID NO: 317

nt: 583

ALIGNMENTS

Identities = 583/583 (100%), Gaps = 0/583 (0%)

Query	1	GAACCCTGCGGAGGGACTTCAATCACATCAATGTAGAACTCAGCCTTCTTGAAAGaaaa	60
Sbjct	1	GAACCCTGCGGAGGGACTTCAATCACATCAATGTAGAACTCAGCCTTCTTGAAAGAAAA	60
Query	61	aaaaGAGGCTCCGGGTTGACAAATGGTGGGGTAACAGAAAGGAACTGGCTACCGTTCGGA	120
Sbjct	61	AAAAGAGGCTCCGGGTTGACAAATGGTGGGGTAACAGAAAGGAACTGGCTACCGTTCGGA	120
Query	121	CTATTTGTAGTCATGTACAGAACATGATCAAGGGTGTTTACTGGGCTTCCGTTACAAGA	180
Sbjct	121	CTATTTGTAGTCATGTACAGAACATGATCAAGGGTGTTTACTGGGCTTCCGTTACAAGA	180
Query	181	TGAGGTCTGTGTATGCTCACTTCCCCATCAACGTTGTTATCCAGGAGAATGGGTCTCTTG	240
Sbjct	181	TGAGGTCTGTGTATGCTCACTTCCCCATCAACGTTGTTATCCAGGAGAATGGGTCTCTTG	240
Query	241	TTGAAATCCGAAATTTCTTGGGTGAAAAATACATCCGCAGGGTTCGGATGAGACCAGGTG	300
Sbjct	241	TTGAAATCCGAAATTTCTTGGGTGAAAAATACATCCGCAGGGTTCGGATGAGACCAGGTG	300
Query	301	TTGCTTGTTTCAAGTATCTCAAGCCCAGAAAGATGAATTAATCCTTGAAGGAAATGACATTG	360
Sbjct	301	TTGCTTGTTTCAAGTATCTCAAGCCCAGAAAGATGAATTAATCCTTGAAGGAAATGACATTG	360
Query	361	AGCTTGTTTCAAATTCAGCGGCTTTGATTCAGCAAGCCACAACAGTTAAAAACAAGGATA	420
Sbjct	361	AGCTTGTTTCAAATTCAGCGGCTTTGATTCAGCAAGCCACAACAGTTAAAAACAAGGATA	420
Query	421	TCAGGAAATTTTGGATGGTATCTATGTCTCTGAAAAAGGAACTGTTTTCAGCAGGCTGATG	480
Sbjct	421	TCAGGAAATTTTGGATGGTATCTATGTCTCTGAAAAAGGAACTGTTTTCAGCAGGCTGATG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AATAAGATCTAAGAGTTACCTGGCTACAGAAAGAAGATGCCAGATGACACTTAAGACCTA  540
          |||
Sbjct  481  AATAAGATCTAAGAGTTACCTGGCTACAGAAAGAAGATGCCAGATGACACTTAAGACCTA  540

Query  541  CTTGTGATATTTAAATGATGCAATAAAAGACCTATTGATTTGG  583
          |||
Sbjct  541  CTTGTGATATTTAAATGATGCAATAAAAGACCTATTGATTTGG  583
```


Sequence 758 matched with Sequence 318

Query= Sequence ID - 758
Length=424

nt: 424

SEQ ID NO: 318

nt: 424

ALIGNMENTS

Identities = 424/424 (100%), Gaps = 0/424 (0%)

Query	1	CTTGGCTCCTGTGGAGGCCTGCTGGGAACGGGACTTCTAAAAGGAACTATGTCTGGAAGG	60
Sbjct	1	CTTGGCTCCTGTGGAGGCCTGCTGGGAACGGGACTTCTAAAAGGAACTATGTCTGGAAGG	60
Query	61	CTGTGGTCCAAGGCCATTTTTGCTGGCTATAAGCGGGGTCTCCGGAACCAAAGGGAGCAC	120
Sbjct	61	CTGTGGTCCAAGGCCATTTTTGCTGGCTATAAGCGGGGTCTCCGGAACCAAAGGGAGCAC	120
Query	121	ACAGCTCTTCTTAAAATTGAAGGTGTTTACGCCCAGATGAAACAGAATTCTATTTGGGC	180
Sbjct	121	ACAGCTCTTCTTAAAATTGAAGGTGTTTACGCCCAGATGAAACAGAATTCTATTTGGGC	180
Query	181	AAGAGATGCGCTTATGTATATAAAGCAAAGAACAACACAGTCACTCCTGGCGGCAAACCA	240
Sbjct	181	AAGAGATGCGCTTATGTATATAAAGCAAAGAACAACACAGTCACTCCTGGCGGCAAACCA	240
Query	241	AACAAAACCAGAGTCATCTGGGGAAAAGTAACTCGGGCCCATGGAAACAGTGGCATGGTT	300
Sbjct	241	AACAAAACCAGAGTCATCTGGGGAAAAGTAACTCGGGCCCATGGAAACAGTGGCATGGTT	300
Query	301	CGTGCCAAATTCCGAAGCAATCTTCTGCTAAGGCCATTGGACACAGAATCCGAGTGATG	360
Sbjct	301	CGTGCCAAATTCCGAAGCAATCTTCTGCTAAGGCCATTGGACACAGAATCCGAGTGATG	360
Query	361	CTGTACCCCTCAAGGATTTAAACTAACGAAAAATCAATAAATAAATGTGGATTTGTGCTC	420
Sbjct	361	CTGTACCCCTCAAGGATTTAAACTAACGAAAAATCAATAAATAAATGTGGATTTGTGCTC	420
Query	421	TTGT 424	
Sbjct	421	TTGT 424	

Sequence 764 matched with Sequence 319

Query= Sequence ID - 764
Length=626

nt: 626

SEQ ID NO: 319

nt: 626

ALIGNMENTS

Identities = 626/626 (100%), Gaps = 0/626 (0%)

Query	1	GAttttttttttttttttttGAGATGGAGTCTTTCTCTGTGCGCCAGGCTGGAGTGCAGTGG	60
Sbjct	1	GATTTTTTTTTTTTTTTTGGAGATGGAGTCTTTCTCTGTGCGCCAGGCTGGAGTGCAGTGG	60
Query	61	TGAAATCTCGACTCACTGCAACCTCCGTCTCCTGGGTTCAAGCAATTCTCCTGCCTCAGC	120
Sbjct	61	TGAAATCTCGACTCACTGCAACCTCCGTCTCCTGGGTTCAAGCAATTCTCCTGCCTCAGC	120
Query	121	CTCCTGAGTAGCTGGGATTACAGGCACCAGCCACCACGCCCGGCTAATTTTTGTATTTTT	180
Sbjct	121	CTCCTGAGTAGCTGGGATTACAGGCACCAGCCACCACGCCCGGCTAATTTTTGTATTTTT	180
Query	181	AGTAGAGACAGGTTTTTCACCATGTTGGCTAGGCTGATTTTGAAGTCATGACCCCAAGTGA	240
Sbjct	181	AGTAGAGACAGGTTTTTCACCATGTTGGCTAGGCTGATTTTGAAGTCATGACCCCAAGTGA	240
Query	241	TCTGCCCCGCTCGGCCTCCCAAAGTGCTGGAATTACAGGTGTGAGCTACCACTCCCAGCC	300
Sbjct	241	TCTGCCCCGCTCGGCCTCCCAAAGTGCTGGAATTACAGGTGTGAGCTACCACTCCCAGCC	300
Query	301	AATGATTACATTTATAAGGTAAAATAACTTGTGCCAATCTGTACAAGTGAATTCAGATTT	360
Sbjct	301	AATGATTACATTTATAAGGTAAAATAACTTGTGCCAATCTGTACAAGTGAATTCAGATTT	360
Query	361	AAAATTTTAATTGTAAAAAGATATCCAGGTGATATTTCTCCCTGAATAATTTAGTTTCCT	420
Sbjct	361	AAAATTTTAATTGTAAAAAGATATCCAGGTGATATTTCTCCCTGAATAATTTAGTTTCCT	420
Query	421	TTTCTATTTCTTGATATAAAAGTACTCAGCATTGAAGTAATTGCTATCTTCACATTTCTT	480
Sbjct	421	TTTCTATTTCTTGATATAAAAGTACTCAGCATTGAAGTAATTGCTATCTTCACATTTCTT	480

Query	481	CCTATTTGAGCTGTCTAAATAAGTAGTCCTACATATTTTCCCCCAACACAAAAAACCCA	540
Sbjct	481	CCTATTTGAGCTGTCTAAATAAGTAGTCCTACATATTTTCCCCCAACACAAAAAACCCA	540
Query	541	GAAAAGAATTATTTTATACTGGAtttttttGGTTGTAGCAGGAACCTAAAGGNGCCAATT	600
Sbjct	541	GAAAAGAATTATTTTATACTGGATTTTTTTGGTTGTAGCAGGAACCTAAAGGNGCCAATT	600
Query	601	GTAACATGCATGTTCTTTTTGGCAAA	626
Sbjct	601	GTAACATGCATGTTCTTTTTGGCAAA	626

Sequence 766 matched with Sequence 320

Query= Sequence ID 766

Length=618

SEQ ID NO: 320

ALIGNMENTS

Identities = 618/618 (100%), Gaps = 0/618 (0%)

Query	1	GTCCATCCTGCAGGCCACAAGCTCTGGATGAGGAACTTGAGGCAAGTCACCAGCCCCTGA	60
Sbjct	1	GTCCATCCTGCAGGCCACAAGCTCTGGATGAGGAACTTGAGGCAAGTCACCAGCCCCTGA	60
Query	61	TCATTTTCGCCTAAAAGAGCAAGGACTAGAGTTCCTGACCTCCAGGCCAGTCCCTGATCCC	120
Sbjct	61	TCATTTTCGCCTAAAAGAGCAAGGACTAGAGTTCCTGACCTCCAGGCCAGTCCCTGATCCC	120
Query	121	TGACCTAATGTTATCGCGGAATGATGATATATGTATCTACGGGGGCCTGGGGCTGGGCGG	180
Sbjct	121	TGACCTAATGTTATCGCGGAATGATGATATATGTATCTACGGGGGCCTGGGGCTGGGCGG	180
Query	181	GCTCCTGCTTCTGGCAGTGGTCCTTCTGTCCGCCTGCCTGTGTTGGCTGCATCGAAGAGT	240
Sbjct	181	GCTCCTGCTTCTGGCAGTGGTCCTTCTGTCCGCCTGCCTGTGTTGGCTGCATCGAAGAGT	240
Query	241	AAAGAGGCTGGAGAGGAGCTGGGCCCAGGGCTCCTCAGAGCAGGAACTCCACTATGCATC	300
Sbjct	241	AAAGAGGCTGGAGAGGAGCTGGGCCCAGGGCTCCTCAGAGCAGGAACTCCACTATGCATC	300
Query	301	TCTGCAGAGGCTGCCAGTGCCCAGCAGTGAGGGACCTGACCTCAGGGGCAGAGACAAGAG	360
Sbjct	301	TCTGCAGAGGCTGCCAGTGCCCAGCAGTGAGGGACCTGACCTCAGGGGCAGAGACAAGAG	360
Query	361	AGGCACCAAGGAGGATCCAAGAGCTGACTATGCCTGCATTGCTGAGAACAAACCCACCTG	420
Sbjct	361	AGGCACCAAGGAGGATCCAAGAGCTGACTATGCCTGCATTGCTGAGAACAAACCCACCTG	420
Query	421	AGCACCCCAGACACCTTCCTCAACCCAGGCGGGTGGACAGGGTCCCCCTGTGGTCCAGCC	480
Sbjct	421	AGCACCCCAGACACCTTCCTCAACCCAGGCGGGTGGACAGGGTCCCCCTGTGGTCCAGCC	480

Query	481	AGTAAAAACCATGGTCCCCCACTTCTGTGTCTCAGTCCTCTCAGTCATCTCGAGCCTCC	540
Sbjct	481	AGTAAAAACCATGGTCCCCCACTTCTGTGTCTCAGTCCTCTCAGTCATCTCGAGCCTCC	540
Query	541	GTTCAAAATGATCATCATCAAAACTTATGTGGCTTTTTGACCTTTGAATAGGGAAat	600
Sbjct	541	GTTCAAAATGATCATCATCAAAACTTATGTGGCTTTTTGACCTTTGAATAGGGAAATTTT	600
Query	601	taaaat	618
Sbjct	601	TAAAATTTT	618

Sequence 768 matched with Sequence 321

Query= Sequence ID 768

Length=596

SEQ ID NO: 321

ALIGNMENTS

Identities = 596/596 (100%), Gaps = 0/596 (0%)

Query	1	CCAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGttt	60
Sbjct	1	CCAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTT	60
Query	61	ttttCTCTTTGAAAGATAGAGATTAATACAACACTCTTAAAAAATATAGTCAATAGGTTAC	120
Sbjct	61	TTTTCTCTTTGAAAGATAGAGATTAATACAACACTCTTAAAAAATATAGTCAATAGGTTAC	120
Query	121	TAAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGA	180
Sbjct	121	TAAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGA	180
Query	181	AAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAAGGTTTCTAAAACAT	240
Sbjct	181	AAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAAGGTTTCTAAAACAT	240
Query	241	GACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAG	300
Sbjct	241	GACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAG	300
Query	301	AGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAA	360
Sbjct	301	AGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAA	360
Query	361	TGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAATAATTT	420
Sbjct	361	TGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAATAATTT	420
Query	421	GAAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATG	480
Sbjct	421	GAAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATG	480

Query	481	ACGCAGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAA	540
Sbjct	481	ACGCAGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAA	540
Query	541	ATGGAAGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTT	596
Sbjct	541	ATGGAAGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTT	596

Length=534

Identities = 534/534 (100%), Gaps = 0/534 (0%)

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PATENT SEQUENCE ALIGNMENT

Query	481	CCCTTAAAAACGTTTAAAAGAGTAAATTTTATGTTGNGTATATTTTACCATAAT	534
Sbjct	481	CCCTTAAAAACGTTTAAAAGAGTAAATTTTATGTTGNGTATATTTTACCATAAT	534

Sequence 776 matched with Sequence 323

Query= Sequence ID 776
Length=556

SEQ ID NO: 323

ALIGNMENTS

Identities = 556/556 (100%), Gaps = 0/556 (0%)

Query	1	tttttttttCATAAGAGGCAAGTACAAGAAAAAGCTTAATTACTTTAACTTCTAAGTAGT	60
Sbjct	1	TTTTTTTTTCATAAGAGGCAAGTACAAGAAAAAGCTTAATTACTTTAACTTCTAAGTAGT	60
Query	61	TTGGAATCTAAATAAATAGGAGTTACCAAATATATGCGCTTCTGTGAATAGTTTTCCCC	120
Sbjct	61	TTGGAATCTAAATAAATAGGAGTTACCAAATATATGCGCTTCTGTGAATAGTTTTCCCC	120
Query	121	ACATGTTTATTTATATTTTTGCATCTCATCAAACCTAACAGATTCTAAAGTCTCTGGTGA	180
Sbjct	121	ACATGTTTATTTATATTTTTGCATCTCATCAAACCTAACAGATTCTAAAGTCTCTGGTGA	180
Query	181	TAATGACAATATCTGCTACGGAGAGACTAGCCTGGGGGAAGAGGATCTCCCTGAACAAGG	240
Sbjct	181	TAATGACAATATCTGCTACGGAGAGACTAGCCTGGGGGAAGAGGATCTCCCTGAACAAGG	240
Query	241	ATAGCGGAGTTGCTGCAGCTTTCAAATGAAGCTGGACATTTAGCTGCGGGGGTAGCACCC	300
Sbjct	241	ATAGCGGAGTTGCTGCAGCTTTCAAATGAAGCTGGACATTTAGCTGCGGGGGTAGCACCC	300
Query	301	TTTGATCAAGGCAGCCCAAAGATGAGTTTCAGGGATGGGACTGACAGAAGAGAAAAGTTC	360
Sbjct	301	TTTGATCAAGGCAGCCCAAAGATGAGTTTCAGGGATGGGACTGACAGAAGAGAAAAGTTC	360
Query	361	TTCCCAGCCCTTTCTACTTTTTCTCTTTGTTTCTCAGGCTTCTGGCCGTCTTCAGTTTTC	420
Sbjct	361	TTCCCAGCCCTTTCTACTTTTTCTCTTTGTTTCTCAGGCTTCTGGCCGTCTTCAGTTTTC	420
Query	421	ACAAGTTTCACTCTCAACCCTAAACAGTACTTCTGTGAAGTACCCTTTGGCCCCTCGTTT	480
Sbjct	421	ACAAGTTTCACTCTCAACCCTAAACAGTACTTCTGTGAAGTACCCTTTGGCCCCTCGTTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TCAGCTCCTAAACTCACCTGGAAATAGATGTCAATCTAATTTTGGGTCTGACTAGTGCAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TCAGCTCCTAAACTCACCTGGAAATAGATGTCAATCTAATTTTGGGTCTGACTAGTGCAG  540

Query  541  TAGGCATTTTGGTGA  556
          ||||||||||||
Sbjct  541  TAGGCATTTTGGTGA  556
```

Sequence 782 matched with Sequence 324

Query= Sequence ID 782
Length=382

SEQ ID NO: 324

ALIGNMENTS

Identities = 382/382 (100%), Gaps = 0/382 (0%)

Query	1	CTCACACAGAACAAAAATGAATGAGTGTGGCTGTGTGCCACTATCACTGTGTCTACAAAA	60
Sbjct	1	CTCACACAGAACAAAAATGAATGAGTGTGGCTGTGTGCCACTATCACTGTGTCTACAAAA	60
Query	61	ACAGCCAGTGGGCCTGATTTGGCCCTTGGCTGCAGTGCGCCCGTCTCTGTTTTTGAGGAA	120
Sbjct	61	ACAGCCAGTGGGCCTGATTTGGCCCTTGGCTGCAGTGCGCCCGTCTCTGTTTTTGAGGAA	120
Query	121	TAAAATCGCATCATTTTCATATGGCTAATGCAAttttttCCCATCTGGAAGCAACATCTG	180
Sbjct	121	TAAAATCGCATCATTTTCATATGGCTAATGCAATTTTTTTCCCATCTGGAAGCAACATCTG	180
Query	181	ATTGGACTCATCTTGTATGGTGCTTGTTACAGTCTCTGTAAATGGGAGAGGGTCCGAGAA	240
Sbjct	181	ATTGGACTCATCTTGTATGGTGCTTGTTACAGTCTCTGTAAATGGGAGAGGGTCCGAGAA	240
Query	241	TAGCTCTTCCTGTTTTTCATCAGGACTGTTTTTAGGGATGGCAAAGAAGTCAGTGTGTCCA	300
Sbjct	241	TAGCTCTTCCTGTTTTTCATCAGGACTGTTTTTAGGGATGGCAAAGAAGTCAGTGTGTCCA	300
Query	301	GCCTGTGTCCTCCTCACCACGTGGCTGATTCCTGAATCTGCATGTGCANCACNTGCCGTT	360
Sbjct	301	GCCTGTGTCCTCCTCACCACGTGGCTGATTCCTGAATCTGCATGTGCANCACNTGCCGTT	360
Query	361	GTCTGGGGCATGATCTGTGTGA	382
Sbjct	361	GTCTGGGGCATGATCTGTGTGA	382

nt: 556

nt: 556

Identities = 556/556 (100%), Gaps = 0/556 (0%)

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PATENT SEQUENCE ALIGNMENT

```
Query  481  CCCACCCGCTTCAAAAATCATCATGGNGGNTTTAGCACCAATTTAGTAAACACAAACTGT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CCCACCCGCTTCAAAAATCATCATGGNGGNTTTAGCACCAATTTAGTAAACACAAACTGT  540

Query  541  CTGAAATATTTTGGAT  556
          |||||||||||||
Sbjct  541  CTGAAATATTTTGGAT  556
```

Sequence 796 matched with Sequence 326

Query= Sequence ID 796
Length=716

SEQ ID NO: 326

ALIGNMENTS

Identities = 716/716 (100%), Gaps = 0/716 (0%)

Query	1	GAACATTCAAGATAGTGAGAGGAAGAAAAAGATATGGCTGTACGGGACCGAGGTCTCTTC	60
Sbjct	1	GAACATTCAAGATAGTGAGAGGAAGAAAAAGATATGGCTGTACGGGACCGAGGTCTCTTC	60
Query	61	TATTATCGCCTCCTCTTAGTTGGCATTGATGAAGTTAAGCGGATTCTGTGTAGCCCTAAA	120
Sbjct	61	TATTATCGCCTCCTCTTAGTTGGCATTGATGAAGTTAAGCGGATTCTGTGTAGCCCTAAA	120
Query	121	TCTGACCCTACTCTTGGACTTTTGGAGGATCCGGCAGAAAGACCTGTGAATAGCTGGGCC	180
Sbjct	121	TCTGACCCTACTCTTGGACTTTTGGAGGATCCGGCAGAAAGACCTGTGAATAGCTGGGCC	180
Query	181	TCAGACTTCAACACACTGGTGCCAGTGTATGGCAAAGCCCACTGGGCAACTATCTCTAAA	240
Sbjct	181	TCAGACTTCAACACACTGGTGCCAGTGTATGGCAAAGCCCACTGGGCAACTATCTCTAAA	240
Query	241	TGCCAGGGGGCAGAGCGTTGTGACCCAGAGCTTCCTAAAACTTCATCCTTTGCCGCATCA	300
Sbjct	241	TGCCAGGGGGCAGAGCGTTGTGACCCAGAGCTTCCTAAAACTTCATCCTTTGCCGCATCA	300
Query	301	GGACCCTTGATTCTCTGAAGAGAACAAGGAGAGGGTACAAGAACTCCCTGATTCTGGAGCC	360
Sbjct	301	GGACCCTTGATTCTCTGAAGAGAACAAGGAGAGGGTACAAGAACTCCCTGATTCTGGAGCC	360
Query	361	CTCATGCTAGTCCCCAATCGCCAGCTTACTGCTGATTATTTTGAGAAAACCTTGGCTTAGC	420
Sbjct	361	CTCATGCTAGTCCCCAATCGCCAGCTTACTGCTGATTATTTTGAGAAAACCTTGGCTTAGC	420
Query	421	CTTAAAGTTGCTCATCAGCAAGTGTTCCTTGGCGGGGAGAATTCCATCCTGACACCCTC	480
Sbjct	421	CTTAAAGTTGCTCATCAGCAAGTGTTCCTTGGCGGGGAGAATTCCATCCTGACACCCTC	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 CAGATGGCTCTTCAAGTAGTGAACATCCAGACCATCGCAATGAGTAGGGCTGGGTCTCGG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 CAGATGGCTCTTCAAGTAGTGAACATCCAGACCATCGCAATGAGTAGGGCTGGGTCTCGG 540

Query 541 CCATGGAAAGCATACCTCAGTGCTCANGATGATACTGGCTGTCTGTTCTTAACAGAACTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 CCATGGAAAGCATACCTCAGTGCTCANGATGATACTGGCTGTCTGTTCTTAACAGAACTG 600

Query 601 CTATTGGAGCCTGGAAACTCAGAATGCAGATCTTTTGTGAACAAAATGAAGCAAGAACCG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 CTATTGGAGCCTGGAAACTCAGAATGCAGATCTTTTGTGAACAAAATGAAGCAAGAACCG 660

Query 661 GAGACNCTGAATAGTTTTATTTCTGTATTAAAAACTGNGATTGGAACAATTGAAGA 716
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 661 GAGACNCTGAATAGTTTTATTTCTGTATTAAAAACTGNGATTGGAACAATTGAAGA 716
```

Sequence 801 matched with Sequence 327

Query= Sequence ID 801
Length=664

SEQ ID NO: 327

ALIGNMENTS

Identities = 664/664 (100%), Gaps = 0/664 (0%)

Query	1	CCACTCCACCTTACTACCAGACAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGC	60
Sbjct	1	CCACTCCACCTTACTACCAGACAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGC	60
Query	61	GATAGAAATTGAAACCTGGCGCAATAGATATAGTACCGCAAGGGAAAGATGAAAAATTAT	120
Sbjct	61	GATAGAAATTGAAACCTGGCGCAATAGATATAGTACCGCAAGGGAAAGATGAAAAATTAT	120
Query	121	AACCAAGCATAATATAGCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAAGTAGA	180
Sbjct	121	AACCAAGCATAATATAGCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAAGTAGA	180
Query	181	AATGAGGATTCTGACCTTGACTTTGATATCAGCAAATTGGAACAGCAGAGCAAGGTGCAA	240
Sbjct	181	AATGAGGATTCTGACCTTGACTTTGATATCAGCAAATTGGAACAGCAGAGCAAGGTGCAA	240
Query	241	AACACAGGACATGGAACCAAGAGAAAAGTCCATAATAGACGAGAAATTCTTCCAACTC	300
Sbjct	241	AACACAGGACATGGAACCAAGAGAAAAGTCCATAATAGACGAGAAATTCTTCCAACTC	300
Query	301	TCTGAAATGGAGGCTTATTTAGAAAACAGAGAAAAGAAGAGGAACGAAAAGATGATAAT	360
Sbjct	301	TCTGAAATGGAGGCTTATTTAGAAAACAGAGAAAAGAAGAGGAACGAAAAGATGATAAT	360
Query	361	GATGATGAGTCAGGTAAAAGTTCCAGAAATGTGAACAACAAAGAtttttttGATCCAGTT	420
Sbjct	361	GATGATGAGTCAGGTAAAAGTTCCAGAAATGTGAACAACAAAGATTTTTTTGATCCAGTT	420
Query	421	GAAAGTGATGAAGACATAGCAAGTGATCATGATGATGAGCTGGGTTCAAACAAGATGATG	480
Sbjct	421	GAAAGTGATGAAGACATAGCAAGTGATCATGATGATGAGCTGGGTTCAAACAAGATGATG	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 AAATTGCTGAAGAAGAAGCAGAAGAAGGAAGCATTCTGAAATATGAATGaaaaaaTTA 540
          |||
Sbjct 481 AAATTGCTGAAGAAGAAGCAGAAGAAGGAAGCATTCTGAAATATGAATGAAAAAATTA 540

Query 541 CATCTTTAGAAAAAGAGTTATTAGAAAAAAGCCTTGGCAGCCGTCNGGGGAAGTGACGC 600
          |||
Sbjct 541 CATCTTTAGAAAAAGAGTTATTAGAAAAAAGCCTTGGCAGCCGTCNGGGGAAGTGACGC 600

Query 601 ACAGAAGAGACCAGAGAATAGCTTCCTGGANGAGACCCTGCACTTTACCCATGCTGCTGG 660
          |||
Sbjct 601 ACAGAAGAGACCAGAGAATAGCTTCCTGGANGAGACCCTGCACTTTACCCATGCTGCTGG 660

Query 661 ATGG 664
          |||
Sbjct 661 ATGG 664
```

Sequence 808 matched with Sequence 328

Query= Sequence ID - 808
Length=641

nt: 641

SEQ ID NO: 328

nt: 641

ALIGNMENTS

Identities = 641/641 (100%), Gaps = 0/641 (0%)

Query	1	CCGGGTTTTAGTATTTAACCAAGAGCCTTTTAAATATTGAAAACCCATAGTTCAGAAAAT	60
Sbjct	1	CCGGGTTTTAGTATTTAACCAAGAGCCTTTTAAATATTGAAAACCCATAGTTCAGAAAAT	60
Query	61	GTTAGTATTGCTGCCCTTCTTCACATAAAAttttttttAAATTATACTATTATTTTGCTT	120
Sbjct	61	GTTAGTATTGCTGCCCTTCTTCACATAAAATTTTTTTTAAATTATACTATTATTTTGCTT	120
Query	121	AATTTTATATTGGGTAAAAACAACCTTCAAGAAGGTAACTAGGAAAGAAGACCTtttttg	180
Sbjct	121	AATTTTATATTGGGTAAAAACAACCTTCAAGAAGGTAACTAGGAAAGAAGACCTTTTTTG	180
Query	181	ttttatttttACTATTTATATATAGAAGACAAATCAGCATTTGGTGATAGTTTTACATGA	240
Sbjct	181	TTTTATTTTACTATTTATATATAGAAGACAAATCAGCATTTGGTGATAGTTTTACATGA	240
Query	241	CCAGTTATCAAACGGTCATAGTATGAAGTGTGCAGTTGTTTCATTATTAGTAAATTATGTT	300
Sbjct	241	CCAGTTATCAAACGGTCATAGTATGAAGTGTGCAGTTGTTTCATTATTAGTAAATTATGTT	300
Query	301	TGATTTTTAAACTATTTAGTACTAATAGTTGAGATGAAAACCTGAAGAAAAATGCCAATGT	360
Sbjct	301	TGATTTTTAAACTATTTAGTACTAATAGTTGAGATGAAAACCTGAAGAAAAATGCCAATGT	360
Query	361	GACGTTTGTGTATAGCTAGCCTTAAAAAACTTCCCATGTTTTTAGGTGACTTTTTTCCCC	420
Sbjct	361	GACGTTTGTGTATAGCTAGCCTTAAAAAACTTCCCATGTTTTTAGGTGACTTTTTTCCCC	420
Query	421	CTCTTAGTACTCTGGAGAAACAATGAAGATGGGCCATCTCAATTCCAGATGTAAACAAAA	480
Sbjct	421	CTCTTAGTACTCTGGAGAAACAATGAAGATGGGCCATCTCAATTCCAGATGTAAACAAAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGTAATTTTATTTC AACATTTAATGTA ACTGCTATTATTGNGGATTCTTGNCTTGNGTA  540
          |||
Sbjct  481  AGTAATTTTATTTC AACATTTAATGTA ACTGCTATTATTGNGGATTCTTGNCTTGNGTA  540

Query  541  TTTTCTTTCCCTTATTCAAGTAATATAGAATAACTTTCCTTAAAATGATTTGATCCAAGA  600
          |||
Sbjct  541  TTTTCTTTCCCTTATTCAAGTAATATAGAATAACTTTCCTTAAAATGATTTGATCCAAGA  600

Query  601  TACGTCATTTCTGTATTGGCAAAATGCCNCTATTAAAGTGT  641
          |||
Sbjct  601  TACGTCATTTCTGTATTGGCAAAATGCCNCTATTAAAGTGT  641
```

Sequence 814 matched with Sequence 329

Query= Sequence ID - 814 nt: 132
Length=132

SEQ ID NO: 329 nt: 132

ALIGNMENTS

Identities = 132/132 (100%), Gaps = 0/132 (0%)

```
Query 1 GTTAAAGTGATACATTTTTATACCAAATGTGTTTAttttttGTGCAAGTAATCCTTAAA 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GTTAAAGTGATACATTTTTATACCAAATGTGTTTATTTTTTTGTGCAAGTAATCCTTAAA 60

Query 61 ATTGCAATTGTATTAGGTGTtaaaataaagtttttaaaaaattaaaaaaaaaaaaaaaaa 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 ATTGCAATTGTATTAGGTGTTAAAATAAAGTTTTTAAAAATTAAAAAAAAAAAAAAAAAAA 120

Query 121 aaaaaaaaaaaaa 132
      |||||||||||
Sbjct 121 AAAAAAAAAAAAA 132
```

Sequence 817 matched with Sequence 330

Query= Sequence ID 817

Length=666

SEQ ID NO: 330

ALIGNMENTS

Identities = 666/666 (100%), Gaps = 0/666 (0%)

Query	1	GACAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGCGATAGAAATTGAAACCTGG	60
Sbjct	1	GACAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGCGATAGAAATTGAAACCTGG	60
Query	61	CGCAATAGATATAGTACCGTAAGGGAAAGATGAAAAATTATAACCAAGCATAATATAGCA	120
Sbjct	61	CGCAATAGATATAGTACCGTAAGGGAAAGATGAAAAATTATAACCAAGCATAATATAGCA	120
Query	121	AGGACTAACCCCTATACCTTCTGCATAATGAATTAAGTAACTAGAAATAACTTTGCAAGGAGAG	180
Sbjct	121	AGGACTAACCCCTATACCTTCTGCATAATGAATTAAGTAACTAGAAATAACTTTGCAAGGAGAG	180
Query	181	CCAAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCC	240
Sbjct	181	CCAAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCC	240
Query	241	GTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTG	300
Sbjct	241	GTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTG	300
Query	301	GTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAACCC	360
Sbjct	301	GTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAACCC	360
Query	361	TCTAAATCCCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAG	420
Sbjct	361	TCTAAATCCCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAG	420
Query	421	GAAAAAACCTTGTAGAGAGAGTAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCA	480
Sbjct	421	GAAAAAACCTTGTAGAGAGAGTAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTaaaaaaaTCCCAAACATATAAC	540
Sbjct	481	CCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATAAC	540
Query	541	TGAACTCCTCACACCCAATTGGACCAATCTATCACCTATAGAAGACTAATGTTAGTATA	600
Sbjct	541	TGAACTCCTCACACCCAATTGGACCAATCTATCACCTATAGAAGACTAATGTTAGTATA	600
Query	601	AGTAACATGAAAACATTCTTCTNCGCATAAGCCTGCGTCAGATTA AAAACACTGAACTGAC	660
Sbjct	601	AGTAACATGAAAACATTCTTCTNCGCATAAGCCTGCGTCAGATTA AAAACACTGAACTGAC	660
Query	661	AATTAA 666	
Sbjct	661	AATTAA 666	

Sequence 821 matched with Sequence 331

Query= Sequence ID - 821
Length=370

nt: 370

SEQ ID NO: 331

nt: 370

ALIGNMENTS

Identities = 370/370 (100%), Gaps = 0/370 (0%)

Query	1	AAAGAGCTCCCAAATGCTATATCTATT	CAGGGGCTCTCAAGAACAATGGAATATCATCCT	60
Sbjct	1	AAAGAGCTCCCAAATGCTATATCTATT	CAGGGGCTCTCAAGAACAATGGAATATCATCCT	60
Query	61	GATTTANAAAAATTTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAAT	120	
Sbjct	61	GATTTANAAAAATTTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAAT	120	
Query	121	ACCAGGATAGCTGTTGTTTCANAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTC	180	
Sbjct	121	ACCAGGATAGCTGTTGTTTCANAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTC	180	
Query	181	ATTGCTGTAATTTTGGGAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGT	240	
Sbjct	181	ATTGCTGTAATTTTGGGAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGT	240	
Query	241	ACCATGGCTGGTTTCAAAGCTGTGGAATTCAAAGGATAAATTAATGAAGAAAACAAGCGG	300	
Sbjct	241	ACCATGGCTGGTTTCAAAGCTGTGGAATTCAAAGGATAAATTAATGAAGAAAACAAGCGG	300	
Query	301	AGCTGAAGAAGAAAGTACAATATGGTGCTGTCTTCCTAATGAAATAAATTCACTAAATGG	360	
Sbjct	301	AGCTGAAGAAGAAAGTACAATATGGTGCTGTCTTCCTAATGAAATAAATTCACTAAATGG	360	
Query	361	ACATTAAAAA	370	
Sbjct	361	ACATTAAAAA	370	

Sequence 825 matched with Sequence 332

Query= Sequence ID 825

Length=741

SEQ ID NO: 332

ALIGNMENTS

Identities = 735/735 (100%), Gaps = 0/735 (0%)

Query	1	AGACTCGAGCAAGCTTATGCATGCATGCGGCCGCAATTCGAGCTCGGCCACTTGGCCAAT	60
Sbjct	1	AGACTCGAGCAAGCTTATGCATGCATGCGGCCGCAATTCGAGCTCGGCCACTTGGCCAAT	60
Query	61	TCGCCCTATAGTGAGTCGTATTACAATTCAGTGGCCGTCGTTTTACAACGTCGTGACTGG	120
Sbjct	61	TCGCCCTATAGTGAGTCGTATTACAATTCAGTGGCCGTCGTTTTACAACGTCGTGACTGG	120
Query	121	GAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGG	180
Sbjct	121	GAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGG	180
Query	181	CGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGC	240
Sbjct	181	CGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGC	240
Query	241	GAATGGAAATTGTAAGCGTTAATATTTTGTAAAAATTCGCGTTAAATTTTGTAAATCA	300
Sbjct	241	GAATGGAAATTGTAAGCGTTAATATTTTGTAAAAATTCGCGTTAAATTTTGTAAATCA	300
Query	301	GCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGA	360
Sbjct	301	GCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGA	360
Query	361	CCGAGATAGGGTTGAGTGTTGTTCCAGTTTGAACAAGAGTCCACTATTAAAGAACGTGG	420
Sbjct	361	CCGAGATAGGGTTGAGTGTTGTTCCAGTTTGAACAAGAGTCCACTATTAAAGAACGTGG	420
Query	421	ACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCAT	480
Sbjct	421	ACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCAT	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 CACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 CACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAG 540

Query 541 GGAGCCCCCGATTTAAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 GGAGCCCCCGATTTAAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGA 600

Query 601 AAAAAGCCAAAANGGAGCCGGCGCTAGGGCCTGGCAAGTGTACGGGCACGCTGCGCGTAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 AAAAAGCCAAAANGGAGCCGGCGCTAGGGCCTGGCAAGTGTACGGGCACGCTGCGCGTAAC 660

Query 661 CACCCACACCCCGCCGNGCTTAATGCCCCNTTCAGGGCGCGTNCTGATGCCGNATTTTNT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 661 CACCCACACCCCGCCGNGCTTAATGCCCCNTTCAGGGCGCGTNCTGATGCCGNATTTTNT 720

Query 721 CTTACNCATNTGTGC 735
          ||||||||||||||
Sbjct 721 CTTACNCATNTGTGC 735
```

Sequence 833 matched with Sequence 333

Query= Sequence ID 833

Length=719

SEQ ID NO: 333

ALIGNMENTS

Identities = 719/719 (100%), Gaps = 0/719 (0%)

Query	1	TAAATAATGGCaaaaaacaacaaaaaaCAAGTTCTCTAAACAGAAAGGAAATTACTAA	60
Sbjct	1	TAAATAATGGCAAAAAACAAACAAAAACAAGTTCTCTAAACAGAAAGGAAATTACTAA	60
Query	61	AGAAGGAATCTTGAAATAACAGGAAAGAGGAAATACCACAGTAGGCAACATTATGGGTAA	120
Sbjct	61	AGAAGGAATCTTGAAATAACAGGAAAGAGGAAATACCACAGTAGGCAACATTATGGGTAA	120
Query	121	ATAAACAGACTTTCCTTCTTTAGTTTCCTAAATATGTTTGATGATTAATGCAAAAATT	180
Sbjct	121	ATAAACAGACTTTCCTTCTTTAGTTTCCTAAATATGTTTGATGATTAATGCAAAAATT	180
Query	181	ACAATATTTTCTTATGTAGCACTAAAGGTATGTAGAGAAAATATTTAAGATAATTGTACT	240
Sbjct	181	ACAATATTTTCTTATGTAGCACTAAAGGTATGTAGAGAAAATATTTAAGATAATTGTACT	240
Query	241	GTAAGCGGGAGATGACAGTGACATAAAGGCAACGTTTTTATACTTCACTCAAACCTTTATG	300
Sbjct	241	GTAAGCGGGAGATGACAGTGACATAAAGGCAACGTTTTTATACTTCACTCAAACCTTTATG	300
Query	301	TATTAATGTAATCCATAAAGCAACCAAAAAAGCTATACTAAGTACATTCAAAAACACAAT	360
Sbjct	301	TATTAATGTAATCCATAAAGCAACCAAAAAAGCTATACTAAGTACATTCAAAAACACAAT	360
Query	361	AGATAAACCAAACAAAATTCTAAAGGATGTACAAGTAACCCACTGGAAGCTGCaaaaaat	420
Sbjct	361	AGATAAACCAAACAAAATTCTAAAGGATGTACAAGTAACCCACTGGAAGCTGCAAAAAAT	420
Query	421	gtaaacagaaactaaaaacagagaataaatgaaaaattaaaaacgaaatGGCAGACTTAG	480
Sbjct	421	GTAAACAGAACTAAAAACAGAGAATAAATGAAAAATTAAAAACGAAATGGCAGACTTAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCCCTAATATACAAATTATCACATTAAATATAAATGGTCTAAATACACCAACTGTAAGAC	540
Sbjct	481	GCCCTAATATACAAATTATCACATTAAATATAAATGGTCTAAATACACCAACTGTAAGAC	540
Query	541	AGAGATTAGCAAAGTCGATTTAAAAACATGACTCAACTACGTGCTGTCTACAAGAACTC	600
Sbjct	541	AGAGATTAGCAAAGTCGATTTAAAAACATGACTCAACTACGTGCTGTCTACAAGAACTC	600
Query	601	ACTTCAAATATACCAAGATAGGAAGGTTGAAAGTAAAACGATGGAAAAAGATGTATCATG	660
Sbjct	601	ACTTCAAATATACCAAGATAGGAAGGTTGAAAGTAAAACGATGGAAAAAGATGTATCATG	660
Query	661	TGAACATTAATCAAAGGAAAGCAGGGGTGGCTATATTAACATCAGGTAAAATAAACTTT	719
Sbjct	661	TGAACATTAATCAAAGGAAAGCAGGGGTGGCTATATTAACATCAGGTAAAATAAACTTT	719

Sequence 837 matched with Sequence 334

Query= Sequence ID - 837
Length=603

nt: 603

SEQ ID NO: 334

nt: 603

ALIGNMENTS

Identities = 603/603 (100%), Gaps = 0/603 (0%)

Query	1	TGAGGNTGGTCATGATGCANAAGCTACTCAAATGCAGTCGGCTTGTCTGGCTCTTGCCC	60
Sbjct	1	TGAGGNTGGTCATGATGCANAAGCTACTCAAATGCAGTCGGCTTGTCTGGCTCTTGCCC	60
Query	61	TCATCCTGGTTCTGGAATCCTCAGTTCAAGGTTATCCTACGCGGAGAGCCAGGTACCAAT	120
Sbjct	61	TCATCCTGGTTCTGGAATCCTCAGTTCAAGGTTATCCTACGCGGAGAGCCAGGTACCAAT	120
Query	121	GGGTGCGCTGCAATCCAGACAGTAATTCTGCAAACCTGCCTTGAAGAAAAAGGACCAATGT	180
Sbjct	121	GGGTGCGCTGCAATCCAGACAGTAATTCTGCAAACCTGCCTTGAAGAAAAAGGACCAATGT	180
Query	181	TCGAACTACTTCCAGGTGAATCCAACAAGATCCCCCGTCTGAGGACTGACCTTTTTTCCAA	240
Sbjct	181	TCGAACTACTTCCAGGTGAATCCAACAAGATCCCCCGTCTGAGGACTGACCTTTTTTCCAA	240
Query	241	AGACGAGAATCCAGGACTTGAATCGTATCTTCCCACTTTCTGAGGACTACTCTGGATCAG	300
Sbjct	241	AGACGAGAATCCAGGACTTGAATCGTATCTTCCCACTTTCTGAGGACTACTCTGGATCAG	300
Query	301	GCTTCGGCTCCGGCTCCGGCTCTGGATCAGGATCTGGGAGTGGCTTCCTAACGGAAATGG	360
Sbjct	301	GCTTCGGCTCCGGCTCCGGCTCTGGATCAGGATCTGGGAGTGGCTTCCTAACGGAAATGG	360
Query	361	AACAGGATTACCAACTAGTAGACGAAAGTGATGCTTTCATGACAACCTTAGGTCTCTTG	420
Sbjct	361	AACAGGATTACCAACTAGTAGACGAAAGTGATGCTTTCATGACAACCTTAGGTCTCTTG	420
Query	421	ACAGGAATCTGCCCTCAGACAGCCAGGACTTGGGTCAACATGGATTAGAAGAGGATTTTA	480
Sbjct	421	ACAGGAATCTGCCCTCAGACAGCCAGGACTTGGGTCAACATGGATTAGAAGAGGATTTTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TGTTATAAAAGAGGATTTTCCCACCTTGACACCAGGCAATGTAGTTAGCATATTTTATGT	540
Sbjct	481	TGTTATAAAAGAGGATTTTCCCACCTTGACACCAGGCAATGTAGTTAGCATATTTTATGT	540
Query	541	ACCATGGNTATATGATTAATCTTGGGACAAAGAATTTTATAGAAATTTTAAACATCTGA	600
Sbjct	541	ACCATGGNTATATGATTAATCTTGGGACAAAGAATTTTATAGAAATTTTAAACATCTGA	600
Query	601	AAA	603
Sbjct	601	AAA	603

Sequence 839 matched with Sequence 335

Query= Sequence ID - 839 nt: 71
Length=71

SEQ ID NO: 335 nt: 71

ALIGNMENTS

Identities = 71/71 (100%), Gaps = 0/71 (0%)

```
Query 1  ATTTATCTAATATTTGGTTTAATAAAATGTGAATAATGaaaaaaaaaaaaaaaaaaaaa 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  ATTTATCTAATATTTGGTTTAATAAAATGTGAATAATGAAAAAAAAAAAAAAAAAAAAA 60

Query 61  aaaaaaaaaa 71
          |||||||||
Sbjct 61  AAAAAAAAAA 71
```


Sequence 849 matched with Sequence 336

Query= Sequence ID - 849
Length=622

nt: 622

SEQ ID NO: 336

nt: 622

ALIGNMENTS

Identities = 622/622 (100%), Gaps = 0/622 (0%)

Query	1	ttttttttttattttttGAGAATGGAGTCTTGCTCTGCCGTCCAGGCTAGAGTTCAGTGGT	60
Sbjct	1	TTTTTTTTTATTTTTTGAGAATGGAGTCTTGCTCTGCCGTCCAGGCTAGAGTTCAGTGGT	60
Query	61	GCGATCTCAGCTCACTGCCACCTCACCTCCTAGGTTCCAGAGATTCTTGCTTCAGCCT	120
Sbjct	61	GCGATCTCAGCTCACTGCCACCTCACCTCCTAGGTTCCAGAGATTCTTGCTTCAGCCT	120
Query	121	CCTCAGTAGTTGAGAATACAGGAACACGCCACCACGCCTAGCTAATTTTTGTATTTTTAG	180
Sbjct	121	CCTCAGTAGTTGAGAATACAGGAACACGCCACCACGCCTAGCTAATTTTTGTATTTTTAG	180
Query	181	TAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACCTCCTGGCCTAAGTGACCC	240
Sbjct	181	TAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACCTCCTGGCCTAAGTGACCC	240
Query	241	ACCTGCCTCAGCCTCCCAAAGTGCTGGGATTATAGGCGTGAGTCATTGTCCCCAGCCGGA	300
Sbjct	241	ACCTGCCTCAGCCTCCCAAAGTGCTGGGATTATAGGCGTGAGTCATTGTCCCCAGCCGGA	300
Query	301	TGTTTTTCATCTTGATTTGCCTTAGTTTCTAAATCTCATCCTCTCCATTTTCTCCTGTTAG	360
Sbjct	301	TGTTTTTCATCTTGATTTGCCTTAGTTTCTAAATCTCATCCTCTCCATTTTCTCCTGTTAG	360
Query	361	TAGTCACAGAGAACCAAATTCTGTCAAGTTATGAACTAAAGTCTCTCTTCCACAAGTCT	420
Sbjct	361	TAGTCACAGAGAACCAAATTCTGTCAAGTTATGAACTAAAGTCTCTCTTCCACAAGTCT	420
Query	421	TCCTGTGTTCTGCCTCAAGTGAAGTTGAAAGAACATCAGTTTGTGGGAAGGTTGAAGACC	480
Sbjct	421	TCCTGTGTTCTGCCTCAAGTGAAGTTGAAAGAACATCAGTTTGTGGGAAGGTTGAAGACC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GAATGATCTGCTGGGAAATCACTGAGGCATTGCCATTCTCTTGAGGAATTTCAATTTTCAT  540
          |||
Sbjct  481  GAATGATCTGCTGGGAAATCACTGAGGCATTGCCATTCTCTTGAGGAATTTCAATTTTCAT  540

Query  541  CGAAGTTTCGGTTTATATCCCTTTCTTGGTGAGTACTATTGCTGTTATGTAAATTAAATG  600
          |||
Sbjct  541  CGAAGTTTCGGTTTATATCCCTTTCTTGGTGAGTACTATTGCTGTTATGTAAATTAAATG  600

Query  601  AGTCGTCATCCTTCTTNTGAGC  622
          |||
Sbjct  601  AGTCGTCATCCTTCTTNTGAGC  622
```

Sequence 860 matched with Sequence 337

Query= Sequence ID - 860
Length=501

nt: 501

SEQ ID NO: 337

nt: 501

ALIGNMENTS

Identities = 501/501 (100%), Gaps = 0/501 (0%)

Query	1	GTGAAATCACTTTCATGGATTATTAATGGATTAAAGAGGGCATCAATCAGCTCAACTCAA	60
Sbjct	1	GTGAAATCACTTTCATGGATTATTAATGGATTAAAGAGGGCATCAATCAGCTCAACTCAA	60
Query	61	GATTTTCATAATCATTTTTTAGTATTTAGATTGTGCCTCAAAGTTGTAGTACCTCACAATAC	120
Sbjct	61	GATTTTCATAATCATTTTTTAGTATTTAGATTGTGCCTCAAAGTTGTAGTACCTCACAATAC	120
Query	121	CTCCACTGGTTTCCTGTTGTAAAAACCTTCAGTGAGTTTGACCATTGTGCTCTTGGCTCT	180
Sbjct	121	CTCCACTGGTTTCCTGTTGTAAAAACCTTCAGTGAGTTTGACCATTGTGCTCTTGGCTCT	180
Query	181	TGGGCTGGAGTACCGTGGTGAGGGAGTAAACACTAGAAAGTCTTTAGTACAAAAGTCTCT	240
Sbjct	181	TGGGCTGGAGTACCGTGGTGAGGGAGTAAACACTAGAAAGTCTTTAGTACAAAAGTCTCT	240
Query	241	AGGGACACCTGGTGATTTCCTACACAAGTGATGTTTATATTTCTCATAAAGAGTCTTCCCT	300
Sbjct	241	AGGGACACCTGGTGATTTCCTACACAAGTGATGTTTATATTTCTCATAAAGAGTCTTCCCT	300
Query	301	ATCCCAAGGTCTTCATGATGCCAGTAGCCATATATGATAAATTATGTTTCAGTGATAACTT	360
Sbjct	301	ATCCCAAGGTCTTCATGATGCCAGTAGCCATATATGATAAATTATGTTTCAGTGATAACTT	360
Query	361	AGTTATCAGAAATCAGCTCAGTGGTCTTCCCCGCCATGATTCACATTTGATGAGTTTTTA	420
Sbjct	361	AGTTATCAGAAATCAGCTCAGTGGTCTTCCCCGCCATGATTCACATTTGATGAGTTTTTA	420
Query	421	AAAATCAAAGTGATTTTGAAAATCTCTAATGGCTCAGAAAATAAAAAACATCCAGTTTGTG	480
Sbjct	421	AAAATCAAAGTGATTTTGAAAATCTCTAATGGCTCAGAAAATAAAAAACATCCAGTTTGTG	480

PATENT SEQUENCE ALIGNMENT

Query	481	GATGACTATATTTAGATTCT	501
Sbjct	481	GATGACTATATTTAGATTCT	501

Sequence 864 matched with Sequence 338

Query= Sequence ID 864
Length=630

SEQ ID NO: 338

ALIGNMENTS

Identities = 630/630 (100%), Gaps = 0/630 (0%)

Query	1	TTGTGTTTTTAGGACTCCTTATCTAAATTAAGGCAGAGAAGTTACAGTATTTATATCTGC	60
Sbjct	1	TTGTGTTTTTAGGACTCCTTATCTAAATTAAGGCAGAGAAGTTACAGTATTTATATCTGC	60
Query	61	ATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGAAACTATTG	120
Sbjct	61	ATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGAAACTATTG	120
Query	121	ATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATCATTTAATAGGAC	180
Sbjct	121	ATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATCATTTAATAGGAC	180
Query	181	ACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGGCTGTACTCTAAAATAA	240
Sbjct	181	ACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGGCTGTACTCTAAAATAA	240
Query	241	TATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTCAAATGCATACTAATATTTTC	300
Sbjct	241	TATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTCAAATGCATACTAATATTTTC	300
Query	301	AATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATCTACTTGTGATAGCCCTAAGAGCTG	360
Sbjct	301	AATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATCTACTTGTGATAGCCCTAAGAGCTG	360
Query	361	AGATAATTATTTCCAGGAGGTTGAATCCCTGATTCTTAACTGTTCAAGCAATGCATAAGCA	420
Sbjct	361	AGATAATTATTTCCAGGAGGTTGAATCCCTGATTCTTAACTGTTCAAGCAATGCATAAGCA	420
Query	421	AGAGAGAATATGACATAAGAGGACCATTCTACATTAGCCAAttttttttCACAAAGATACC	480
Sbjct	421	AGAGAGAATATGACATAAGAGGACCATTCTACATTAGCCATTTTTTTTCACAAAGATACC	480

Query	481	TATGTGAATACAGGGCACCTGGGAGGGTAAGTGGAGGACTATTTCTAACTATATTTATAA	540
Sbjct	481	TATGTGAATACAGGGCACCTGGGAGGGTAAGTGGAGGACTATTTCTAACTATATTTATAA	540
Query	541	GCACATACTGATATTGGTGAATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGA	600
Sbjct	541	GCACATACTGATATTGGTGAATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGA	600
Query	601	CAATGTGTAAGGAGATCAGGAATTCATTAG	630
Sbjct	601	CAATGTGTAAGGAGATCAGGAATTCATTAG	630

Sequence 865 matched with Sequence 339

Query= Sequence ID - 865 nt: 122
Length=122

SEQ ID NO: 339 nt: 122

ALIGNMENTS

Identities = 122/122 (100%), Gaps = 0/122 (0%)

Query	1	CCANAATCCACTCTCCAGTCTCCCTCCCCTGACTCCCTCTGCTGTCCTCCCCTCTCACGA	60
Sbjct	1	CCANAATCCACTCTCCAGTCTCCCTCCCCTGACTCCCTCTGCTGTCCTCCCCTCTCACGA	60
Query	61	GAATAAAGTGTCAAGCAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	120
Sbjct	61	GAATAAAGTGTCAAGCAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	120
Query	121	aa 122	
Sbjct	121	AA 122	

Sequence 867 matched with Sequence 340

Query= Sequence ID 867
Length=640

SEQ ID NO: 340

ALIGNMENTS

Identities = 640/640 (100%), Gaps = 0/640 (0%)

Query	1	ttttttttttttttttttttCAGAGTCACAGATATTGTATAGCTGAGGTAAGCATTTTACA	60
Sbjct	1	TTTTTTTTTTTTTTTTTTTTCAGAGTCACAGATATTGTATAGCTGAGGTAAGCATTTTACA	60
Query	61	ACTTTTCAGACACAAGTAAGTACATAAAATATTATTTTACAACCAACAATNTTTAATATTT	120
Sbjct	61	ACTTTTCAGACACAAGTAAGTACATAAAATATTATTTTACAACCAACAATNTTTAATATTT	120
Query	121	CCACATTGAANAATAGATGTGATAATTAAATCTTTTATAAGGTTTTAAAAAGACATGAAA	180
Sbjct	121	CCACATTGAANAATAGATGTGATAATTAAATCTTTTATAAGGTTTTAAAAAGACATGAAA	180
Query	181	CATAAACCTAATTATACATAAAAAGAAAAGAATTTTAAACAAGAGCTTATTGNGATGACAT	240
Sbjct	181	CATAAACCTAATTATACATAAAAAGAAAAGAATTTTAAACAAGAGCTTATTGNGATGACAT	240
Query	241	TACTCATAACTTTTACCTTTAAACCTTTTCTTGGGTAGCTATTCAAAAAGTAAAGACCAC	300
Sbjct	241	TACTCATAACTTTTACCTTTAAACCTTTTCTTGGGTAGCTATTCAAAAAGTAAAGACCAC	300
Query	301	AAGTTTGTGTTGCCCANATTTCTTATGTTTNGTATATTTAAGCTCTTTATTTATTGAACAG	360
Sbjct	301	AAGTTTGTGTTGCCCANATTTCTTATGTTTNGTATATTTAAGCTCTTTATTTATTGAACAG	360
Query	361	ATGNGTCATTAATTCATTNGGAGCATTACTATTATCAGTAAAATTTGAtttttttttCCC	420
Sbjct	361	ATGNGTCATTAATTCATTNGGAGCATTACTATTATCAGTAAAATTTGATTTTTTTTTCCC	420
Query	421	CTCAGTCATAGGTAAATCAGCTCCACCTGGAATTTCTAAGGACCCAGTTTATAGTCAATAT	480
Sbjct	421	CTCAGTCATAGGTAAATCAGCTCCACCTGGAATTTCTAAGGACCCAGTTTATAGTCAATAT	480

Query	481	TTTCAAGTAATCATGACCTCAGAAATAGTCTTAATTAAGATAACAAATATTAGCCATCAA	540
Sbjct	481	TTTCAAGTAATCATGACCTCAGAAATAGTCTTAATTAAGATAACAAATATTAGCCATCAA	540
Query	541	AATGGAACCAAGACAAGATTCTAATGTTTGTA AACAGTCAATCCATATTTATGAATATTA	600
Sbjct	541	AATGGAACCAAGACAAGATTCTAATGTTTGTA AACAGTCAATCCATATTTATGAATATTA	600
Query	601	GCATATATTGGNGAATAGTTAAGGCAAAAGGGTCTAGCAG	640
Sbjct	601	GCATATATTGGNGAATAGTTAAGGCAAAAGGGTCTAGCAG	640

Sequence 869 matched with Sequence 341

Query= Sequence ID - 869
Length=667

nt: 667

SEQ ID NO: 341

nt: 667

ALIGNMENTS

Identities = 667/667 (100%), Gaps = 0/667 (0%)

Query	1	TTGTGTTTTTAGGACTCCTTATCTAAATTAAGGCAGAGAAGTTACAGTATTTATATCTGC	60
Sbjct	1	TTGTGTTTTTAGGACTCCTTATCTAAATTAAGGCAGAGAAGTTACAGTATTTATATCTGC	60
Query	61	ATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGAAACTATTG	120
Sbjct	61	ATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGAAACTATTG	120
Query	121	ATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATCATTTAATAGGAC	180
Sbjct	121	ATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATCATTTAATAGGAC	180
Query	181	ACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGGCTGTACTCTAAAATAA	240
Sbjct	181	ACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGGCTGTACTCTAAAATAA	240
Query	241	TATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTCAAATGCATACTAATATTTTC	300
Sbjct	241	TATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTCAAATGCATACTAATATTTTC	300
Query	301	AATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATCTACTTGTGATAGCCCTAAGAGCTG	360
Sbjct	301	AATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATCTACTTGTGATAGCCCTAAGAGCTG	360
Query	361	AGATAATTATTTCCAGGAGGTTGAATCCCTGATTCTTAACTGTTTCAAGCAATGCATAAGCA	420
Sbjct	361	AGATAATTATTTCCAGGAGGTTGAATCCCTGATTCTTAACTGTTTCAAGCAATGCATAAGCA	420
Query	421	AGAGAGAATATGACATAAGAGGACCATTCTACATTAGCCAttttttttCACAAAGATACC	480
Sbjct	421	AGAGAGAATATGACATAAGAGGACCATTCTACATTAGCCATTTTTTTTCACAAAGATACC	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 TATGTGAATACAGGGCACCTGGGANGGTAAGTGGAGGACTATTTCTAACTATATTTATAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 TATGTGAATACAGGGCACCTGGGANGGTAAGTGGAGGACTATTTCTAACTATATTTATAA 540

Query 541 GCACATACTGATATTGNTGAATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 GCACATACTGATATTGNTGAATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGA 600

Query 601 CAATGTGTAAGGAGATCAGGAATTCATTAGTCACCTTTCAGATGGTTTAATGCATACAGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 CAATGTGTAAGGAGATCAGGAATTCATTAGTCACCTTTCAGATGGTTTAATGCATACAGC 660

Query 661 TGTACCG 667
          |||||||
Sbjct 661 TGTACCG 667
```

Sequence 870 matched with Sequence 342

Query= Sequence ID 870

Length=591

SEQ ID NO: 342

ALIGNMENTS

Identities = 591/591 (100%), Gaps = 0/591 (0%)

Query	1	GGAGTTTGAGCAGATCCTTCAGGAGCGGAATGAACTCAAAGCCAAAGTGTTCTGCTCAA	60
Sbjct	1	GGAGTTTGAGCAGATCCTTCAGGAGCGGAATGAACTCAAAGCCAAAGTGTTCTGCTCAA	60
Query	61	GGAGGAACTGGCCTACTTCCAGCGGGAGCTGCTCACAGACCACCGGGTCCCCGGCCTTCT	120
Sbjct	61	GGAGGAACTGGCCTACTTCCAGCGGGAGCTGCTCACAGACCACCGGGTCCCCGGCCTTCT	120
Query	121	GCTCGAGGCCATGAAGGTGGCTGTCCGGAAGCAGCGGAAGAAGATCAAGGCCAAGATGTT	180
Sbjct	121	GCTCGAGGCCATGAAGGTGGCTGTCCGGAAGCAGCGGAAGAAGATCAAGGCCAAGATGTT	180
Query	181	AGGGACACCAGAGGAAGCAGAGAGCAGTGAGGATGAGGCTGGCCCATGGATCCTGCTCTC	240
Sbjct	181	AGGGACACCAGAGGAAGCAGAGAGCAGTGAGGATGAGGCTGGCCCATGGATCCTGCTCTC	240
Query	241	CGATGACAAGGGAGACCATCCCCACCCCCGGAGTCCAAAATACAGAGTTTCTTTGGCCT	300
Sbjct	241	CGATGACAAGGGAGACCATCCCCACCCCCGGAGTCCAAAATACAGAGTTTCTTTGGCCT	300
Query	301	ATGGTATCGGGGTAAAGCTGAATCCTCTGAGGATGAGACCAGCAGCCCTGCACCCAGCAA	360
Sbjct	301	ATGGTATCGGGGTAAAGCTGAATCCTCTGAGGATGAGACCAGCAGCCCTGCACCCAGCAA	360
Query	361	GCTAGGGGGAGAAGAGGAGGCCCAACCACAGTCTCCAGCTCCTGATCCGCCCTGTTCTGC	420
Sbjct	361	GCTAGGGGGAGAAGAGGAGGCCCAACCACAGTCTCCAGCTCCTGATCCGCCCTGTTCTGC	420
Query	421	CCTCCACGAACACCTTTGTCTGGGGGCCTCAGCCGCCCCAGAGGCCTGACTTAGGGGTCT	480
Sbjct	421	CCTCCACGAACACCTTTGTCTGGGGGCCTCAGCCGCCCCAGAGGCCTGACTTAGGGGTCT	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 GGCTGTGGAAGGATGTGTGGCCTCAAATGAGGACAGGGCTCCCGCCTTCACAGCCCTCGC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 GGCTGTGGAAGGATGTGTGGCCTCAAATGAGGACAGGGCTCCCGCCTTCACAGCCCTCGC 540

Query 541 CAGGGGTCTGCCCCAATCCTGGCCTGCATCAGGCAAGGACGGGGTCTCAGC 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 CAGGGGTCTGCCCCAATCCTGGCCTGCATCAGGCAAGGACGGGGTCTCAGC 591
```

Sequence 871 matched with Sequence 343

Query= Sequence ID - 871
Length=642

nt: 642

SEQ ID NO: 343

nt: 642

ALIGNMENTS

Identities = 642/642 (100%), Gaps = 0/642 (0%)

Query	1	GCAAGTCTTCAGTATGTACATTTATCCCCTAGAAGAAGAAAAATTAGTTGTGCATGAAAA	60
Sbjct	1	GCAAGTCTTCAGTATGTACATTTATCCCCTAGAAGAAGAAAAATTAGTTGTGCATGAAAA	60
Query	61	AGAAACATTAAGTAAAGCTAAATGCTCACACTCTAAATCAGTGCTCTCCAAAGTACAG	120
Sbjct	61	AGAAACATTAAGTAAAGCTAAATGCTCACACTCTAAATCAGTGCTCTCCAAAGTACAG	120
Query	121	CAGGCGGGAAAAAGAAAATGGTAGAAttttttCTTCCAATTACTTTAACTTATTCTTTTTTA	180
Sbjct	121	CAGGCGGGAAAAAGAAAATGGTAGATTTTTTTCTTCCAATTACTTTAACTTATTCTTTTTTA	180
Query	181	ATGGACACTTcatacataaatatattcacatataatataacataatgtataagca	240
Sbjct	181	ATGGACACTTCATACATAAATATATTCACAATATATTAATATATACATAATGTATAAGCA	240
Query	241	tacatatTGAATGTGCAGTCAAAAAATGTACTAATGGAATGCTCTACCAAAACAAGTTCA	300
Sbjct	241	TACATATTGAATGTGCAGTCAAAAAATGTACTAATGGAATGCTCTACCAAAACAAGTTCA	300
Query	301	CGTTCATCTGTAAAATGGGAATAATATTTTTTAAAAGGCATACAGTCTGAACATTTTTTAGA	360
Sbjct	301	CGTTCATCTGTAAAATGGGAATAATATTTTTTAAAAGGCATACAGTCTGAACATTTTTTAGA	360
Query	361	TTATTCATAAAATCTATTCAGAAAGTTAAACTAAAAAATTTAACGTATGCCTATAACAAA	420
Sbjct	361	TTATTCATAAAATCTATTCAGAAAGTTAAACTAAAAAATTTAACGTATGCCTATAACAAA	420
Query	421	TTTTGTAAGTAAATGTAATTGNTTTTCATCCTGAGATCTAATATCCTCGTTTTTAAGTAGA	480
Sbjct	421	TTTTGTAAGTAAATGTAATTGNTTTTCATCCTGAGATCTAATATCCTCGTTTTTAAGTAGA	480

Sequence 873 matched with Sequence 344

Query= Sequence ID 873
Length=661

SEQ ID NO: 344

ALIGNMENTS

Identities = 661/661 (100%), Gaps = 0/661 (0%)

Query	1	GTTTTCCACCGTGAAGAGAACATTTCTCTGGGAATGACAAAGCCCTCAGGAACNGCTTT	60
Sbjct	1	GTTTTCCACCGTGAAGAGAACATTTCTCTGGGAATGACAAAGCCCTCAGGAACNGCTTT	60
Query	61	TATTTCTATTGGAAGATGCCCATCATACTTCTGGCAGGATAAAATGATAAATTTATTTAT	120
Sbjct	61	TATTTCTATTGGAAGATGCCCATCATACTTCTGGCAGGATAAAATGATAAATTTATTTAT	120
Query	121	TCAACAGATGATACTCAATTCCTGCTGTTTTACTAAAGGTTCTTTACGTTTTATAGAAG	180
Sbjct	121	TCAACAGATGATACTCAATTCCTGCTGTTTTACTAAAGGTTCTTTACGTTTTATAGAAG	180
Query	181	CTAAATTTACTGTCATAGAAATTGCAATTGTAGATGTTACTGTAATCTAGTCAGAATATC	240
Sbjct	181	CTAAATTTACTGTCATAGAAATTGCAATTGTAGATGTTACTGTAATCTAGTCAGAATATC	240
Query	241	CTTATCCTTCTAAAATAAACTAGTTAAAATTATTAACATACGTACTGATATTAATTTTT	300
Sbjct	241	CTTATCCTTCTAAAATAAACTAGTTAAAATTATTAACATACGTACTGATATTAATTTTT	300
Query	301	AAGTTTAATGCTGCCACGTGCTTCTGCTAAGAACATTTATCACTACAAGTGGCAGAAAAT	360
Sbjct	301	AAGTTTAATGCTGCCACGTGCTTCTGCTAAGAACATTTATCACTACAAGTGGCAGAAAAT	360
Query	361	TCCAAACTCATCAAAACCAAAGTGTGCTTCTTCCCTGCTTTTTTTCAGAAAATGAGAAAGG	420
Sbjct	361	TCCAAACTCATCAAAACCAAAGTGTGCTTCTTCCCTGCTTTTTTTCAGAAAATGAGAAAGG	420
Query	421	ATGACTTTATTCCAACATATTCTAAAAGTATTCCAAGAACACTACCTTTATTCTAAATTC	480
Sbjct	421	ATGACTTTATTCCAACATATTCTAAAAGTATTCCAAGAACACTACCTTTATTCTAAATTC	480

PATENT SEQUENCE ALIGNMENT

Query	481	GTTATTTTCACAAAATAAAGGCTGCAGATTGAAAGATAAAGGATTGCTATTAAAGAACAA	540
Sbjct	481	GTTATTTTCACAAAATAAAGGCTGCAGATTGAAAGATAAAGGATTGCTATTAAAGAACAA	540
Query	541	AAGAAAACAAAACCGAGAGAGAAGGAGAGCTAGGGAAATCCCTGCanaanaaCCGAATAN	600
Sbjct	541	AAGAAAACAAAACCGAGAGAGAAGGAGAGCTAGGGAAATCCCTGCANAANAACCGAATAN	600
Query	601	GGTCCCTCTATTCTGGGCCGGGGCCTGAAACTATGAAACAGGCCAACACAGAATCTTGGC	660
Sbjct	601	GGTCCCTCTATTCTGGGCCGGGGCCTGAAACTATGAAACAGGCCAACACAGAATCTTGGC	660
Query	661	A	661
Sbjct	661	A	661

Sequence 875 matched with Sequence 345

Query= Sequence ID 875
Length=661

SEQ ID NO: 345

ALIGNMENTS

Identities = 661/661 (100%), Gaps = 0/661 (0%)

Query	1	CCTCTGACTCGCTCAGCTCACCCACGCTGCTGGCCCTGTGAGGGGGCAGGGAAGGGGAGG	60
Sbjct	1	CCTCTGACTCGCTCAGCTCACCCACGCTGCTGGCCCTGTGAGGGGGCAGGGAAGGGGAGG	60
Query	61	CAGCCGGCACCCACAAGTGCCACTGCCCCGAGCTGGTGCATTACAGAGAGGAGAAACACAT	120
Sbjct	61	CAGCCGGCACCCACAAGTGCCACTGCCCCGAGCTGGTGCATTACAGAGAGGAGAAACACAT	120
Query	121	CTTCCCTAGAGGGTTCCTGTANACCTAGGGAGGACCTTATCTGTGCGTGAAACACACCAG	180
Sbjct	121	CTTCCCTAGAGGGTTCCTGTANACCTAGGGAGGACCTTATCTGTGCGTGAAACACACCAG	180
Query	181	GCTGTGGGCCTCAAGGACTTGAAAGCATCCATGTGTGGACTCAAGTCCTTACCTCTTCCG	240
Sbjct	181	GCTGTGGGCCTCAAGGACTTGAAAGCATCCATGTGTGGACTCAAGTCCTTACCTCTTCCG	240
Query	241	GAGATGTAGCAAAACGCATGGAGTGTGTATTGTTCCCAGTGACACTTCANAGAGCTGGTA	300
Sbjct	241	GAGATGTAGCAAAACGCATGGAGTGTGTATTGTTCCCAGTGACACTTCANAGAGCTGGTA	300
Query	301	GTTAGTAGCATGTTGAGCCAGGCCTGGGTCTGTGTCTCTTTTCTCTTTCTCCTTAGTCTT	360
Sbjct	301	GTTAGTAGCATGTTGAGCCAGGCCTGGGTCTGTGTCTCTTTTCTCTTTCTCCTTAGTCTT	360
Query	361	CTCATAGCATTAACCTAATCTATTGGGTTTATTGGAATTAACCTGGTGCTGGATATTT	420
Sbjct	361	CTCATAGCATTAACCTAATCTATTGGGTTTATTGGAATTAACCTGGTGCTGGATATTT	420
Query	421	TCAAATTGTATCTAGTGCAGCTGATTTTAAACAATAACTACTGTGTTTCTGGCAATAGTGT	480
Sbjct	421	TCAAATTGTATCTAGTGCAGCTGATTTTAAACAATAACTACTGTGTTTCTGGCAATAGTGT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GTTCTGATTAGAAATGACCAATATTATACTAAGAAAAGATACGACTTTATTTTCTGGTAG	540
Sbjct	481	GTTCTGATTAGAAATGACCAATATTATACTAAGAAAAGATACGACTTTATTTTCTGGTAG	540
Query	541	ATAGAAATAAATAGCTATATCCATGTACTGNAGTTTTTCTTCAACATCAATGGTCATTGN	600
Sbjct	541	ATAGAAATAAATAGCTATATCCATGTACTGNAGTTTTTCTTCAACATCAATGGTCATTGN	600
Query	601	AATGTTACTGATCATGCATTGGTGAGGNGGTCTGAATGTTCTGACATTAACAATTTTCCA	660
Sbjct	601	AATGTTACTGATCATGCATTGGTGAGGNGGTCTGAATGTTCTGACATTAACAATTTTCCA	660
Query	661	T	661
Sbjct	661	T	661

Sequence 876 matched with Sequence 346

Query= Sequence ID - 876 nt: 115
Length=115

SEQ ID NO: 346 nt: 115

ALIGNMENTS

Identities = 115/115 (100%), Gaps = 0/115 (0%)

```
Query 1  AAACTTTGTGGCAACAGTGCACTAATTGGATAATGTTTGTTCCTCAATAAATTAAGAGC 60
          |||
Sbjct 1  AAACTTTGTGGCAACAGTGCACTAATTGGATAATGTTTGTTCCTCAATAAATTAAGAGC 60

Query 61  CAAATTGTaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 115
          |||
Sbjct 61  CAAATTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 115
```

Sequence 878 matched with Sequence 347

Query= Sequence ID - 878
Length=634

nt: 634

SEQ ID NO: 347

nt: 634

ALIGNMENTS

Identities = 634/634 (100%), Gaps = 0/634 (0%)

Query	1	GCCAGGCTTTGTGAATTACAGGACATTTGAGACAATCGTGAAACAGCAAATCAAGGCACT	60
Sbjct	1	GCCAGGCTTTGTGAATTACAGGACATTTGAGACAATCGTGAAACAGCAAATCAAGGCACT	60
Query	61	GGAAGAGCCGGCTGTGGATATGCTACACACCGTGACGGATATGGTCCGGCTTGCTTTTCA	120
Sbjct	61	GGAAGAGCCGGCTGTGGATATGCTACACACCGTGACGGATATGGTCCGGCTTGCTTTTCA	120
Query	121	AGATGTTTCGATAAAAAATTTTGAAGAGTTTTTTAACCTCCACAGAACCGCCAAGTCCAA	180
Sbjct	121	AGATGTTTCGATAAAAAATTTTGAAGAGTTTTTTAACCTCCACAGAACCGCCAAGTCCAA	180
Query	181	AATTGAAGACATTAGAGCAGAACAAGAGAGAGAAGGTGAGAAGCTGATCCGCCTCCACTT	240
Sbjct	181	AATTGAAGACATTAGAGCAGAACAAGAGAGAGAAGGTGAGAAGCTGATCCGCCTCCACTT	240
Query	241	CCAGATGGAACAGATTGTCTACTGCCAGGACCAGGTATACAGGGGTGCATTGCagaaggt	300
Sbjct	241	CCAGATGGAACAGATTGTCTACTGCCAGGACCAGGTATACAGGGGTGCATTGCAGAAGGT	300
Query	301	cagagagaaggagctggaagaagaaaagaagaagaaATCCTGGGATTTTGGGGCTTTCCA	360
Sbjct	301	CAGAGAGAAGGAGCTGGAAGAAGAAAAGAAGAAGAAATCCTGGGATTTTGGGGCTTTCCA	360
Query	361	ATCCAGCTCGGCAACAGACTCTTCCATGGAGGAGATCTTTCAGCACCTGATGGCCTATCA	420
Sbjct	361	ATCCAGCTCGGCAACAGACTCTTCCATGGAGGAGATCTTTCAGCACCTGATGGCCTATCA	420
Query	421	CCAGGAGGCCAGCAAGCGCATCTCCAGCCACATCCCTTTGATCATCCAGTTCTTCATGCT	480
Sbjct	421	CCAGGAGGCCAGCAAGCGCATCTCCAGCCACATCCCTTTGATCATCCAGTTCTTCATGCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCAGACGTACGGCCAGCAGCTTCAAAAGGCCATGCTGCAGCTCCTGCAGGGACAAGGACA	540
Sbjct	481	CCAGACGTACGGCCAGCAGCTTCAAAAGGCCATGCTGCAGCTCCTGCAGGGACAAGGACA	540
Query	541	CCTACAGCTGGCTCCTGAAGGAGCGGAGCGACACCAGCGACAAGCGGAAGTTNCTGAAGG	600
Sbjct	541	CCTACAGCTGGCTCCTGAAGGAGCGGAGCGACACCAGCGACAAGCGGAAGTTNCTGAAGG	600
Query	601	AGCGGCTTGACACGGCTGACGCAGGCTCGGCGCCG	634
Sbjct	601	AGCGGCTTGACACGGCTGACGCAGGCTCGGCGCCG	634

Sequence 879 matched with Sequence 348

Query= Sequence ID 879
Length=528

SEQ ID NO: 348

ALIGNMENTS

Identities = 528/528 (100%), Gaps = 0/528 (0%)

Query	1	GTTGCCGGGTCCTGTGATAACTCTGTTTAACATTTTGAGGAACTGTTGAATGGTTTTTCA	60
Sbjct	1	GTTGCCGGGTCCTGTGATAACTCTGTTTAACATTTTGAGGAACTGTTGAATGGTTTTTCA	60
Query	61	CAGCAGCTGCCTCATTTTTTATTCCCATCAGCAGTACTTCTTGGTTCTAATACCTCCACG	120
Sbjct	61	CAGCAGCTGCCTCATTTTTTATTCCCATCAGCAGTACTTCTTGGTTCTAATACCTCCACG	120
Query	121	TTCTCGCCAACACTTGTTGTTGTCTGTAATTCGTTGTTAGCCATCCCAGTGGGGATGAA	180
Sbjct	121	TTCTCGCCAACACTTGTTGTTGTCTGTAATTCGTTGTTAGCCATCCCAGTGGGGATGAA	180
Query	181	GTAGTATCTTACTGTGGTTTTTCAGTTGCGTTTCCCTGATAATTAATGATGGTGAACATCT	240
Sbjct	181	GTAGTATCTTACTGTGGTTTTTCAGTTGCGTTTCCCTGATAATTAATGATGGTGAACATCT	240
Query	241	TTTCATGTTCTTGTTGGCCATTTGTATGTCTTCTTGGGaaaaaaaaaTGTCTGTTCAAA	300
Sbjct	241	TTTCATGTTCTTGTTGGCCATTTGTATGTCTTCTTGGGAAAAAAAAAATGTCTGTTCAAA	300
Query	301	TCCTTTACAAAGTATTTATTTTTTATGTCAACAATATAACCACTCAGTACACTGCTTTTT	360
Sbjct	301	TCCTTTACAAAGTATTTATTTTTTATGTCAACAATATAACCACTCAGTACACTGCTTTTT	360
Query	361	ANACAATGATCTTTTAAAGGTTTGTTTACAACATTTAGCACTTGAAAATTTAAGGTTATG	420
Sbjct	361	ANACAATGATCTTTTAAAGGTTTGTTTACAACATTTAGCACTTGAAAATTTAAGGTTATG	420
Query	421	CCCTCaaaaaaTTGCTGAGGGAGCTAAGCTATGAAGATGCAAAGGCATAANAATTATAC	480
Sbjct	421	CCCTCAAAAAAATTGCTGAGGGAGCTAAGCTATGAAGATGCAAAGGCATAANAATTATAC	480

Query	481	AATGGACTTTGGGGGAATCCAGGGAAGGGTGGGAGGGGGGTGANGGA	528
Sbjct	481	AATGGACTTTGGGGGAATCCAGGGAAGGGTGGGAGGGGGGTGANGGA	528

Sequence 881 matched with Sequence 349

Query= Sequence ID 881
Length=573

SEQ ID NO: 349

ALIGNMENTS

Identities = 573/573 (100%), Gaps = 0/573 (0%)

Query	1	TCGACTCTGAttttttttCTCCTTCCTCGCAGCCGCGCCAGGGAGCTCGCGNGCGCGG	60
Sbjct	1	TCGACTCTGATTTTTTTTCTCCTTCCTCGCAGCCGCGCCAGGGAGCTCGCGNGCGCGG	60
Query	61	CCCCTGTCTCCGGCCCGAGATGAATCCTGCGGCAGAAGCCGAGTTCAACATCCTCCTGG	120
Sbjct	61	CCCCTGTCTCCGGCCCGAGATGAATCCTGCGGCAGAAGCCGAGTTCAACATCCTCCTGG	120
Query	121	CCACCGACTCCTACAAGGTTACTCACTATAAACAATATCCACCCAACACAAGCAAAGTTT	180
Sbjct	121	CCACCGACTCCTACAAGGTTACTCACTATAAACAATATCCACCCAACACAAGCAAAGTTT	180
Query	181	ATTCTACTTTGAATGCCGTGAAAAGAAGACAGAAACTCCAAATTAAGGAAGGTGAAAT	240
Sbjct	181	ATTCTACTTTGAATGCCGTGAAAAGAAGACAGAAACTCCAAATTAAGGAAGGTGAAAT	240
Query	241	ATGAGGAAACAGTATTTTATGGGTTGCAGTACATTCTTAATAAGTACTTAAAAGGTAAAG	300
Sbjct	241	ATGAGGAAACAGTATTTTATGGGTTGCAGTACATTCTTAATAAGTACTTAAAAGGTAAAG	300
Query	301	TAGTAACCAAAGAGAAAATCCAGGAAGCCAAAGATGTCTACAAAGAACATTTCCAAGATG	360
Sbjct	301	TAGTAACCAAAGAGAAAATCCAGGAAGCCAAAGATGTCTACAAAGAACATTTCCAAGATG	360
Query	361	ATGTCTTTAATGAAAAGGGATGGAACCTACATTCTTGAGAAGTATGATGGGCATCTTCCAA	420
Sbjct	361	ATGTCTTTAATGAAAAGGGATGGAACCTACATTCTTGAGAAGTATGATGGGCATCTTCCAA	420
Query	421	TANAAATAAAAAGCTGTTTCCTGAGGGCTTTGTCATTCCCAGAGGAAATGTTCTCTTCACGG	480
Sbjct	421	TANAAATAAAAAGCTGTTTCCTGAGGGCTTTGTCATTCCCAGAGGAAATGTTCTCTTCACGG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TGGAAAACACAGATCCAGAGTGTTACTGGCTTACAAATTGGATTGAGACTATTCTTG TTC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TGGAAAACACAGATCCAGAGTGTTACTGGCTTACAAATTGGATTGAGACTATTCTTG TTC  540

Query  541  AGTCCTGGTATCCAATCACAGTGGCCACAAATT  573
          ||||||||||||||||||||||||||||
Sbjct  541  AGTCCTGGTATCCAATCACAGTGGCCACAAATT  573
```

Sequence 883 matched with Sequence 350

Query= Sequence ID 883
Length=659

SEQ ID NO: 350

ALIGNMENTS

Identities = 659/659 (100%), Gaps = 0/659 (0%)

Query	1	TCATTTACATTAATACTCAAACTGCTCGATTAAGCAGGTGCTGTTCTTATCGCCATTTT	60
Sbjct	1	TCATTTACATTAATACTCAAACTGCTCGATTAAGCAGGTGCTGTTCTTATCGCCATTTT	60
Query	61	GCATATGATGAGAAAGGTAAGGTCACCCAGCTAGTATTTGGCTCACAGCAGGCCTTAAG	120
Sbjct	61	GCATATGATGAGAAAGGTAAGGTCACCCAGCTAGTATTTGGCTCACAGCAGGCCTTAAG	120
Query	121	ACTTGGTTTGTGTGACTCATCAGTCCACGCTCCTAAAACCACTAAGTTGTTCTACCCTTT	180
Sbjct	121	ACTTGGTTTGTGTGACTCATCAGTCCACGCTCCTAAAACCACTAAGTTGTTCTACCCTTT	180
Query	181	AATGTTGAATTAACATTGGATAGTGTTCAAGTTTANATGGGTGGGTGAGGGCCCAAGGAC	240
Sbjct	181	AATGTTGAATTAACATTGGATAGTGTTCAAGTTTANATGGGTGGGTGAGGGCCCAAGGAC	240
Query	241	CTTTCAAACCTCAGATCTCTTATTTAATAACCTGGTCCCAGATCCATTCCTCTGTCTGAAGA	300
Sbjct	241	CTTTCAAACCTCAGATCTCTTATTTAATAACCTGGTCCCAGATCCATTCCTCTGTCTGAAGA	300
Query	301	GGAAGTCATCCTTCAGTGGCTATTCATTGTGGGGTTAAGAGCGCAGACTATGAATTCAGT	360
Sbjct	301	GGAAGTCATCCTTCAGTGGCTATTCATTGTGGGGTTAAGAGCGCAGACTATGAATTCAGT	360
Query	361	CTTTTGGGTCCCAGTTTGCCAGACCTTGAGTGAGTGCCCCGAGTTTACTTACTTGTAAG	420
Sbjct	361	CTTTTGGGTCCCAGTTTGCCAGACCTTGAGTGAGTGCCCCGAGTTTACTTACTTGTAAG	420
Query	421	GGTAGGTGGAGGtaatatataattaaataaaacttaaaaaactaattaaaaacaaaacaaatG	480
Sbjct	421	GGTAGGTGGAGGTAATATAATTAAATAAACTTAAAAAACTAATTAAAAAACAAAACAAATG	480

PATENT SEQUENCE ALIGNMENT

Query	481	AACTAAGGTCTTAGGATATCTGGCGTCTATTTTGCGCCAAATCACATAATGTCTATTGTT	540
Sbjct	481	AACTAAGGTCTTAGGATATCTGGCGTCTATTTTGCGCCAAATCACATAATGTCTATTGTT	540
Query	541	GTGTGTTGGACTATAGGATTGTCCTTTAACAGGGAAGGGTTTATTTCTGTAATCAAGTCT	600
Sbjct	541	GTGTGTTGGACTATAGGATTGTCCTTTAACAGGGAAGGGTTTATTTCTGTAATCAAGTCT	600
Query	601	GTCAATATTATGACCATGTTGATAATAGCTACCTTTAATTGAGGGCTTCCATGTGCCAA	659
Sbjct	601	GTCAATATTATGACCATGTTGATAATAGCTACCTTTAATTGAGGGCTTCCATGTGCCAA	659

Sequence 885 matched with Sequence 351

Query= Sequence ID 885
Length=517

SEQ ID NO: 351

ALIGNMENTS

Identities = 517/517 (100%), Gaps = 0/517 (0%)

Query	1	TCAGTGGAAAAGGGCAGGTTGAATCAAGGTGAATCAATCTGAAATTGAGCACACCTGCCT	60
Sbjct	1	TCAGTGGAAAAGGGCAGGTTGAATCAAGGTGAATCAATCTGAAATTGAGCACACCTGCCT	60
Query	61	GCCATCGCTGTTTCCTTCAACTGAGTGCTGCACATCATGGGCTCTGTCTGTGAGAGAAAAA	120
Sbjct	61	GCCATCGCTGTTTCCTTCAACTGAGTGCTGCACATCATGGGCTCTGTCTGTGAGAGAAAAA	120
Query	121	TCCCGGTGCTTGGTGTCTTGCATGACATGGAGTTTTGCATGTAGATCAATTTAAAATGT	180
Sbjct	121	TCCCGGTGCTTGGTGTCTTGCATGACATGGAGTTTTGCATGTAGATCAATTTAAAATGT	180
Query	181	ACCTCTTGTTTACATAATTTGCATAATTTTAAAAGATAATGTTGCCAAACTTTGGAAATG	240
Sbjct	181	ACCTCTTGTTTACATAATTTGCATAATTTTAAAAGATAATGTTGCCAAACTTTGGAAATG	240
Query	241	TTAATGTTCANACTGAAAATCTCCACTACATGTAACCTTCTCCTCTGGATCAGTGGCAT	300
Sbjct	241	TTAATGTTCANACTGAAAATCTCCACTACATGTAACCTTCTCCTCTGGATCAGTGGCAT	300
Query	301	GGCTTATAATCCCAGCCAGTGGTTTGAAGTGTTCAGTGTCAACTGCCATGTGCTCTGCT	360
Sbjct	301	GGCTTATAATCCCAGCCAGTGGTTTGAAGTGTTCAGTGTCAACTGCCATGTGCTCTGCT	360
Query	361	TCAAGGGGGAAGTAGCCTTTTGTGAATTTTTGTACATAAGTATTTGTTACAAATATTTT	420
Sbjct	361	TCAAGGGGGAAGTAGCCTTTTGTGAATTTTTGTACATAAGTATTTGTTACAAATATTTT	420
Query	421	AGCAAATGCTTTCTATTTCTCTTGCTTGTGCATATCTTGGCTGGCGTTACAGAAAAATAG	480
Sbjct	421	AGCAAATGCTTTCTATTTCTCTTGCTTGTGCATATCTTGGCTGGCGTTACAGAAAAATAG	480

SEQ ID NO: 352

Identities = 174/174 (100%), Gaps = 0/174 (0%)

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Sequence 889 matched with Sequence 353

Query= Sequence ID 889

Length=664

SEQ ID NO: 353

ALIGNMENTS

Identities = 664/664 (100%), Gaps = 0/664 (0%)

Query	1	CAGAGAGCTTGTTCCCTCCCTCCCTGTGCATGCAAACAAGAGGGCATGGGAGCACACAGA	60
Sbjct	1	CAGAGAGCTTGTTCCCTCCCTCCCTGTGCATGCAAACAAGAGGGCATGGGAGCACACAGA	60
Query	61	GAGATGGCAGCCACCTACAAGCCAAGAGGAGAAGCCTCACAATCAAACCTCTCGCTGCTGG	120
Sbjct	61	GAGATGGCAGCCACCTACAAGCCAAGAGGAGAAGCCTCACAATCAAACCTCTCGCTGCTGG	120
Query	121	CGAGAGTCTTGGA	180
Sbjct	121	CGAGAGTCTTGGA	180
Query	181	TTGTTTCAGCTTCTCAGTCTCTGGTGT	240
Sbjct	181	TTGTTTCAGCTTCTCAGTCTCTGGTGT	240
Query	241	ATTATNAGGGAAACAGAAAACACTGATACTTAACAATGCTAATGCAATTATTTATTTGCT	300
Sbjct	241	ATTATNAGGGAAACAGAAAACACTGATACTTAACAATGCTAATGCAATTATTTATTTGCT	300
Query	301	TTTCAGTCTCTACAAAACGTTCTAAAACACTAATCTAAATATTAACAGTAAAATATTTGC	360
Sbjct	301	TTTCAGTCTCTACAAAACGTTCTAAAACACTAATCTAAATATTAACAGTAAAATATTTGC	360
Query	361	ATAACTAATGGAAACTAAGAAATCATATGACCAATATTTCACTTATTGGTAATCTTACTC	420
Sbjct	361	ATAACTAATGGAAACTAAGAAATCATATGACCAATATTTCACTTATTGGTAATCTTACTC	420
Query	421	TACTGATTTCCCCCAGACTGTGATTTTGA	480
Sbjct	421	TACTGATTTCCCCCAGACTGTGATTTTGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GTTTATTCATGGAATTCCAGTTATCTGGGCTTGAAATTGCAGGCTCTCCTAACTTAAGCA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTTTATTCATGGAATTCCAGTTATCTGGGCTTGAAATTGCAGGCTCTCCTAACTTAAGCA  540

Query  541  AAATCTGACAGATCAGCAAAATGAGATAAAATGTTTCTTTTTTCTTTCTGACTGCATTAAA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAATCTGACAGATCAGCAAAATGAGATAAAATGTTTCTTTTTTCTTTCTGACTGCATTAAA  600

Query  601  TCAGATACAACCTCAGCATTAAAAAGCTATCTTTGNAAAATGNTGGTACTAATAAATTAGT  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TCAGATACAACCTCAGCATTAAAAAGCTATCTTTGNAAAATGNTGGTACTAATAAATTAGT  660

Query  661  CTTA  664
          |||
Sbjct  661  CTTA  664
```

Sequence 890 matched with Sequence 354

Query= Sequence ID 890

Length=661

SEQ ID NO: 354

ALIGNMENTS

Identities = 661/661 (100%), Gaps = 0/661 (0%)

Query	1	CCAGTTCCACATTTCAGTGAAGTCATGAACTTGAAATTGGCCATGATCAAAAAGTATTTAA	60
Sbjct	1	CCAGTTCCACATTTCAGTGAAGTCATGAACTTGAAATTGGCCATGATCAAAAAGTATTTAA	60
Query	61	ATCACAGAAGTTGCAAATGCCACAAATCAAGGTCTTTTTCTCTTGGAGAACCTGTAAAC	120
Sbjct	61	ATCACAGAAGTTGCAAATGCCACAAATCAAGGTCTTTTTCTCTTGGAGAACCTGTAAAC	120
Query	121	ATTTACCAACTCACGACCGCCATGCACCCAATACTGCAATAGGTCTATAGATGCAGATAC	180
Sbjct	121	ATTTACCAACTCACGACCGCCATGCACCCAATACTGCAATAGGTCTATAGATGCAGATAC	180
Query	181	TGTCTCCATGAATCTTATAGGCTAGAAAGGAAATAGATAAGTAGTCCTACCAGAAGAACA	240
Sbjct	181	TGTCTCCATGAATCTTATAGGCTAGAAAGGAAATAGATAAGTAGTCCTACCAGAAGAACA	240
Query	241	TGATGAAGGCATTTGTGGTAAACAGAATGATGGCCCCCAAAGATGTCCACATCCTAATC	300
Sbjct	241	TGATGAAGGCATTTGTGGTAAACAGAATGATGGCCCCCAAAGATGTCCACATCCTAATC	300
Query	301	CCTGAAGCCTATGAATATACTACTTTACTTGGCAAAAGGGACTTTGCCACAGGTTTTTAA	360
Sbjct	301	CCTGAAGCCTATGAATATACTACTTTACTTGGCAAAAGGGACTTTGCCACAGGTTTTTAA	360
Query	361	TTAAGGACCTTGAAATAGAGAGATTATCCTGGATAATCCAGATGGCCCCAGTGTAAATCCC	420
Sbjct	361	TTAAGGACCTTGAAATAGAGAGATTATCCTGGATAATCCAGATGGCCCCAGTGTAAATCCC	420
Query	421	AAGGGTCCTCACAAAGGGTAGGAAGGAGAGCCAGAGTCAGAGAAGGAGACGTAGCAATGG	480
Sbjct	421	AAGGGTCCTCACAAAGGGTAGGAAGGAGAGCCAGAGTCAGAGAAGGAGACGTAGCAATGG	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 AGGCAGAGGTCANAGAGAGATCTGCAGATGCTGCTGTGTTGGCTTTGAAAATGAGGAATG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AGGCAGAGGTCANAGAGAGATCTGCAGATGCTGCTGTGTTGGCTTTGAAAATGAGGAATG 540

Query 541 CAGGTGACCTCAANGNGCTAGATGATGCAAGGAAACAAATAATCTCCTATGAACCCTAGG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 CAGGTGACCTCAANGNGCTAGATGATGCAAGGAAACAAATAATCTCCTATGAACCCTAGG 600

Query 601 ATGGGCATTATTATGAGTCCTATTTTATAAACAAGGAACTGACNTCCAGAAAGATAAATG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 ATGGGCATTATTATGAGTCCTATTTTATAAACAAGGAACTGACNTCCAGAAAGATAAATG 660

Query 661 C 661
          |
Sbjct 661 C 661
```

nt: 626

nt: 626

Identities = 626/626 (100%), Gaps = 0/626 (0%)

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PATENT SEQUENCE ALIGNMENT

```
Query 481 TGaaaaaaaaTAGAGACACGCAAATAAGTAAAAAGGCACTCCATGCTCATGAATTTAAAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 TGAAAAAAAAATAGAGACACGCAAATAAGTAAAAAGGCACTCCATGCTCATGAATTTAAAG 540

Query 541 AATCAATATAATTAAAATGTCCGNGCTGCCTAAAGCAACTTACAGATTAAAGGCTATTTC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 AATCAATATAATTAAAATGTCCGNGCTGCCTAAAGCAACTTACAGATTAAAGGCTATTTC 600

Query 601 TCTCAAACCTATAAATGCACCTTTTTTA 626
          ||||||||||||||||||||
Sbjct 601 TCTCAAACCTATAAATGCACCTTTTTTA 626
```

Sequence 893 matched with Sequence 356

Query= Sequence ID - 893
Length=585

nt: 585

SEQ ID NO: 356

nt: 585

ALIGNMENTS

Identities = 585/585 (100%), Gaps = 0/585 (0%)

Query	1	GTCATTGCTGGGTGGCGCCAGCCCTCAGACTTGCCTCTTTGCAGTAGGAAGAAGGCCTCC	60
Sbjct	1	GTCATTGCTGGGTGGCGCCAGCCCTCAGACTTGCCTCTTTGCAGTAGGAAGAAGGCCTCC	60
Query	61	CCACATACCTTCCCACACTCATCACCTTAAGCCAGACTCGGTGTCCAGTGAATATGACCA	120
Sbjct	61	CCACATACCTTCCCACACTCATCACCTTAAGCCAGACTCGGTGTCCAGTGAATATGACCA	120
Query	121	TCTCTTGCCCATTTTCTAATGAGTGTTTTCATTAATGAGTTATAAGAATGTGGTGGGTAA	180
Sbjct	121	TCTCTTGCCCATTTTCTAATGAGTGTTTTCATTAATGAGTTATAAGAATGTGGTGGGTAA	180
Query	181	ATCTATGGGCTTTGAACTAGTGAATCAACTTGGTTTCAGAATCTGGCACTGCTACTTACT	240
Sbjct	181	ATCTATGGGCTTTGAACTAGTGAATCAACTTGGTTTCAGAATCTGGCACTGCTACTTACT	240
Query	241	AGTGAATTTAAGCAAGTTATTTACCTTTCAGAGTGTCAGTTCCCTCATGCATACAAGGA	300
Sbjct	241	AGTGAATTTAAGCAAGTTATTTACCTTTCAGAGTGTCAGTTCCCTCATGCATACAAGGA	300
Query	301	AGATAAAAAATAATGTNTACNAAAGTATTGGAGTAATTAATACATGGAGAACTACATGTA	360
Sbjct	301	AGATAAAAAATAATGTNTACNAAAGTATTGGAGTAATTAATACATGGAGAACTACATGTA	360
Query	361	AAGCGTTTAGCATGATGTCTGACATATTAAGCATCCAATATTAGTNGCTTGCAGAATTAT	420
Sbjct	361	AAGCGTTTAGCATGATGTCTGACATATTAAGCATCCAATATTAGTNGCTTGCAGAATTAT	420
Query	421	TAGTAAAAGAGATTGCTTCTGAAAGCCATTCCAATTCTTAAATTTTATAATGCCACATTT	480
Sbjct	421	TAGTAAAAGAGATTGCTTCTGAAAGCCATTCCAATTCTTAAATTTTATAATGCCACATTT	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 GAGGTCACCTGAAGTCGTGTATAACATGTGTACATTTTTCGATTATTTTTTCAATTCC 540
          |||
Sbjct 481 GAGGTCACCTGAAGTCGTGTATAACATGTGTACATTTTTCGATTATTTTTTCAATTCC 540

Query 541 CANATTAAAGGCATAGAGATATCCTAGCNANGGACTCCAAGTGTG 585
          |||
Sbjct 541 CANATTAAAGGCATAGAGATATCCTAGCNANGGACTCCAAGTGTG 585
```

Sequence 895 matched with Sequence 357

Query= Sequence ID - 895
Length=560

nt: 560

SEQ ID NO: 357

nt: 560

ALIGNMENTS

Identities = 560/560 (100%), Gaps = 0/560 (0%)

Query	1	GTAATTGCAGCCTGGGCAACGGAGTGAGAGACTGTCTCAGG	60
Sbjct	1	GTAATTGCAGCCTGGGCAACGGAGTGAGAGACTGTCTCAGG	60
Query	61	CTACTGAGGTAGTTGAATATATCCTCCATTCCCCATTTGTGGATTAGTTAGTAAATGGGG	120
Sbjct	61	CTACTGAGGTAGTTGAATATATCCTCCATTCCCCATTTGTGGATTAGTTAGTAAATGGGG	120
Query	121	CATCTTAGGGTTTAAATATGTCCAGGGTCACTGAGGATCAGATCCTAGGGTTCCTTTGAC	180
Sbjct	121	CATCTTAGGGTTTAAATATGTCCAGGGTCACTGAGGATCAGATCCTAGGGTTCCTTTGAC	180
Query	181	TCAAGGCTTTTGTCTCAGCAAAACGTACCTTCCAGCAGGAAGGCTTTCTCAGGCAAGTA	240
Sbjct	181	TCAAGGCTTTTGTCTCAGCAAAACGTACCTTCCAGCAGGAAGGCTTTCTCAGGCAAGTA	240
Query	241	GCAGGGTGGCTACTATGTATCGCTTCTTTA	300
Sbjct	241	GCAGGGTGGCTACTATGTATCGCTTCTTTA	300
Query	301	GTGCGCATAATTTAAAAAATCAGTGCTAAAACCCTT	360
Sbjct	301	GTGCGCATAATTTAAAAAATCAGTGCTAAAACCCTT	360
Query	361	CCTGTCTtttctttttttttctttttattttttctttttattattattatactttaagtt	420
Sbjct	361	CCTGTCTTTCTTTTTTTTTCTTTTATTTTTTCTTTTATTATTATTATACTTTAAGTT	420
Query	421	ttaGGGTACATGTGCACAACGTGCAGGTTTGTTACATATGTATACATGTGCCATGTNGGT	480
Sbjct	421	TTAGGGTACATGTGCACAACGTGCAGGTTTGTTACATATGTATACATGTGCCATGTNGGT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GAGCTGCACCCATTAACTCGTCATTTAGCATTAGGTATATCTCCTAATGCTATccctccc  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAGCTGCACCCATTAACTCGTCATTTAGCATTAGGTATATCTCCTAATGCTATCCCTCCC  540

Query  541  ccctccccccctttttttttt  560
          ||||||||||||||||
Sbjct  541  CCCTCCCCCCTTTTTTTTTT  560
```

Length=645

SEQ ID NO: 358

Identities = 645/645 (100%), Gaps = 0/645 (0%)

Query	1	GGGAATGTCTTAGGCACTGGGACTGTAAGTGCAAAGACCCTGTGGCACAAGGGAATGTTA	60
Sbjct	1	GGGAATGTCTTAGGCACTGGGACTGTAAGTGCAAAGACCCTGTGGCACAAGGGAATGTTA	60
Query	61	ATTATCTACCTTTCANAACTGGAANAAGGCCTAGCCTAGAGCATTGAAAACAATAAGGG	120
Sbjct	61	ATTATCTACCTTTCANAACTGGAANAAGGCCTAGCCTAGAGCATTGAAAACAATAAGGG	120
Query	121	AAAGGAGGAGTAAGGCTGGANAGATAGGAATGGTTTAAAGTCTTTGTTAAAAAAttttttt	180
Sbjct	121	AAAGGAGGAGTAAGGCTGGANAGATAGGAATGGTTTAAAGTCTTTGTTAAAAATTTTTTT	180
Query	181	aaaaaaaTCTTTATCACAAGAAGAGGATTGGCNTGATCAAATTTGACTTTTaaaaanaTT	240
Sbjct	181	AAAAAAATCTTTATCACAAGAAGAGGATTGGCNTGATCAAATTTGACTTTTAAAAANATT	240
Query	241	ACTTGGGTTGGGCATGATCAAATACTACTTAGGGAGATTAGTTTANATGATAATGGCATT	300
Sbjct	241	ACTTGGGTTGGGCATGATCAAATACTACTTAGGGAGATTAGTTTANATGATAATGGCATT	300
Query	301	CTGGACCANAGTGGAGTCAGAGGTGAAAAGAGGTAGATATTCCANAATTGAGGGATTTGT	360
Sbjct	301	CTGGACCANAGTGGAGTCAGAGGTGAAAAGAGGTAGATATTCCANAATTGAGGGATTTGT	360
Query	361	GAGGTGAAATCATTGTGTTACAGATATTAAAGGATAAGGAGCTTTGTCAAAGGGGATCTTA	420
Sbjct	361	GAGGTGAAATCATTGTGTTACAGATATTAAAGGATAAGGAGCTTTGTCAAAGGGGATCTTA	420
Query	421	AGTTTCTGGTATGGTAACTGGGTTAGAGAGCCCTGGAACATGACCAGCTTTAAGGGAAGA	480
Sbjct	421	AGTTTCTGGTATGGTAACTGGGTTAGAGAGCCCTGGAACATGACCAGCTTTAAGGGAAGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GAGCTTGAGCTCTGTTCTTGTTAAGCTCAGTTTGAGATCTTTGTGGAATCAAGTGGAGAG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAGCTTGAGCTCTGTTCTTGTTAAGCTCAGTTTGAGATCTTTGTGGAATCAAGTGGAGAG  540

Query  541  GTCTAAGCAGGGAAGTGGCTTAGGCTGTAAAGATGAATCTGAGAGTCCCAAGAATA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GTCTAAGCAGGGAAGTGGCTTAGGCTGTAAAGATGAATCTGAGAGTCCCAAGAATA  600

Query  601  TGGTAATTATTAATAAAAGCCTTAGGTANATGAAATTGTTTTGGG  645
          |||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TGGTAATTATTAATAAAAGCCTTAGGTANATGAAATTGTTTTGGG  645
```

Sequence 897 matched with Sequence 359

Query= Sequence ID - 897
Length=509

nt: 509

SEQ ID NO: 359

nt: 509

ALIGNMENTS

Identities = 509/509 (100%), Gaps = 0/509 (0%)

Query	1	GCAAATCTACACATTTGATTAAATGATAGGGA	ACTATGCACACACATAATACATATAATG	60
Sbjct	1	GCAAATCTACACATTTGATTAAATGATAGGGA	ACTATGCACACACATAATACATATAATG	60
Query	61	CTAGTTTCTTGGTTTTGATATTGTACCATAGTTATGTAAGATGTAACCAT	TGGGGGAAAC	120
Sbjct	61	CTAGTTTCTTGGTTTTGATATTGTACCATAGTTATGTAAGATGTAACCAT	TGGGGGAAAC	120
Query	121	TGGGTGAAGGCTACATGAGACCTCTCTGTACTTAATCTTTGCAACTTATGTGAATCTATA		180
Sbjct	121	TGGGTGAAGGCTACATGAGACCTCTCTGTACTTAATCTTTGCAACTTATGTGAATCTATA		180
Query	181	ATTATTCCAAAATAAAAAAGTTTTAAAGAACCTAAGTATCCTTATTACTGAGGGTCATCGT		240
Sbjct	181	ATTATTCCAAAATAAAAAAGTTTTAAAGAACCTAAGTATCCTTATTACTGAGGGTCATCGT		240
Query	241	GCTAGACAGCAAGGTTGGGCCAGAGCTTCTAGTTATTTAAAATACTAAATACCAGCCTGG		300
Sbjct	241	GCTAGACAGCAAGGTTGGGCCAGAGCTTCTAGTTATTTAAAATACTAAATACCAGCCTGG		300
Query	301	GCAACATAGCAAGACCCTGCCTCTACaaaaagcaaaaaaATTAGCTGGGCATGGTGGTAC		360
Sbjct	301	GCAACATAGCAAGACCCTGCCTCTACAAAAAGCAAAAAAATTAGCTGGGCATGGTGGTAC		360
Query	361	ATGCCTGTGGTCCTAGTTACTCTTGGAGGAGTCTGAGGTGGGGAGCTTGAGCCTAGGAGT		420
Sbjct	361	ATGCCTGTGGTCCTAGTTACTCTTGGAGGAGTCTGAGGTGGGGAGCTTGAGCCTAGGAGT		420
Query	421	TTGAGGCCGCAGTGAGCCTTGATTGTGTCTCTGTACTCCAGTCTGGGCCACAGAGCAAGA		480
Sbjct	421	TTGAGGCCGCAGTGAGCCTTGATTGTGTCTCTGTACTCCAGTCTGGGCCACAGAGCAAGA		480

PATENT SEQUENCE ALIGNMENT

Query	481	CCCGGTCTCTAAAAATAAATAAATAAATA	509
Sbjct	481	CCCGGTCTCTAAAAATAAATAAATAAATA	509

Sequence 898 matched with Sequence 360

Query= Sequence ID 898
Length=511

SEQ ID NO: 360

ALIGNMENTS

Identities = 509/509 (100%), Gaps = 0/509 (0%)

Query	3	TGCACTCCAGCTTGGTGACAGAGGGAGACTCCATNTTaaaaaaaaaaaaaaaaaaaaa	62
Sbjct	3	TGCACTCCAGCTTGGTGACAGAGGGAGACTCCATNTTAAAAAAAAAAAAAAAAAAAAA	62
Query	63	aGGGAGTAGCTTGAAGCCACATAGTAGTTAGTGGTAAAGGCCACCCCTTTTCCCACAAC	122
Sbjct	63	AGGGAGTAGCTTGAAGCCACATAGTAGTTAGTGGTAAAGGCCACCCCTTTTCCCACAAC	122
Query	123	CACACCAGCACCACAAGCTAGCCTTTNTAATTTCCAAGCCAGTGCCCTTTCAACGCACAC	182
Sbjct	123	CACACCAGCACCACAAGCTAGCCTTTNTAATTTCCAAGCCAGTGCCCTTTCAACGCACAC	182
Query	183	ACCCCTGTGTCAGTTCCCTTTCTGCTGCAAGCTCTCTGGAGGCAGATACTGTTGAGTCCC	242
Sbjct	183	ACCCCTGTGTCAGTTCCCTTTCTGCTGCAAGCTCTCTGGAGGCAGATACTGTTGAGTCCC	242
Query	243	TGGCCTGCCTATGAGAACGGCTCATGATCTCTATTTCTTCTGCTTAATGACCATCTCGAA	302
Sbjct	243	TGGCCTGCCTATGAGAACGGCTCATGATCTCTATTTCTTCTGCTTAATGACCATCTCGAA	302
Query	303	GTAACAAGTTTAGCCTAAAATAAACTTGCTAAGTTAGCAAAGGAAGTCCTTAGCAGCCAC	362
Sbjct	303	GTAACAAGTTTAGCCTAAAATAAACTTGCTAAGTTAGCAAAGGAAGTCCTTAGCAGCCAC	362
Query	363	CATTTCTCGATTCTCCATCACCTCCCCTGCCCCTCAACTCCCTCATTTCTCCCAAGATA	422
Sbjct	363	CATTTCTCGATTCTCCATCACCTCCCCTGCCCCTCAACTCCCTCATTTCTCCCAAGATA	422
Query	423	TGGGCTCCAGGCTGGGCGCGGTGGCTCACGCCTATAATCCTAGCACTTTGGGAGGCTGAG	482
Sbjct	423	TGGGCTCCAGGCTGGGCGCGGTGGCTCACGCCTATAATCCTAGCACTTTGGGAGGCTGAG	482

PATENT SEQUENCE ALIGNMENT

Query	483	GTGAGCAGATCACTGAGGTCAGGAGTTCG	511
Sbjct	483	GTGAGCAGATCACTGAGGTCAGGAGTTCG	511

Sequence 899 matched with Sequence 361

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 899
Length=16

SEQ ID NO: 361	26.3	2e-06
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ALIGNMENTS

Identities = 13/13 (100%), Gaps = 0/13 (0%)

Query	4	TTCGGAACGCGCC	16
Sbjct	4	TTCGGAACGCGCC	16

Sequence 900 matched with Sequence 362

Query= Sequence ID 900

Length=579

SEQ ID NO: 362

ALIGNMENTS

Identities = 579/579 (100%), Gaps = 0/579 (0%)

Query	1	CTGGAGGGATGGGTAGGATTTTGACAAGAGTGGTTGAAGGTATTCTAATTCACCTAGTAC	60
Sbjct	1	CTGGAGGGATGGGTAGGATTTTGACAAGAGTGGTTGAAGGTATTCTAATTCACCTAGTAC	60
Query	61	CTACATGTGCGAGGCAGCATGAAGGCAAAAAAGCCTGGGGCATGTTTCAGAGAATAGCAAG	120
Sbjct	61	CTACATGTGCGAGGCAGCATGAAGGCAAAAAAGCCTGGGGCATGTTTCAGAGAATAGCAAG	120
Query	121	TATTCTAGTTTGAGTGGCACCTGGTACGTATATAAGGGAATAGTAAAAGATCTGGCTGGA	180
Sbjct	121	TATTCTAGTTTGAGTGGCACCTGGTACGTATATAAGGGAATAGTAAAAGATCTGGCTGGA	180
Query	181	AAGGAAAAGTAGGGGCAGGTTACGAAGGACCTCTGAAAGTCAGACTGTGGAAGTGGAACT	240
Sbjct	181	AAGGAAAAGTAGGGGCAGGTTACGAAGGACCTCTGAAAGTCAGACTGTGGAAGTGGAACT	240
Query	241	TTTATCAGGAAGCAGTAGTTAGTTTTTTCAAGCAAAAGCTAATTAGAGTTGATATTTAGG	300
Sbjct	241	TTTATCAGGAAGCAGTAGTTAGTTTTTTCAAGCAAAAGCTAATTAGAGTTGATATTTAGG	300
Query	301	AGGATGAATCTAACAGTTGTGTGCAAGGATGCCTTCAAAGTGAAGTGAAGTGAAGTGAAGT	360
Sbjct	301	AGGATGAATCTAACAGTTGTGTGCAAGGATGCCTTCAAAGTGAAGTGAAGTGAAGTGAAGT	360
Query	361	GACTGGTTAAGAGACTACAACAATAACCTGAGTAAGAATTAATACAGGCCTGACCTAGTT	420
Sbjct	361	GACTGGTTAAGAGACTACAACAATAACCTGAGTAAGAATTAATACAGGCCTGACCTAGTT	420
Query	421	TTGAGTGAGTAGGATTGGAAACAAGAGTTTTAGGTATTATAGGATTTATGCATATAAAAT	480
Sbjct	421	TTGAGTGAGTAGGATTGGAAACAAGAGTTTTAGGTATTATAGGATTTATGCATATAAAAT	480

PATENT SEQUENCE ALIGNMENT

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Query  481  GGACTTGACAGAACTTGAAGAAAGAGAAAGTGTCAAAGGACACAGAAAGTGAGGCAGGA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGACTTGACAGAACTTGAAGAAAGAGAAAGTGTCAAAGGACACAGAAAGTGAGGCAGGA  540

Query  541  TATCTTACAATGTTAAAGGAAAGGAATAATAGAAGTTAC  579
          |||||||||||||||||||||||||||||||||||
Sbjct  541  TATCTTACAATGTTAAAGGAAAGGAATAATAGAAGTTAC  579
```

Sequence 903 matched with Sequence 363

Query= Sequence ID 903
Length=185

SEQ ID NO: 363

ALIGNMENTS

Identities = 185/185 (100%), Gaps = 0/185 (0%)

Query	1	GGAAACATAAGCTTGTTTCAGTACACTCACGCTGTAGATTAATTCTGATATTACATATCT	60
Sbjct	1	GGAAACATAAGCTTGTTTCAGTACACTCACGCTGTAGATTAATTCTGATATTACATATCT	60
Query	61	CCATCAGACTTTGTACCCTCTCTCTTCCATCCCTTACCCTTACCGATTAGGTTGGTATTA	120
Sbjct	61	CCATCAGACTTTGTACCCTCTCTCTTCCATCCCTTACCCTTACCGATTAGGTTGGTATTA	120
Query	121	CCTAAAAATCCATAGAAAATGTCCAGGTGAATTGCCTTATGCTTTCTACCCCATAAGGTA	180
Sbjct	121	CCTAAAAATCCATAGAAAATGTCCAGGTGAATTGCCTTATGCTTTCTACCCCATAAGGTA	180
Query	181	TAATT 185	
Sbjct	181	TAATT 185	

Sequence 904 matched with Sequence 364

Query= Sequence ID 904
Length=649

SEQ ID NO: 364

ALIGNMENTS

Identities = 648/648 (100%), Gaps = 0/648 (0%)

Query	1	CTCTGTGGTGTGAGAACACAGTGGGTGACCAAGGCTTTCCAGATGAACCCAAGGAAAGTG	60
Sbjct	1	CTCTGTGGTGTGAGAACACAGTGGGTGACCAAGGCTTTCCAGATGAACCCAAGGAAAGTG	60
Query	61	AAAAAGCTGATGCTAATAACCAGACAACAGAACCTCAGCTTAAGAAAGGCAGCCAAGTGG	120
Sbjct	61	AAAAAGCTGATGCTAATAACCAGACAACAGAACCTCAGCTTAAGAAAGGCAGCCAAGTGG	120
Query	121	AGGCACTCTTCAGTTATGAGGCTACCCAACCAGAGGACCTGGAGTTTCAGGAAGGGGATA	180
Sbjct	121	AGGCACTCTTCAGTTATGAGGCTACCCAACCAGAGGACCTGGAGTTTCAGGAAGGGGATA	180
Query	181	TAATCCTGGTGTATCAAAGGTGAATGAAGAATGGCTGGAAGGGGAGTGCAAAGGGAAGG	240
Sbjct	181	TAATCCTGGTGTATCAAAGGTGAATGAAGAATGGCTGGAAGGGGAGTGCAAAGGGAAGG	240
Query	241	TGGGCATTTTCCCCAAAGTTTTTGTGTAAGACTGCGCAACTACAGATTTGGAAAGCACTC	300
Sbjct	241	TGGGCATTTTCCCCAAAGTTTTTGTGTAAGACTGCGCAACTACAGATTTGGAAAGCACTC	300
Query	301	GGAGAGAAGTCTAGGATGTTTCACAAACTACAAAGCTGAAGAAAATGAAGCCCTATTACT	360
Sbjct	301	GGAGAGAAGTCTAGGATGTTTCACAAACTACAAAGCTGAAGAAAATGAAGCCCTATTACT	360
Query	361	TGTTTGTAAGATTTAGCACCTTCTGCTGTATACTGTACTGAGACATTACAGTTTGGAAG	420
Sbjct	361	TGTTTGTAAGATTTAGCACCTTCTGCTGTATACTGTACTGAGACATTACAGTTTGGAAG	420
Query	421	TGTAACTATTTATTCCCTGTGTTAAATTTAACCTACTAGACAATGATGTGAGTACCCAGG	480
Sbjct	421	TGTAACTATTTATTCCCTGTGTTAAATTTAACCTACTAGACAATGATGTGAGTACCCAGG	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 ATGATTTCTGGGGCACAGTGGGTGAGGAGATGGGGACAGGTGAATGGAGGAGTTAGGGG 540
          |||
Sbjct 481 ATGATTTCTGGGGCACAGTGGGTGAGGAGATGGGGACAGGTGAATGGAGGAGTTAGGGG 540

Query 541 AGAGGAAAAGTGGATGGAAGTGTCTGGAAAGGGCACCAAAAAGTCTTCCAGGTCTGATC 600
          |||
Sbjct 541 AGAGGAAAAGTGGATGGAAGTGTCTGGAAAGGGCACCAAAAAGTCTTCCAGGTCTGATC 600

Query 601 CTGTTTCTTGCTCTGAGTGCTAGCTACCACTGTGTCACACTGTAACAT 648
          |||
Sbjct 601 CTGTTTCTTGCTCTGAGTGCTAGCTACCACTGTGTCACACTGTAACAT 648
```

Sequence 905 matched with Sequence 365

Query= Sequence ID - 905
Length=655

nt: 655

SEQ ID NO: 365

nt: 655

ALIGNMENTS

Identities = 655/655 (100%), Gaps = 0/655 (0%)

Query	1	CTCAGCTCTTGCCTGGTCACCTTGTGGCTTTTACCATCCTCATCCCCTGTGCCACCCACA	60
Sbjct	1	CTCAGCTCTTGCCTGGTCACCTTGTGGCTTTTACCATCCTCATCCCCTGTGCCACCCACA	60
Query	61	TCCTGCCACTTCTGCATGGAGTTGGGGTGGGGCCATTGGAGAAAAGAGGTTAAACAAGCA	120
Sbjct	61	TCCTGCCACTTCTGCATGGAGTTGGGGTGGGGCCATTGGAGAAAAGAGGTTAAACAAGCA	120
Query	121	GTAATTTACTTGAGTACAGTCTTTGAGCCAATGAAATGCCAGTCATCATTTCCCAGGGGT	180
Sbjct	121	GTAATTTACTTGAGTACAGTCTTTGAGCCAATGAAATGCCAGTCATCATTTCCCAGGGGT	180
Query	181	ACTTGTCATCTTGTCAACAACCCGCTGATAATGCTCCTTCAATGTGAATAGCAAAAGTAG	240
Sbjct	181	ACTTGTCATCTTGTCAACAACCCGCTGATAATGCTCCTTCAATGTGAATAGCAAAAGTAG	240
Query	241	GGAGAGACGCTGAATGAAGAAGATGCCTACCCCTCAGGAAGACTGCTGTCCGCCTCCAGG	300
Sbjct	241	GGAGAGACGCTGAATGAAGAAGATGCCTACCCCTCAGGAAGACTGCTGTCCGCCTCCAGG	300
Query	301	CCtgcacacacacccatgcccacctgcacccccagcaccacgcccacactcactcgca	360
Sbjct	301	CCTGCATGCACACACCCATGCCCACCTGCACCCCAGCACCACGCCCACACTCACTCGCA	360
Query	361	cacacccacatgccagTGTGTTTGGGGTTGGCAGCCTGGACACTGCTGAGGCAAACACAAG	420
Sbjct	361	CACACCCACATGCCAGTGTGTTTGGGGTTGGCAGCCTGGACACTGCTGAGGCAAACACAAG	420
Query	421	TCATCAAGCATAATTCTCATTCTCTCCTTCTGTCTCTGTTTTAGTTACAGGAATTTGGTC	480
Sbjct	421	TCATCAAGCATAATTCTCATTCTCTCCTTCTGTCTCTGTTTTAGTTACAGGAATTTGGTC	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGTTTAGAGGATTTAATAAGTCCGTGGAAAATTTGTTTCTGTCTCTTGCTACCCACGTGA	540
Sbjct	481	AGTTTAGAGGATTTAATAAGTCCGTGGAAAATTTGTTTCTGTCTCTTGCTACCCACGTGA	540
Query	541	AAAGTAAGTGCATGCTTCATGATGTGTTTTCCCACTACCTTCCAGGCCAGCCGAGCCCAC	600
Sbjct	541	AAAGTAAGTGCATGCTTCATGATGTGTTTTCCCACTACCTTCCAGGCCAGCCGAGCCCAC	600
Query	601	TGGCCANGGCCTGGCCCGGTGACCTCGGTTGACACTGTCCTCANGCCACTCACTT	655
Sbjct	601	TGGCCANGGCCTGGCCCGGTGACCTCGGTTGACACTGTCCTCANGCCACTCACTT	655

Sequence 906 matched with Sequence 366

Query= Sequence ID 906
Length=334

SEQ ID NO: 366

ALIGNMENTS

Identities = 334/334 (100%), Gaps = 0/334 (0%)

Query	1	CAGAATTTTCATGTTTATGCTGCACAAGGCCTGTATTTTATAATGGTGGCTCTTTTGGACG	60
Sbjct	1	CAGAATTTTCATGTTTATGCTGCACAAGGCCTGTATTTTATAATGGTGGCTCTTTTGGACG	60
Query	61	ATGACTTCCTCGATGGTGAAACTTCCAGTAATCTCCCTCATCATACTGAAATGATATCAG	120
Sbjct	61	ATGACTTCCTCGATGGTGAAACTTCCAGTAATCTCCCTCATCATACTGAAATGATATCAG	120
Query	121	TATATCATCAGAACACCATGGAGCTTGTCATTTGAGGGACACAGCTTGCTTGTGTGCTTG	180
Sbjct	121	TATATCATCAGAACACCATGGAGCTTGTCATTTGAGGGACACAGCTTGCTTGTGTGCTTG	180
Query	181	GGAAAGAAGAGGTTTAGCATGGTTTCAGGTCAGTGATGAGTCCAATGATCTCTGCAAGTT	240
Sbjct	181	GGAAAGAAGAGGTTTAGCATGGTTTCAGGTCAGTGATGAGTCCAATGATCTCTGCAAGTT	240
Query	241	CCCTTAGCTCTGANAATTCTGATGTCATATGCACTTCTGCCGCCAGAGTTGCTGCTTACT	300
Sbjct	241	CCCTTAGCTCTGANAATTCTGATGTCATATGCACTTCTGCCGCCAGAGTTGCTGCTTACT	300
Query	301	GGATGCGTAAGAAGAAAAGaaaaaaaaaaaaaaaaa	334
Sbjct	301	GGATGCGTAAGAAGAAAAGAAAAAAAAAAAAAAAAA	334

Sequence 907 matched with Sequence 367

Query= Sequence ID - 907
Length=582

nt: 582

SEQ ID NO: 367

nt: 582

ALIGNMENTS

Identities = 582/582 (100%), Gaps = 0/582 (0%)

Query	1	CTTCCATTGGGGGTAAAGATCAAACCTTAGGCGAGCCAGGTCTGTATCTCCATTCCTGTC	60
Sbjct	1	CTTCCATTGGGGGTAAAGATCAAACCTTAGGCGAGCCAGGTCTGTATCTCCATTCCTGTC	60
Query	61	TCTGACTGCTTCCCTGTAGGGATTGTCTGCAAGCGCACACCTGCATTTTCTTGTCCACAA	120
Sbjct	61	TCTGACTGCTTCCCTGTAGGGATTGTCTGCAAGCGCACACCTGCATTTTCTTGTCCACAA	120
Query	121	GTCTATGCTCTAACTCTGTACCTGCATGGCTGCAAATTAGCTTCCTTCTTCCTGCCCTC	180
Sbjct	121	GTCTATGCTCTAACTCTGTACCTGCATGGCTGCAAATTAGCTTCCTTCTTCCTGCCCTC	180
Query	181	TTCTCTCTAGCTTGGATTTTGAATTTGAATGGCAGGCATGGGATGTCCGTGTGTGTGTAC	240
Sbjct	181	TTCTCTCTAGCTTGGATTTTGAATTTGAATGGCAGGCATGGGATGTCCGTGTGTGTGTAC	240
Query	241	TGCTGATGTGTACAGCCGCTTGTTAGCGCTCTCATTGTCTTCAAATGTAAGTCATTTTGG	300
Sbjct	241	TGCTGATGTGTACAGCCGCTTGTTAGCGCTCTCATTGTCTTCAAATGTAAGTCATTTTGG	300
Query	301	CTGGGTGCGGTGGCTCATGCGTATAATCCCACGCTTTGGGAGGCTGAGGTGAGCTGATCA	360
Sbjct	301	CTGGGTGCGGTGGCTCATGCGTATAATCCCACGCTTTGGGAGGCTGAGGTGAGCTGATCA	360
Query	361	TTTGAGGTAGGAGTTCGAGACCAGCCTGGCCAACATGGCAAACTCCATCTCTACCAAA	420
Sbjct	361	TTTGAGGTAGGAGTTCGAGACCAGCCTGGCCAACATGGCAAACTCCATCTCTACCAAA	420
Query	421	AATACAAAAATTAGCTGGGTATGGTAGTGACGCCTGTAATCCCAGCTACTTGGAATGCT	480
Sbjct	421	AATACAAAAATTAGCTGGGTATGGTAGTGACGCCTGTAATCCCAGCTACTTGGAATGCT	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 GAAGCAGGAGAATTGCCTGAACCCANGAGGCGGAGGTTGCGGTGAGCCAAGATCACGCCA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 GAAGCAGGAGAATTGCCTGAACCCANGAGGCGGAGGTTGCGGTGAGCCAAGATCACGCCA 540

Query 541 CTGCACTCCAACCTGGGTGACAGAGCAAGGCTGTGTCTCAAA 582
          ||||||||||||||||||||||||||||||||||||||||
Sbjct 541 CTGCACTCCAACCTGGGTGACAGAGCAAGGCTGTGTCTCAAA 582
```

Sequence 908 matched with Sequence 368

Query= Sequence ID 908
Length=530

SEQ ID NO: 368

ALIGNMENTS

Identities = 530/530 (100%), Gaps = 0/530 (0%)

Query	1	ACCTGACTTCAAACCTATACTACGAGGCTACAGTAATCAAAACAGCATGGTACTAGTACAA	60
Sbjct	1	ACCTGACTTCAAACCTATACTACGAGGCTACAGTAATCAAAACAGCATGGTACTAGTACAA	60
Query	61	AAACAGACCAATGGAACAGAATAGAGATCTCAGAAATAAACTGCACATCTACAACCATC	120
Sbjct	61	AAACAGACCAATGGAACAGAATAGAGATCTCAGAAATAAACTGCACATCTACAACCATC	120
Query	121	TGATCTTCAACAAACCTGACAAAACGAGCAATGGGGAAAGGATTCCCTATTTAATAAATG	180
Sbjct	121	TGATCTTCAACAAACCTGACAAAACGAGCAATGGGGAAAGGATTCCCTATTTAATAAATG	180
Query	181	GTGCTGGGAGAACTGGCTAGCCATGTGCAGAAAATTGAAACTGGACCCCTTCCTTACACC	240
Sbjct	181	GTGCTGGGAGAACTGGCTAGCCATGTGCAGAAAATTGAAACTGGACCCCTTCCTTACACC	240
Query	241	TTATACAAAAATTAACCTCAAGATGGATTAAAGACTTAAATGTAGAACCCAAAACGATAAA	300
Sbjct	241	TTATACAAAAATTAACCTCAAGATGGATTAAAGACTTAAATGTAGAACCCAAAACGATAAA	300
Query	301	AACCCTAGAAGAAAATCTAGGCAATATCATTAAGGACATAGACATGGGCAAAAATTTTCAT	360
Sbjct	301	AACCCTAGAAGAAAATCTAGGCAATATCATTAAGGACATAGACATGGGCAAAAATTTTCAT	360
Query	361	GATGAAAACATCAAAAGCAATGGCAACAAAAGCAGAACTGACAAATGGGCTTCTGCACA	420
Sbjct	361	GATGAAAACATCAAAAGCAATGGCAACAAAAGCAGAACTGACAAATGGGCTTCTGCACA	420
Query	421	GCAAAAAGAACTATCGTCAGAGTGAACAGACAACCTACAGAATGGGAGACAGTTTTTGCA	480
Sbjct	421	GCAAAAAGAACTATCGTCAGAGTGAACAGACAACCTACAGAATGGGAGACAGTTTTTGCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	ATCTATCCATCTGACAAAAGTCTAATATCCAGAATCTACAAGGAATTAA	530
Sbjct	481	ATCTATCCATCTGACAAAAGTCTAATATCCAGAATCTACAAGGAATTAA	530

Sequence 910 matched with Sequence 369

Query= Sequence ID 910
Length=653

SEQ ID NO: 369

ALIGNMENTS

Identities = 653/653 (100%), Gaps = 0/653 (0%)

Query	1	CAAAAAACAAGAATTACCCGGGCTTGGTGGTGCATGTCTGTAGTCCTATCTACTCAGGAG	60
Sbjct	1	CAAAAAACAAGAATTACCCGGGCTTGGTGGTGCATGTCTGTAGTCCTATCTACTCAGGAG	60
Query	61	GCTGAGGCTGAAGGATCACTTGAGCCCAGGAGTTTGAGGCTGCAGTGAGTGAGCCATGAT	120
Sbjct	61	GCTGAGGCTGAAGGATCACTTGAGCCCAGGAGTTTGAGGCTGCAGTGAGTGAGCCATGAT	120
Query	121	CATGCCAGTGTACTCCAGCCTTGGCAGACTGAGCAAACTTGGTCCCTCGCAAAATGTTG	180
Sbjct	121	CATGCCAGTGTACTCCAGCCTTGGCAGACTGAGCAAACTTGGTCCCTCGCAAAATGTTG	180
Query	181	AAGCCCAGTTTTCACTATTAACCTGTATTTCAAGTTTCCCATGCTAACTTTGAAACACTG	240
Sbjct	181	AAGCCCAGTTTTCACTATTAACCTGTATTTCAAGTTTCCCATGCTAACTTTGAAACACTG	240
Query	241	GGGCTGGCCTGAGGGTATAAAGGCTTATTCAAACCTCAGTAATTTAAACTTAAATCCTAA	300
Sbjct	241	GGGCTGGCCTGAGGGTATAAAGGCTTATTCAAACCTCAGTAATTTAAACTTAAATCCTAA	300
Query	301	GGAACCTCAAAAAGTGTAATCTAGTCCAAATGGGGCATCAATTCTAAAGCATTGCTTGT	360
Sbjct	301	GGAACCTCAAAAAGTGTAATCTAGTCCAAATGGGGCATCAATTCTAAAGCATTGCTTGT	360
Query	361	TTGAGCAGATTTTCTGTGTCTGAGGTATATAGATAACTTATCTTTTATGACTAAATCCA	420
Sbjct	361	TTGAGCAGATTTTCTGTGTCTGAGGTATATAGATAACTTATCTTTTATGACTAAATCCA	420
Query	421	AGTCCTTAGTTCCTGTTGGAATTCAAAATCATATTTAAAAATTGATGCTTTGTTCTATAA	480
Sbjct	421	AGTCCTTAGTTCCTGTTGGAATTCAAAATCATATTTAAAAATTGATGCTTTGTTCTATAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTAATGCTTTGATTGTATAAATAATAAGTATTCTTCCAAATCCCTTTTTACAGATGATGA	540
Sbjct	481	TTAATGCTTTGATTGTATAAATAATAAGTATTCTTCCAAATCCCTTTTTACAGATGATGA	540
Query	541	TTCTGATACCGAGACGTCAAATGACTTGCCAAAATTTGCAGATGGAATCAAGGCCNGAAA	600
Sbjct	541	TTCTGATACCGAGACGTCAAATGACTTGCCAAAATTTGCAGATGGAATCAAGGCCNGAAA	600
Query	601	CAGAAATCAGAACTACCTGGNTCCCAGTCCTGTNCTTAAAATTCTAACTCGAC	653
Sbjct	601	CAGAAATCAGAACTACCTGGNTCCCAGTCCTGTNCTTAAAATTCTAACTCGAC	653

Sequence 911 matched with Sequence 370

Query= Sequence ID - 911
Length=595

nt: 595

SEQ ID NO: 370

nt: 595

ALIGNMENTS

Identities = 595/595 (100%), Gaps = 0/595 (0%)

Query	1	GAGGGTGTAGAAGAGAAGAAGAAGGAGGTTCTGCTGTGCCANAAACCCTTAAGAAAAAG	60
Sbjct	1	GAGGGTGTAGAAGAGAAGAAGAAGGAGGTTCTGCTGTGCCANAAACCCTTAAGAAAAAG	60
Query	61	CGAAGGAATTCGCAGAGCTGAAGATCAAGCGCCTGAGAAAGAAGTTTGCCCAAAGATG	120
Sbjct	61	CGAAGGAATTCGCAGAGCTGAAGATCAAGCGCCTGAGAAAGAAGTTTGCCCAAAGATG	120
Query	121	CTTCGAAAGGCAAGGAGGAAGCTTATCTATGAAAAANCAAAGCACTATCACAAGGAATAT	180
Sbjct	121	CTTCGAAAGGCAAGGAGGAAGCTTATCTATGAAAAANCAAAGCACTATCACAAGGAATAT	180
Query	181	AGGCAGATGTACAAANCTGAAATTCGAATGGCGAGGATGGCAAGAAAAGCTGGCAACTTC	240
Sbjct	181	AGGCAGATGTACAAANCTGAAATTCGAATGGCGAGGATGGCAAGAAAAGCTGGCAACTTC	240
Query	241	TATGTACCTGCAGAACCCAAATTGGCGTTTGTTCATCAGAATCAGAGGTATCAATGGAGTG	300
Sbjct	241	TATGTACCTGCAGAACCCAAATTGGCGTTTGTTCATCAGAATCAGAGGTATCAATGGAGTG	300
Query	301	AGCCCAAAGGTTTCGAAAGGTGTTGCAGCTTCTTCGCCTTCGTCAAATCTTCAATGGAACC	360
Sbjct	301	AGCCCAAAGGTTTCGAAAGGTGTTGCAGCTTCTTCGCCTTCGTCAAATCTTCAATGGAACC	360
Query	361	TTTGTGAAGCTCAACAAGGCTTCGATTAACATGCTGAGGATTGTAGAGCCATATATTGCA	420
Sbjct	361	TTTGTGAAGCTCAACAAGGCTTCGATTAACATGCTGAGGATTGTAGAGCCATATATTGCA	420
Query	421	TGGGGGTACCCCAATCTGAAGTCAGTAAATGAACTAATCTACAAGCGTGGTTATGGCAA	480
Sbjct	421	TGGGGGTACCCCAATCTGAAGTCAGTAAATGAACTAATCTACAAGCGTGGTTATGGCAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	ATCAATAAGAAGCGAATTGCTTTGACAGATAACGCTTTGATTGCTCGATCTCTTGGTAAA	540
Sbjct	481	ATCAATAAGAAGCGAATTGCTTTGACAGATAACGCTTTGATTGCTCGATCTCTTGGTAAA	540
Query	541	TACNGCATCATCTGCATGGAGGATTTGATTCATGAGATCTATACTGTTGAAAAAC	595
Sbjct	541	TACNGCATCATCTGCATGGAGGATTTGATTCATGAGATCTATACTGTTGAAAAAC	595

Sequence 912 matched with Sequence 371

Query= Sequence ID - 912
Length=651

nt: 651

SEQ ID NO: 371

nt: 651

ALIGNMENTS

Identities = 651/651 (100%), Gaps = 0/651 (0%)

Query	1	CATTTCCAGAGTTTATGTGAATTGAATTGAACTATGGTTTTATGTTACTGTCAGTAGAAT	60
Sbjct	1	CATTTCCAGAGTTTATGTGAATTGAATTGAACTATGGTTTTATGTTACTGTCAGTAGAAT	60
Query	61	GAAGTACGAATATTTGAAAAATACACCTTCAACTTCAAAGTGATTCTTGACAAAAATTAT	120
Sbjct	61	GAAGTACGAATATTTGAAAAATACACCTTCAACTTCAAAGTGATTCTTGACAAAAATTAT	120
Query	121	AAGGAATCATTTTGGACACATTTTCTGGTAGAGCCTTGTA AAAAATTA AACCAAGTGTTG	180
Sbjct	121	AAGGAATCATTTTGGACACATTTTCTGGTAGAGCCTTGTA AAAAATTA AACCAAGTGTTG	180
Query	181	TTTTCAAGAAGAACTGTAATACATAATCAGGAATTTGAGTAGGGAGATTATTTTGTTATT	240
Sbjct	181	TTTTCAAGAAGAACTGTAATACATAATCAGGAATTTGAGTAGGGAGATTATTTTGTTATT	240
Query	241	TAAAATTAAAGTGGCTGTGTAGTTTAACTTTAGTATTGCAGGTAGAGTAAGCTTACATG	300
Sbjct	241	TAAAATTAAAGTGGCTGTGTAGTTTAACTTTAGTATTGCAGGTAGAGTAAGCTTACATG	300
Query	301	ATAACAAAAATCTTGGTCTTAGTGACTTAATGATTCTGATATTTATTGATTGATTGGTTA	360
Sbjct	301	ATAACAAAAATCTTGGTCTTAGTGACTTAATGATTCTGATATTTATTGATTGATTGGTTA	360
Query	361	TCATTCCAAATATTTTAAAAGATAATAGCTGGCTGGGTGCGGTGGCTCATGCCTGTAATC	420
Sbjct	361	TCATTCCAAATATTTTAAAAGATAATAGCTGGCTGGGTGCGGTGGCTCATGCCTGTAATC	420
Query	421	CCAGCACTTTGGGAGGCCAGGACGGGCGGATCACGAGGTCAGGAGATCAAGACCATCCTG	480
Sbjct	421	CCAGCACTTTGGGAGGCCAGGACGGGCGGATCACGAGGTCAGGAGATCAAGACCATCCTG	480

Query	481	GCTAACACGGTGAAACCCCGTCTCTACTaaaaatcaaaaaaTTAGCCGGGTGTAGTGGCG	540
Sbjct	481	GCTAACACGGTGAAACCCCGTCTCTACTAAAAATCAAAAAATTAGCCGGGTGTAGTGGCG	540
Query	541	GGCACCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGCATGAACCTGGGAG	600
Sbjct	541	GGCACCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGCATGAACCTGGGAG	600
Query	601	GCGGAGCTTGCAGTGAGCTGAAATCGTGCCACTGCCTCCACCTGGCGACAA	651
Sbjct	601	GCGGAGCTTGCAGTGAGCTGAAATCGTGCCACTGCCTCCACCTGGCGACAA	651

Sequence 913 matched with Sequence 372

Query= Sequence ID 913
Length=531

SEQ ID NO: 372

ALIGNMENTS

Identities = 531/531 (100%), Gaps = 0/531 (0%)

Query	1	GTGAGGTGGGGACTTCATTCA	60
Sbjct	1	GTGAGGTGGGGACTTCATTCA	60
Query	61	TCAGGGGAGGTGGAGGAGGAG	120
Sbjct	61	TCAGGGGAGGTGGAGGAGGAG	120
Query	121	CCAGTTACTTGGGGGAGGACAG	180
Sbjct	121	CCAGTTACTTGGGGGAGGACAG	180
Query	181	CGGCTGCATCTTTGTCCCGAT	240
Sbjct	181	CGGCTGCATCTTTGTCCCGAT	240
Query	241	TTNCCCTGGGCTGCGCCCACT	300
Sbjct	241	TTNCCCTGGGCTGCGCCCACT	300
Query	301	CACCCTCTGCTTCCTGGTGCT	360
Sbjct	301	CACCCTCTGCTTCCTGGTGCT	360
Query	361	AGGGAAGAGGAGTGTCCGTAG	420
Sbjct	361	AGGGAAGAGGAGTGTCCGTAG	420
Query	421	TGGGTGATTTTAGTCTCTACA	480
Sbjct	421	TGGGTGATTTTAGTCTCTACA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TGACCCTTTGCTGATGCTGGGGGGAGGGGATCTAAATCCTCATTATCTCT	531
Sbjct	481	TGACCCTTTGCTGATGCTGGGGGGAGGGGATCTAAATCCTCATTATCTCT	531

Sequence 914 matched with Sequence 373

Query= Sequence ID 914
Length=602

SEQ ID NO: 373

ALIGNMENTS

Identities = 602/602 (100%), Gaps = 0/602 (0%)

Query	1	GGCGCCTGCTGGAGGAGGAGAGAGCTCTGCTGGCATGAGCCACAGTTTCTTGA	60
Sbjct	1	GGCGCCTGCTGGAGGAGGAGAGAGCTCTGCTGGCATGAGCCACAGTTTCTTGA	60
Query	61	CCATCAACCCTCTTGGTTGAGGCCTTGTTCTGAGCCCTGACATGTGCTTGGGCA	120
Sbjct	61	CCATCAACCCTCTTGGTTGAGGCCTTGTTCTGAGCCCTGACATGTGCTTGGGCA	120
Query	121	GGCCTGGGCTTCTGAGGTGGCCTCCTGCCCTGATCAGGGACCCTCCCCGCTT	180
Sbjct	121	GGCCTGGGCTTCTGAGGTGGCCTCCTGCCCTGATCAGGGACCCTCCCCGCTT	180
Query	181	CTCTCAGTTGAACAAAGCAGCAAAACAAAGGCAGTTTTATATGAAAGATTANA	240
Sbjct	181	CTCTCAGTTGAACAAAGCAGCAAAACAAAGGCAGTTTTATATGAAAGATTANA	240
Query	241	AATAATCAGGCTTTTTAAATGATGTAATCCCACTGTAATAGCATAGGGATTT	300
Sbjct	241	AATAATCAGGCTTTTTAAATGATGTAATCCCACTGTAATAGCATAGGGATTT	300
Query	301	AGCTGCTGGTGGCTTGGGACATCAGTGGGGCCAAGGGTTCTCTGTCCCTGGT	360
Sbjct	301	AGCTGCTGGTGGCTTGGGACATCAGTGGGGCCAAGGGTTCTCTGTCCCTGGT	360
Query	361	GATTTGGCTTTCCCGTGTCTTTCTGGTGATGCCTTGTTGGGGTTCTGTGGGT	420
Sbjct	361	GATTTGGCTTTCCCGTGTCTTTCTGGTGATGCCTTGTTGGGGTTCTGTGGGT	420
Query	421	GGGAAGAGGGCCATCTGCCTGAATGTAACCTGCTAGCTCTCCGAAGCCCTGC	480
Sbjct	421	GGGAAGAGGGCCATCTGCCTGAATGTAACCTGCTAGCTCTCCGAAGCCCTGC	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTGTGTGAACCGTGTGGACAGTGGTGGCCGCGCTGTGCCTGCTCGTGTTGCCTACATGTC	540
Sbjct	481	TTGTGTGAACCGTGTGGACAGTGGTGGCCGCGCTGTGCCTGCTCGTGTTGCCTACATGTC	540
Query	541	CCTGGCTGTTGAGGCGCTGCTTTAACCTGCACCCCTNCCTTGCTCATANATGCTCCTTTT	600
Sbjct	541	CCTGGCTGTTGAGGCGCTGCTTTAACCTGCACCCCTNCCTTGCTCATANATGCTCCTTTT	600
Query	601	GA	602
Sbjct	601	GA	602

Sequence 915 matched with Sequence 374

Query= Sequence ID - 915 nt: 230
Length=230

SEQ ID NO: 374 nt: 230

ALIGNMENTS

Identities = 230/230 (100%), Gaps = 0/230 (0%)

Query	1	TTTGAGACCAGCCTAGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAATTAG	60
Sbjct	1	TTTGAGACCAGCCTAGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAATTAG	60
Query	61	CCGGGCGTGGCGGCACATGCCTATAATCCCACTTACTTGGGAGGCTGANGTAGGAGAATC	120
Sbjct	61	CCGGGCGTGGCGGCACATGCCTATAATCCCACTTACTTGGGAGGCTGANGTAGGAGAATC	120
Query	121	GCTTGAACCCANANAGGCAGAGTTTGCAGTGAGCCGAGATTGTGCCATTGCACTCCAGCC	180
Sbjct	121	GCTTGAACCCANANAGGCAGAGTTTGCAGTGAGCCGAGATTGTGCCATTGCACTCCAGCC	180
Query	181	TGGGCGACAGAGCGAGACTCCATCTaaaaaTAAATGAATAAAATAA	230
Sbjct	181	TGGGCGACAGAGCGAGACTCCATCTAAAAAATAAATGAATAAAATAA	230

Sequence 917 matched with Sequence 375

Query= Sequence ID 917
Length=483

SEQ ID NO: 375

ALIGNMENTS

Identities = 481/481 (100%), Gaps = 0/481 (0%)

Query	3	CAGAtttttttttttttttttCAGNGTTAGACCATCTTTCAATTCCTGGAACAACTTAACT	62
Sbjct	3	CAGATTTTttttttttttttttttCAGNGTTAGACCATCTTTCAATTCCTGGAACAACTTAACT	62
Query	63	TTCCATGATATGtattttttatacattgctggattttatttgctaataattttacttagga	122
Sbjct	63	TTCCATGATATGTATTTTttttatacATTGCTGGATTTTATTTGCTAATATTTTACTTAGGA	122
Query	123	tttaattttCTAAGTNGACCTATAATTNTCCTGTATAAAATTGCATTGTGCACATTTTAG	182
Sbjct	123	TTTAATTTTCTAAGTNGACCTATAATTNTCCTGTATAAAATTGCATTGTGCACATTTTAG	182
Query	183	TATCAAGGTTGTCCTANCNCCATGAAATGGATTTANAATGGTTTATGTAANATAAAGTAC	242
Sbjct	183	TATCAAGGTTGTCCTANCNCCATGAAATGGATTTANAATGGTTTATGTAANATAAAGTAC	242
Query	243	ATTTCTTCTAAAGGTTTGNGTGGATTAACCTTTCAAATCTGCCANAGNGNGtttttttccct	302
Sbjct	243	ATTTCTTCTAAAGGTTTGNGTGGATTAACCTTTCAAATCTGCCANAGNGNGTTTTTTTCTCT	302
Query	303	ttttttttttttttttCATTtTNAAGGGAGNGCAAGTANCtttttcaaatnctgatttaatttt	362
Sbjct	303	TTTTTTTTTTTTTTTCATTtTNAAGGGAGNGCAAGTANCtttttcaaatNCTGATTTAATTTT	362
Query	363	taaaatatttncaagtntntttanagtttttattntntntngaangttaacattttttata	422
Sbjct	363	TAAAATATTNCAAGTNTNTTTANAGTTTTTATTTNTNTNGAANGTTAACATTTTTTATA	422
Query	423	naaaanGGTNTTATCTTTTTAAATTCTTTGACATCAGTTTCTTCANAATTCCTTCTTTTA	482
Sbjct	423	NAAAANGGTNTTATCTTTTTAAATTCTTTGACATCAGTTTCTTCANAATTCCTTCTTTTA	482

PATENT SEQUENCE ALIGNMENT

Query	483	A	483
Sbjct	483	A	483

Sequence 926 matched with Sequence 376

Query= Sequence ID 926

Length=538

SEQ ID NO: 376

ALIGNMENTS

Identities = 538/538 (100%), Gaps = 0/538 (0%)

Query	1	GTCATATCTCTTCCCAGGGAAAGCAGGAGCCCTTCTGGAGCCCTTCAGCAGGGTCAGGGC	60
Sbjct	1	GTCATATCTCTTCCCAGGGAAAGCAGGAGCCCTTCTGGAGCCCTTCAGCAGGGTCAGGGC	60
Query	61	CCCTCGTCTTCCCCTCCTTTCCAGAGCCATCTTCCCAGTCCACCATCCCCATCGTGGGC	120
Sbjct	61	CCCTCGTCTTCCCCTCCTTTCCAGAGCCATCTTCCCAGTCCACCATCCCCATCGTGGGC	120
Query	121	ATTGTTGCTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTGGTCGCTACTGTG	180
Sbjct	121	ATTGTTGCTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTGGTCGCTACTGTG	180
Query	181	ATGTGTAGGAGGAAGAGCTCAGGTAGGGAAGGGGTGAGGGGTGGGGTCTGGGTTTTCTTG	240
Sbjct	181	ATGTGTAGGAGGAAGAGCTCAGGTAGGGAAGGGGTGAGGGGTGGGGTCTGGGTTTTCTTG	240
Query	241	TCCCACTGGGGGTTTCAAGCCCCAGGTAGAAGTGTTCCCTGCCTCATTACTGGGAAGCAG	300
Sbjct	241	TCCCACTGGGGGTTTCAAGCCCCAGGTAGAAGTGTTCCCTGCCTCATTACTGGGAAGCAG	300
Query	301	CATCCACACAGGGGCTAACGCAGCCTGGGACCCTGTGTGCCAGCACTTACTCTTTTGTGC	360
Sbjct	301	CATCCACACAGGGGCTAACGCAGCCTGGGACCCTGTGTGCCAGCACTTACTCTTTTGTGC	360
Query	361	AGCACATGTGACAATGAAGGACGGATGTATCACCTTGATGGTTGTGGTGTGGGGTCCTG	420
Sbjct	361	AGCACATGTGACAATGAAGGACGGATGTATCACCTTGATGGTTGTGGTGTGGGGTCCTG	420
Query	421	ATTTTCAGCATTCATGAGTCAGGGGAAGGTCCCTGCTAAGGACAGACCTTAGGAGGGCAGT	480
Sbjct	421	ATTTTCAGCATTCATGAGTCAGGGGAAGGTCCCTGCTAAGGACAGACCTTAGGAGGGCAGT	480

Sequence 938 matched with Sequence 377

Query= Sequence ID 938

Length=440

SEQ ID NO: 377

ALIGNMENTS

Identities = 440/440 (100%), Gaps = 0/440 (0%)

Query	1	TGGCCATCCTTTTCCCCCAAACACACCCCCTTAACCTATCTCTTGGGACTTAGCCCGAC	60
Sbjct	1	TGGCCATCCTTTTCCCCCAAACACACCCCCTTAACCTATCTCTTGGGACTTAGCCCGAC	60
Query	61	CCTCCCTCTCATTTCCTTCCCATTAAGTCTGAGAGGCAAGAGCTAGGTTAGGCAAGGAGGTGGT	120
Sbjct	61	CCTCCCTCTCATTTCCTTCCCATTAAGTCTGAGAGGCAAGAGCTAGGTTAGGCAAGGAGGTGGT	120
Query	121	TGGCCAGAGATGGGGAACAGCCAGGTGCCCCAGTCCTCTGATTTTTCCTCCATCCTGCTT	180
Sbjct	121	TGGCCAGAGATGGGGAACAGCCAGGTGCCCCAGTCCTCTGATTTTTCCTCCATCCTGCTT	180
Query	181	ACCACCTCCCTGGGTACTTACAGCCTTCTCTTGGGAACAGCCGGGGCCAGGACTGGGTCA	240
Sbjct	181	ACCACCTCCCTGGGTACTTACAGCCTTCTCTTGGGAACAGCCGGGGCCAGGACTGGGTCA	240
Query	241	CCTATGAGCTGAATCAGCATCTCCTCCTGAGTCCCAGGGCCCCTGCAGTTCCCAGTCTCT	300
Sbjct	241	CCTATGAGCTGAATCAGCATCTCCTCCTGAGTCCCAGGGCCCCTGCAGTTCCCAGTCTCT	300
Query	301	TCTGTCCTGCAGCCCTTGCTCTTTCCCACAGGTTCCACTTTATATCCACcttttccttt	360
Sbjct	301	TCTGTCCTGCAGCCCTTGCTCTTTCCCACAGGTTCCACTTTATATCCACCTTTTCCTTT	360
Query	361	tgttcaattttttatTTTTATTTTTTTTATTATTAAATGATGTGGTCTATGGaaaaaaaaa	420
Sbjct	361	TGTTCAATTTTATTTTTATTTTTTTTATTATTAAATGATGTGGTCTATGGAAAAAAAAA	420
Query	421	taaaaaTCTGACTTAGTTTT	440
Sbjct	421	TAAAAATCTGACTTAGTTTT	440

nt: 513

nt: 513

Identities = 513/513 (100%), Gaps = 0/513 (0%)

Query	1	GGAACCCAGTGTATTACCTGCTGGAACCAAGGAAACTAACAATGTAGGTTACTAGTGAAT 	60
Sbjct	1	GGAACCCAGTGTATTACCTGCTGGAACCAAGGAAACTAACAATGTAGGTTACTAGTGAAT 	60
Query	61	ACCCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATAAAACAAAATTCTCTAA 	120
Sbjct	61	ACCCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATAAAACAAAATTCTCTAA 	120
Query	121	CACTGCAAAGAGTGAGCCATGCCTGTTAACACTGTAAAGAATGTAACATGTGGGGGACAC 	180
Sbjct	121	CACTGCAAAGAGTGAGCCATGCCTGTTAACACTGTAAAGAATGTAACATGTGGGGGACAC 	180
Query	181	ACAGGGGCAGATGGGATGGTTTAGTTTAGGATTTTATTAGTGCATGCCCTACCCTCTGGG 	240
Sbjct	181	ACAGGGGCAGATGGGATGGTTTAGTTTAGGATTTTATTAGTGCATGCCCTACCCTCTGGG 	240
Query	241	GGAACGTCCCATCTGAGGTTTTCTTCTCGGTGGGGGGATTAACTTCTGTCTTAGGGAAA 	300
Sbjct	241	GGAACGTCCCATCTGAGGTTTTCTTCTCGGTGGGGGGATTAACTTCTGTCTTAGGGAAA 	300
Query	301	ACAGTGTCTGATGAGGAGTGTTCCAACACAGGCTACATGAATCCCCTATACCAGTGCG 	360
Sbjct	301	ACAGTGTCTGATGAGGAGTGTTCCAACACAGGCTACATGAATCCCCTATACCAGTGCG 	360
Query	361	AAAGCAGCCAGGAGTCCCCGTTGAAAAGAACAATGCCACTCTCTTTTATGTATCTTGGT 	420
Sbjct	361	AAAGCAGCCAGGAGTCCCCGTTGAAAAGAACAATGCCACTCTCTTTTATGTATCTTGGT 	420
Query	421	TCTGCAACTCATTGTGTGTAAGTAGGGTTAATCGAGTATCAGGTTACAGTATCCTGCCC 	480
Sbjct	421	TCTGCAACTCATTGTGTGTAAGTAGGGTTAATCGAGTATCAGGTTACAGTATCCTGCCC 	480

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Query    481  TTATTATTTTATGATTCACTGACTCAAGTTCCA  513
        ||||||||||||||||||||||||||||
Sbjct    481  TTATTATTTTATGATTCACTGACTCAAGTTCCA  513
```

Sequence 947 matched with Sequence 379

Query= Sequence ID 947
Length=646

SEQ ID NO: 379

ALIGNMENTS

Identities = 641/641 (100%), Gaps = 0/641 (0%)

Query	1	GAGAGTGAAAAAATTCTGGTACAAATTGGGAAATTAGTATATAACAACATAGTGTTAAAT	60
Sbjct	1	GAGAGTGAAAAAATTCTGGTACAAATTGGGAAATTAGTATATAACAACATAGTGTTAAAT	60
Query	61	TCAATGGGAAAAGTTTAATAAGAGGATTGGTATCAACTGGCTGTCCAAAGATAAAAATG	120
Sbjct	61	TCAATGGGAAAAGTTTAATAAGAGGATTGGTATCAACTGGCTGTCCAAAGATAAAAATG	120
Query	121	GACCGTCCTATCACATACAAAATTGTTTTTTAGATAAAGATTTAAATACAGGCACTCCTT	180
Sbjct	121	GACCGTCCTATCACATACAAAATTGTTTTTTAGATAAAGATTTAAATACAGGCACTCCTT	180
Query	181	CATTTGCGTGGTGCACCTTGAGGTGTTGCAGAAATGATGAGAGCTGAAACTGCAAAGCAA	240
Sbjct	181	CATTTGCGTGGTGCACCTTGAGGTGTTGCAGAAATGATGAGAGCTGAAACTGCAAAGCAA	240
Query	241	TTTTAATACTTTATCTGTTGGAAATCTTATAGTTTTCTGTGACCGTTAAAATTTTCATT	300
Sbjct	241	TTTTAATACTTTATCTGTTGGAAATCTTATAGTTTTCTGTGACCGTTAAAATTTTCATT	300
Query	301	AAACTATTAAAAACACCCATGACTGGTCACaaatgtattgggaaatggaaaagaattaat	360
Sbjct	301	AAACTATTAAAAACACCCATGACTGGTCACAAATGTATTGGGAAATGGAAAAGAATTAAT	360
Query	361	acactaaaaatacaaaaaatagaaaatatTTAAATTATCTAAAAATTGAAACATTAGA	420
Sbjct	361	ACACTAAAAATACAAAAATAGAAAATATTTAAATTATCTAAAAATTGAAACATTAGA	420
Query	421	aaaattGAGAACTAGGCAGGGCGTGGTGGCTCACATCTGTAATTTTAGCCCTTTGGGAGG	480
Sbjct	421	AAAATTGAGAACTAGGCAGGGCGTGGTGGCTCACATCTGTAATTTTAGCCCTTTGGGAGG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CTGANGCAGGTGGATCACCTGANGTCAGGAGTTCGAGACCAGCCTGCCAACGTGGGGAAA	540
Sbjct	481	CTGANGCAGGTGGATCACCTGANGTCAGGAGTTCGAGACCAGCCTGCCAACGTGGGGAAA	540
Query	541	CCCCGTCTCTACTGAAAATACAAAAATTANCCGGGCATGGTGGCACAAGCCTGTAATNCT	600
Sbjct	541	CCCCGTCTCTACTGAAAATACAAAAATTANCCGGGCATGGTGGCACAAGCCTGTAATNCT	600
Query	601	TGCTNACCAGGANGCTGAGGCAGGAGAATCACTTGAACCCA	641
Sbjct	601	TGCTNACCAGGANGCTGAGGCAGGAGAATCACTTGAACCCA	641

Sequence 949 matched with Sequence 380

Query= Sequence ID 949
Length=362

SEQ ID NO: 380

ALIGNMENTS

Identities = 362/362 (100%), Gaps = 0/362 (0%)

Query	1	GTTTCACATGAGAAGGTAGTATTATGTACAGTGACCTTGTTTAAAGTGTCNGTTTAATGT	60
Sbjct	1	GTTTCACATGAGAAGGTAGTATTATGTACAGTGACCTTGTTTAAAGTGTCNGTTTAATGT	60
Query	61	TACCACTAAGGCCCTGCCCCAGCTTTATCACCTGAGCACTAACAAGTGCTGTGTGGAGTT	120
Sbjct	61	TACCACTAAGGCCCTGCCCCAGCTTTATCACCTGAGCACTAACAAGTGCTGTGTGGAGTT	120
Query	121	CAGTCCATGCTGGTAACTNTTGAGTATTCAGTGGGTCTTTTAAACAATTACCACCGTGGAG	180
Sbjct	121	CAGTCCATGCTGGTAACTNTTGAGTATTCAGTGGGTCTTTTAAACAATTACCACCGTGGAG	180
Query	181	GANANAGCAAGGAAGAGAAATGCTGTGATCTTTTNCTGTTTTTAATTAGNGAAAGAGGGA	240
Sbjct	181	GANANAGCAAGGAAGAGAAATGCTGTGATCTTTTNCTGTTTTTAATTAGNGAAAGAGGGA	240
Query	241	TTANATTAAACAAATGTTACAGAGNTGTGACTNTGATCCCCCAGNGGTAAGCAATAATTG	300
Sbjct	241	TTANATTAAACAAATGTTACAGAGNTGTGACTNTGATCCCCCAGNGGTAAGCAATAATTG	300
Query	301	TANAGACTGGATTTNANAAGCCCTGAGAGTTTATTTTCAACCTATNTATTATAGNNCAAT	360
Sbjct	301	TANAGACTGGATTTNANAAGCCCTGAGAGTTTATTTTCAACCTATNTATTATAGNNCAAT	360
Query	361	CC 362	
Sbjct	361	CC 362	

Sequence 1028 matched with Sequence 381

Query= Sequence ID 1028
Length=80

SEQ ID NO: 381

ALIGNMENTS

Identities = 80/80 (100%), Gaps = 0/80 (0%)

```
Query   1   ACAAGGCTTGGGGGCTGGACTCCCTCTACTGCCTCTGGCCATACCCCCTCCTGGAGATGG   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1   ACAAGGCTTGGGGGCTGGACTCCCTCTACTGCCTCTGGCCATACCCCCTCCTGGAGATGG   60

Query   61   GGTCAAGGCACCAGGACTGA   80
          ||||||||||||||||
Sbjct   61   GGTCAAGGCACCAGGACTGA   80
```

Sequence 1056 matched with Sequence 382

Query= Sequence ID - 1056 nt: 435
Length=435

SEQ ID NO: 382 nt: 435

ALIGNMENTS

Identities = 435/435 (100%), Gaps = 0/435 (0%)

Query	1	TCGCTTGTAAGCCTGAGACAGCTGCCTGTGTGGGACTGAGATGCAGGATTTCTTCACAC	60
Sbjct	1	TCGCTTGTAAGCCTGAGACAGCTGCCTGTGTGGGACTGAGATGCAGGATTTCTTCACAC	60
Query	61	CTCTCCTTTGTGACTTCAAGAGCCTCTGGCATCTCTTTCTGCAAAGGCATCTGAATGTGT	120
Sbjct	61	CTCTCCTTTGTGACTTCAAGAGCCTCTGGCATCTCTTTCTGCAAAGGCATCTGAATGTGT	120
Query	121	CTGCGTTCCTGTTAGCATAATGTGAGGAGGTGGAGAGACAGCCACCCCGTGTCCACCG	180
Sbjct	121	CTGCGTTCCTGTTAGCATAATGTGAGGAGGTGGAGAGACAGCCACCCCGTGTCCACCG	180
Query	181	TGACCCCTGTCCCCACACTGACCTGTGTTCCCTCCCGATCATCTTTCCTGTTCCAGAGA	240
Sbjct	181	TGACCCCTGTCCCCACACTGACCTGTGTTCCCTCCCGATCATCTTTCCTGTTCCAGAGA	240
Query	241	AGTGGGCTGGATGTCTCCATCTCTGTCTCAACTTCATGGTGCCTGAGCTGCAACTTCTT	300
Sbjct	241	AGTGGGCTGGATGTCTCCATCTCTGTCTCAACTTCATGGTGCCTGAGCTGCAACTTCTT	300
Query	301	ACTTCCCTAATGAAGTTAAGAACCTGAATATAAATTTGTTTTCTCAAATATTTGCTATGA	360
Sbjct	301	ACTTCCCTAATGAAGTTAAGAACCTGAATATAAATTTGTTTTCTCAAATATTTGCTATGA	360
Query	361	AGGGTTGATGGATTAATTAAATAAGTCAATTCCTGGAAGTTGAGAGAGCAAATAAGACC	420
Sbjct	361	AGGGTTGATGGATTAATTAAATAAGTCAATTCCTGGAAGTTGAGAGAGCAAATAAGACC	420
Query	421	TGAGAACCTTCCAGA	435
Sbjct	421	TGAGAACCTTCCAGA	435

Sequence 1071 matched with Sequence 383

Query= Sequence ID 1071

Length=571

SEQ ID NO: 383

ALIGNMENTS

Identities = 569/569 (100%), Gaps = 0/569 (0%)

Query	2	GATATAGTNCCGCATGGGAAAGATGANCAGGTATAACCNAGCNTNATATAGCAAGGACTA	61
Sbjct	2	GATATAGTNCCGCATGGGAAAGATGANCAGGTATAACCNAGCNTNATATAGCAAGGACTA	61
Query	62	ACCCCCCTGCCTTCTGCATAATGAATTAAGTAGAAATAAAGTTNGCAAGGAGAGCCAAAGC	121
Sbjct	62	ACCCCCCTGCCTTCTGCATAATGAATTAAGTAGAAATAAAGTTNGCAAGGAGAGCCAAAGC	121
Query	122	TAAGACCCCNAGAAACAGACGAGCTACCTAAGAACAGNTAAAAGAGCACACCCGTCTATG	181
Sbjct	122	TAAGACCCCNAGAAACAGACGAGCTACCTAAGAACAGNTAAAAGAGCACACCCGTCTATG	181
Query	182	TAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGTGATAG	241
Sbjct	182	TAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGTGATAG	241
Query	242	CTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTNGCCACAGAACCCTCTAAAT	301
Sbjct	242	CTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTNGCCACAGAACCCTCTAAAT	301
Query	302	CCCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAA	361
Sbjct	302	CCCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAA	361
Query	362	CCTTGTTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTA	421
Sbjct	362	CCTTGTTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTA	421
Query	422	AGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATAACTGAACTCC	481
Sbjct	422	AGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATAACTGAACTCC	481

PATENT SEQUENCE ALIGNMENT

```
Query 482 TNACACCCAATTGGACCAATCTATCACCCCTATAGAAGAACTAATGTTAGTATAAGTAACA 541
          |||
Sbjct 482 TNACACCCAATTGGACCAATCTATCACCCCTATAGAAGAACTAATGTTAGTATAAGTAACA 541

Query 542 TGAAAACATTCTCCTCCGCATAAGCCTGC 570
          |||
Sbjct 542 TGAAAACATTCTCCTCCGCATAAGCCTGC 570
```

Sequence 1074 matched with Sequence 384

Query= Sequence ID - 1074
Length=689

nt: 689

SEQ ID NO: 384

nt: 689

ALIGNMENTS

Identities = 689/689 (100%), Gaps = 0/689 (0%)

Query	1	GGGAGGCGGAGGCTGCAGTGAGCTGAGATCGTGCCACTTCATTCCAGCCTGGGCAACAAA	60
Sbjct	1	GGGAGGCGGAGGCTGCAGTGAGCTGAGATCGTGCCACTTCATTCCAGCCTGGGCAACAAA	60
Query	61	GCGAAACTCTGTCTCaaaaaaaaaaaaaaaaaaaaaTTTGTTGACTGTTGTAATTTAAAGC	120
Sbjct	61	GCGAAACTCTGTCTCAAAAAAAAAAAAAAAAAAAAAATTTGTTGACTGTTGTAATTTAAAGC	120
Query	121	TTGTCATTTTTTATTTAGTAATAACACTCATTAGTGTAGTATCTATGATGAACCAGGTTC	180
Sbjct	121	TTGTCATTTTTTATTTAGTAATAACACTCATTAGTGTAGTATCTATGATGAACCAGGTTC	180
Query	181	TGCACAAAGTACCTTATGTTTCATGGCCTCATATCGTCTTCTCCAAAACTCTGCAAGATAG	240
Sbjct	181	TGCACAAAGTACCTTATGTTTCATGGCCTCATATCGTCTTCTCCAAAACTCTGCAAGATAG	240
Query	241	GATTCATCACCACTTATAGGGAGAGATCTGAAAGTTTAAAATTGTACCCAAGGTCACACA	300
Sbjct	241	GATTCATCACCACTTATAGGGAGAGATCTGAAAGTTTAAAATTGTACCCAAGGTCACACA	300
Query	301	GCTGGTAAGTGCCAGAGCTGGGATTCCGTAGGGTGTTTCANAGTGCCTCTCCTGCCGTAGG	360
Sbjct	301	GCTGGTAAGTGCCAGAGCTGGGATTCCGTAGGGTGTTTCANAGTGCCTCTCCTGCCGTAGG	360
Query	361	CTTATCACAAAAAGTCAAAGTTTGGTCATAATAAAGCCTGAAGTTTGGCAGGATTTAAAA	420
Sbjct	361	CTTATCACAAAAAGTCAAAGTTTGGTCATAATAAAGCCTGAAGTTTGGCAGGATTTAAAA	420
Query	421	ATAGTCACCANACTTTTGAGTTGGAGCATCCACCTCACTGCTGTTACCTTCTGTGGCA	480
Sbjct	421	ATAGTCACCANACTTTTGAGTTGGAGCATCCACCTCACTGCTGTTACCTTCTGTGGCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	GGGAGAGTCATCATTTCCATTTTCAGCTTGTGGAATATCTTGTCATTAACATTCTCATGCA	540
Sbjct	481	GGGAGAGTCATCATTTCCATTTTCAGCTTGTGGAATATCTTGTCATTAACATTCTCATGCA	540
Query	541	AAAGCCATTTTATGGTGCCCAATGAANATGGTTAAGCTACTGCCCCAAGCCTNTGGAAGC	600
Sbjct	541	AAAGCCATTTTATGGTGCCCAATGAANATGGTTAAGCTACTGCCCCAAGCCTNTGGAAGC	600
Query	601	CTTCCTAATTTTGGACTTGCACTATGCAAATTGNATAATATTTTCTCTACCCTAAGCCAA	660
Sbjct	601	CTTCCTAATTTTGGACTTGCACTATGCAAATTGNATAATATTTTCTCTACCCTAAGCCAA	660
Query	661	ATATTTTCTTCACTTTTCATTCTAC	689
Sbjct	661	ATATTTTCTTCACTTTTCATTCTAC	689

Sequence 1081 matched with Sequence 385

Query= Sequence ID 1081

Length=542

SEQ ID NO: 385

ALIGNMENTS

Identities = 542/542 (100%), Gaps = 0/542 (0%)

Query	1	cgccgccgcgcgcgcgcgtcgctctccaacgccagcgccgcctctcgctcgccgagctccag	60
Sbjct	1	CGCCGCCGCGCCGCCGTCGCTCTCCAACGCCAGCGCCGCCTCTCGCTCGCCGAGCTCCAG	60
Query	61	ccgAAGGAGAAGGGGGTAAGTAAGGAGGTCTCTGTACCATGGCTCGTACAAAGCAGACT	120
Sbjct	61	CCGAAGGAGAAGGGGGTAAGTAAGGAGGTCTCTGTACCATGGCTCGTACAAAGCAGACT	120
Query	121	GCCCGCAAATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACAAAAGCCGCTCGC	180
Sbjct	121	GCCCGCAAATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACAAAAGCCGCTCGC	180
Query	181	AAGAGTGCGCCCTCTACTGGAGGGGTGAAGAAACCTCATCGTTACAGGCCTGGTACTGTG	240
Sbjct	181	AAGAGTGCGCCCTCTACTGGAGGGGTGAAGAAACCTCATCGTTACAGGCCTGGTACTGTG	240
Query	241	GCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAACTTCTGATTCGCAAACCTCCC	300
Sbjct	241	GCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAACTTCTGATTCGCAAACCTCCC	300
Query	301	TTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAAACAGATCTGCGCTTCCAGAGC	360
Sbjct	301	TTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAAACAGATCTGCGCTTCCAGAGC	360
Query	361	GCANCTATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTATCTGGTTGGCCTTTTTGAAGAC	420
Sbjct	361	GCANCTATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTATCTGGTTGGCCTTTTTGAAGAC	420
Query	421	ACCAACCTGTGTGCTATCCATGCCAAACGTGTAACAATTATGCCAAAAGACATCCAGCTA	480
Sbjct	421	ACCAACCTGTGTGCTATCCATGCCAAACGTGTAACAATTATGCCAAAAGACATCCAGCTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCACGCCGCATACGTGGAGAACGTGCTTAAGAATCCACTATGATGGGAAACATTTTCATTC	540
Sbjct	481	GCACGCCGCATACGTGGAGAACGTGCTTAAGAATCCACTATGATGGGAAACATTTTCATTC	540
Query	541	TC	542
Sbjct	541	TC	542

Sequence 1083 matched with Sequence 386

Query= Sequence ID - 1083 nt: 198
Length=198

SEQ ID NO: 386 nt: 198

ALIGNMENTS

Identities = 198/198 (100%), Gaps = 0/198 (0%)

Query	1	GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTTAAAGGCACAATTAATCACATTGG	60
Sbjct	1	GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTTAAAGGCACAATTAATCACATTGG	60
Query	61	TTGTACTCTGNNGACAGCCTTCTTTaaaaaaaaataaacaattttaaacaaaaaaaaa	120
Sbjct	61	TTGTACTCTGNNGACAGCCTTCTTTAAAAAAAAAATAACAATTTAAACAAAAAAAAAA	120
Query	121	aa	180
Sbjct	121	AA	180
Query	181	aaaaaaaaanTTTTAACC	198
Sbjct	181	AAAAAAAANTTTTAACC	198

Sequence 1084 matched with Sequence 387

Query= Sequence ID - 1084 nt: 198
Length=198

SEQ ID NO: 387 nt: 198

ALIGNMENTS

Identities = 198/198 (100%), Gaps = 0/198 (0%)

Query	1	GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTTAAAGGCACAATTAATCACATTGG	60
Sbjct	1	GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTTAAAGGCACAATTAATCACATTGG	60
Query	61	TTGTACTCTGNNGACAGCCTTCTTTaaaaaaaaataaacaattttaaacaaaaaaaaa	120
Sbjct	61	TTGTACTCTGNNGACAGCCTTCTTTAAAAAAAAAATAACAATTTAAACAAAAAAAAAA	120
Query	121	aa	180
Sbjct	121	AA	180
Query	181	aaaaaaaaanTTTTAACC	198
Sbjct	181	AAAAAAAANTTTTAACC	198

Sequence 1099 matched with Sequence 388

Query= Sequence ID - 1099 nt: 561
Length=561

SEQ ID NO: 388 nt: 561

ALIGNMENTS

Identities = 561/561 (100%), Gaps = 0/561 (0%)

Query	1	TGCATGCTTGTGGATTGGAAAACTTTGGAGACTGATTACTTTTCATTATATATGTGTCA	60
Sbjct	1	TGCATGCTTGTGGATTGGAAAACTTTGGAGACTGATTACTTTTCATTATATATGTGTCA	60
Query	61	CAGTGAAACAGCTTTTATGTGTCATGTAAGATTACTGCTTGCCTCTCTAAGGAAGGTCGT	120
Sbjct	61	CAGTGAAACAGCTTTTATGTGTCATGTAAGATTACTGCTTGCCTCTCTAAGGAAGGTCGT	120
Query	121	GACTGTTTAAATAGACGGGCAAGGTGGAACCTTTTGAAAGATGAGCTTTTGAATATAAGT	180
Sbjct	121	GACTGTTTAAATAGACGGGCAAGGTGGAACCTTTTGAAAGATGAGCTTTTGAATATAAGT	180
Query	181	TGTCTGCTAGATCATGGTTTGTATTGAACTAACAAGGTTTGCAGATCTGCTGACTTATAT	240
Sbjct	181	TGTCTGCTAGATCATGGTTTGTATTGAACTAACAAGGTTTGCAGATCTGCTGACTTATAT	240
Query	241	AAAGCTTTTTGATTCCTACTAAGCTTTAAGATTTAAAAAATGTTCAATGTTGAAATTTCT	300
Sbjct	241	AAAGCTTTTTGATTCCTACTAAGCTTTAAGATTTAAAAAATGTTCAATGTTGAAATTTCT	300
Query	301	GTGGGGCTCTATTTTTGCTTTGGCTTTCTGGTGAGAGAGTGAGGAAGCATTCTTTCCTTC	360
Sbjct	301	GTGGGGCTCTATTTTTGCTTTGGCTTTCTGGTGAGAGAGTGAGGAAGCATTCTTTCCTTC	360
Query	361	ACTAAGTTTGTCTTTCTTGTCTTCTGGATAGATTGATTTTAAGAGACTAAGGGAATTTAC	420
Sbjct	361	ACTAAGTTTGTCTTTCTTGTCTTCTGGATAGATTGATTTTAAGAGACTAAGGGAATTTAC	420
Query	421	AAACTAAAGATTTTAGTCATCTGGTGAAAAAGGAGACTTTAAGATTGTTTAGGGCTGGGC	480
Sbjct	421	AAACTAAAGATTTTAGTCATCTGGTGAAAAAGGAGACTTTAAGATTGTTTAGGGCTGGGC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGGGTGACTCACATCTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGCAGAACACTTGA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGGGTGACTCACATCTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGCAGAACACTTGA  540

Query  541  AGGAGTTCAAGACCAGCGTGG  561
          ||||||||||||||||
Sbjct  541  AGGAGTTCAAGACCAGCGTGG  561
```

Sequence 1109 matched with Sequence 389

Length=601

Identities = 594/594 (100%), Gaps = 0/594 (0%)

Query	1	TTTGNCGGTNTTGGAnnnnnnanaanTTTCTTCCANNCNTNACNTNTTGGTGGNCTAAATT	60
Sbjct	1	TTTGNCGGTNTTGGANNNNNANAANTTTCTTCCANNCNTNACNTNTTGGTGGNCTAAATT	60
Query	61	AANATGGNTTTNGNGGGTTCNTTNCTNNNTNNNNCATGGGANANAATTNATTNTCNTNCN	120
Sbjct	61	AANATGGNTTTNGNGGGTTCNTTNCTNNNTNNNNCATGGGANANAATTNATTNTCNTNCN	120
Query	121	NNTTCCTTNNCCCTNAANCTACCTTCCCCCNATTTTCTCCCCTNTTCNTNAATTANCATC	180
Sbjct	121	NNTTCCTTNNCCCTNAANCTACCTTCCCCCNATTTTCTCCCCTNTTCNTNAATTANCATC	180
Query	181	CTCTCCNCNTANNTCNANACNTTAATGGCAANACTATCTAATANCNANNATAANANCTCC	240
Sbjct	181	CTCTCCNCNTANNTCNANACNTTAATGGCAANACTATCTAATANCNANNATAANANCTCC	240
Query	241	TGTNNNCCACATNTCTTATTNNNCGCNCNCANGTTNCANNCCCNCAGAGTNAACTCATCCT	300
Sbjct	241	TGTNNNCCACATNTCTTATTNNNCGCNCNCANGTTNCANNCCCNCAGAGTNAACTCATCCT	300
Query	301	CNNCNNAANTTCATATCGTGNNCTNTNNNCNNTNGCGCGANATATTaannanaccngtan	360
Sbjct	301	CNNCNNAANTTCATATCGTGNNCTNTNNNCNNTNGCGCGANATATTAANNANACCNGTAN	360
Query	361	ntnnnanacannanntnngnaanaanccttctnannTTTTAGCNTCNNGCNNTAACNNNN	420
Sbjct	361	NTNNNANACANNANNTNNGNAANAANCCTTCTNANNTTTTAGCNTCNNGCNNTAACNNNN	420
Query	421	NTCTTNGTGNNNNCNCAGCTTTCNCNNCATNATNCTNCNNCGAANTNTCANNCNTCTCCN	480
Sbjct	421	NTCTTNGTGNNNNCNCAGCTTTCNCNNCATNATNCTNCNNCGAANTNTCANNCNTCTCCN	480
Query	481	CTTNAATGNNTTCCCATGNATTAANTNCCTCGNNNANAGCACTATCGTNNNNGAGNNNAT	540
Sbjct	481	CTTNAATGNNTTCCCATGNATTAANTNCCTCGNNNANAGCACTATCGTNNNNGAGNNNAT	540
Query	541	TATNGNCNNTTTACNTCATGTGGTCCANTNNCGTTNGNCGCNNNNAATNTTCGT	594

Sbjct 541 TATNGNCNNTTTACNTCATGTGGTCCANTNNCGTTNGNCGCNNNNAATNTTCGT 594

Sequence 1118 matched with Sequence 390

Query= Sequence ID 1118
Length=616

SEQ ID NO: 390

ALIGNMENTS

Identities = 616/616 (100%), Gaps = 0/616 (0%)

Query	1	GGATTTTAGAGGAAGGCGCTNGGTTACATTGGAGAACTGGAGTGGTCTGGAGTTCACGG	60
Sbjct	1	GGATTTTAGAGGAAGGCGCTNGGTTACATTGGAGAACTGGAGTGGTCTGGAGTTCACGG	60
Query	61	TGTAGTGGACCAGAGGCCACCTCTCCTGGGCTTCTCAGTGTCTCGCCGGCGGGGTTCTGGC	120
Sbjct	61	TGTAGTGGACCAGAGGCCACCTCTCCTGGGCTTCTCAGTGTCTCGCCGGCGGGGTTCTGGC	120
Query	121	CTGAGCTGGATTGACATAGCCCTTGGCGGATTTAAACAACCTAAACATTAAGCAGTACAG	180
Sbjct	121	CTGAGCTGGATTGACATAGCCCTTGGCGGATTTAAACAACCTAAACATTAAGCAGTACAG	180
Query	181	CTGCCTCAAACCTTTGGGATTTTCAGAATGACTGACACTGCCGAAGCTGTTCCAAAGTTT	240
Sbjct	181	CTGCCTCAAACCTTTGGGATTTTCAGAATGACTGACACTGCCGAAGCTGTTCCAAAGTTT	240
Query	241	GAAGAGATGTTTGCTAGTAGATTACAGAAAATGACAAGGAGTATCAGGAATACCTGAAA	300
Sbjct	241	GAAGAGATGTTTGCTAGTAGATTACAGAAAATGACAAGGAGTATCAGGAATACCTGAAA	300
Query	301	CGCCCTCCTGAGTCTCCTCCAATTGTTGAGGAATGGAATAGCANAGCTGGTGGGAACCAA	360
Sbjct	301	CGCCCTCCTGAGTCTCCTCCAATTGTTGAGGAATGGAATAGCANAGCTGGTGGGAACCAA	360
Query	361	AGAAACAGAGGCAATCGGTTGCAAGACAACAGACAGTTCAGAGGCAGGGACAACAGATGG	420
Sbjct	361	AGAAACAGAGGCAATCGGTTGCAAGACAACAGACAGTTCAGAGGCAGGGACAACAGATGG	420
Query	421	GGGTGGCCAAGTGACAATCGATCCAATCAGTGGCATGGACGATCCTGGGGTAACAACACTAC	480
Sbjct	421	GGGTGGCCAAGTGACAATCGATCCAATCAGTGGCATGGACGATCCTGGGGTAACAACACTAC	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCGCAACACAGACAAGAACCTTACTATCCCCAGCAATATGGACATTATGGTTACAACCAG	540
Sbjct	481	CCGCAACACAGACAAGAACCTTACTATCCCCAGCAATATGGACATTATGGTTACAACCAG	540
Query	541	CGGCCTCCTTACGGTTACTACTGATAGAAAATGTTGGCAGCTTTTAGTAAAAGCATTACT	600
Sbjct	541	CGGCCTCCTTACGGTTACTACTGATAGAAAATGTTGGCAGCTTTTAGTAAAAGCATTACT	600
Query	601	CTGTTACCATGAGAAA	616
Sbjct	601	CTGTTACCATGAGAAA	616

Sequence 1125 matched with Sequence 391

Query= Sequence ID 1125
Length=407

SEQ ID NO: 391

ALIGNMENTS

Identities = 404/404 (100%), Gaps = 0/404 (0%)

Query	2	GACTGGCTCCCGAAAAGAAGGGTGGCGAGaanaaaaaGGGCCGTTCTGCCATGGACGAAG	61
Sbjct	2	GACTGGCTCCCGAAAAGAAGGGTGGCGAGANAAGGGGCCGTTCTGCCATGGACGAAG	61
Query	62	TGGTAACCCGCGAATACACCATCAACATTNACAAGCGCATCCATGGAGTGGGCTTCAAGA	121
Sbjct	62	TGGTAACCCGCGAATACACCATCAACATTNACAAGCGCATCCATGGAGTGGGCTTCAAGA	121
Query	122	ANCGTGACCTCGGGCACTCAAAGAGATTCGGAATTTGCCATGAAGGAGATGGGAACTC	181
Sbjct	122	ANCGTGACCTCGGGCACTCAAAGAGATTCGGAATTTGCCATGAAGGAGATGGGAACTC	181
Query	182	CATATGTGCGCATTGACACCAGGCTCAACAAANCTGTCTGGGCCAAAGGAATAAGGAATG	241
Sbjct	182	CATATGTGCGCATTGACACCAGGCTCAACAAANCTGTCTGGGCCAAAGGAATAAGGAATG	241
Query	242	TGCCATACCGAATCCGTGTGCGGCTGTCCANAAACGTAATGAGGATGAAGATTCACCAA	301
Sbjct	242	TGCCATACCGAATCCGTGTGCGGCTGTCCANAAACGTAATGAGGATGAAGATTCACCAA	301
Query	302	ATAAGCTNTATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAG	361
Sbjct	302	ATAAGCTNTATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAG	361
Query	362	TCAATGTGGATGANAACNAATCGCTGATCGTCAGATCaaanaaa	405
Sbjct	362	TCAATGTGGATGANAACNAATCGCTGATCGTCAGATCAANAAA	405

Sequence 1139 matched with Sequence 392

Query= Sequence ID - 1139 nt: 503
Length=503

SEQ ID NO: 392 nt: 503

ALIGNMENTS

Identities = 503/503 (100%), Gaps = 0/503 (0%)

Query	1	CAGCACTGCCAGTGGAGATGGGCGTCACTACTGCTACCCTCATTTCACCTGCGCTGTGGA	60
Sbjct	1	CAGCACTGCCAGTGGAGATGGGCGTCACTACTGCTACCCTCATTTCACCTGCGCTGTGGA	60
Query	61	CACTGAGAACATCCGCCGTGTGTTCAACGACTGCCGTGACATCATTACAGCGCATGCACCT	120
Sbjct	61	CACTGAGAACATCCGCCGTGTGTTCAACGACTGCCGTGACATCATTACAGCGCATGCACCT	120
Query	121	TCGTCAGTACGAGCTGCTCTAAGAAGGGAACCCCAAATTTAATTAAAGCCTTAAGCACA	180
Sbjct	121	TCGTCAGTACGAGCTGCTCTAAGAAGGGAACCCCAAATTTAATTAAAGCCTTAAGCACA	180
Query	181	ATTAATTAAAAAGTGAAACGTAATTGTACAAGCAGTTAATCACCCACCATAGGGCATGATT	240
Sbjct	181	ATTAATTAAAAAGTGAAACGTAATTGTACAAGCAGTTAATCACCCACCATAGGGCATGATT	240
Query	241	AACAAAGCAACCTTTCCCTTCCCCCGAGTGATTTTGCGAAACCCCCTTTCCCTTCAGCT	300
Sbjct	241	AACAAAGCAACCTTTCCCTTCCCCCGAGTGATTTTGCGAAACCCCCTTTCCCTTCAGCT	300
Query	301	TGCTTAGATGTTCCAAATTTAGAAAGCTTAAGGCGGCCTACAGaaaaaggaaaaaggcc	360
Sbjct	301	TGCTTAGATGTTCCAAATTTAGAAAGCTTAAGGCGGCCTACAGAAAAAGGAAAAAGGCC	360
Query	361	acaaaagttccctctcactttcagtaaaaaataataaaacagcagcagcaacaaataaaa	420
Sbjct	361	ACAAAAGTTCCTCTCACTTTCAGTAAAAATAAATAAACAGCAGCAGCAAACAAATAAAA	420
Query	421	atgaaataaaagaaacaaatgaaataaatattgtgttgagcattaaaaaaaaatcaaa	480
Sbjct	421	ATGAAATAAAAGAAACAAATGAAATAAATATTGTGTTGTGCAGCATTAATAAAAAATCAAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	ataaaaaattaaatGTGAGCAAAG	503
Sbjct	481	ATAAAAAATTAAATGTGAGCAAAG	503

Sequence 1148 matched with Sequence 393

Query= Sequence ID - 1148
Length=587

nt: 587

SEQ ID NO: 393

nt: 587

ALIGNMENTS

Identities = 587/587 (100%), Gaps = 0/587 (0%)

Query	1	TGAAAAATAAAGTTTTTATGTATATTCTACATATGTATATGTTGGTAGAAAGCAAAAACG	60
Sbjct	1	TGAAAAATAAAGTTTTTATGTATATTCTACATATGTATATGTTGGTAGAAAGCAAAAACG	60
Query	61	CTAGGTAAAAATAAATGTAATACAATTTTAGCTATGAACCAAAAAACCATTTGTGGTGTG	120
Sbjct	61	CTAGGTAAAAATAAATGTAATACAATTTTAGCTATGAACCAAAAAACCATTTGTGGTGTG	120
Query	121	GATGCAAGAAAGTCTGGATGGGTGCAGAGTTCTCCATGTTTCACTTCTGACATTTGAAAA	180
Sbjct	121	GATGCAAGAAAGTCTGGATGGGTGCAGAGTTCTCCATGTTTCACTTCTGACATTTGAAAA	180
Query	181	TACGCAGTTTGCATTTGATACGTCAAATGTTATTTTAAAGAAAACCAATAAAATCATTAA	240
Sbjct	181	TACGCAGTTTGCATTTGATACGTCAAATGTTATTTTAAAGAAAACCAATAAAATCATTAA	240
Query	241	AACCGAAAAAGGCAGTTTGTCTGTTTTTACCTTAGTTGGAGTTATCTGCAATTGCCGTAT	300
Sbjct	241	AACCGAAAAAGGCAGTTTGTCTGTTTTTACCTTAGTTGGAGTTATCTGCAATTGCCGTAT	300
Query	301	TAGTGTTTTAAGGAACCTTGTAAGTAAGCTCCTTAGTCCCCTTTAGAGCTACGAAACATGT	360
Sbjct	301	TAGTGTTTTAAGGAACCTTGTAAGTAAGCTCCTTAGTCCCCTTTAGAGCTACGAAACATGT	360
Query	361	CAATTTTACTTTTCTCCAGCTTTTTGGAATCTTATCTAAATTACCATGTAGAGTTCTGCA	420
Sbjct	361	CAATTTTACTTTTCTCCAGCTTTTTGGAATCTTATCTAAATTACCATGTAGAGTTCTGCA	420
Query	421	TAGCTTCAAATTCTCTTAGCCAATGTGGTCTGTAAGTGTCTATCGATGAATTTACCGTT	480
Sbjct	421	TAGCTTCAAATTCTCTTAGCCAATGTGGTCTGTAAGTGTCTATCGATGAATTTACCGTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AATTGCCGTAGTATACTGTCCTGTACCGGATGTGAAGAGGAGCAACTCTGCACAGTGCAC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AATTGCCGTAGTATACTGTCCTGTACCGGATGTGAAGAGGAGCAACTCTGCACAGTGCAC  540

Query  541  TGGTTGCTCCCATGGTAGGAANGAATGGCTTATCAATGGTCGGATTT  587
          |||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGGTTGCTCCCATGGTAGGAANGAATGGCTTATCAATGGTCGGATTT  587
```


Sequence 1160 matched with Sequence 394

Query= Sequence ID - 1160
Length=650

nt: 650

SEQ ID NO: 394

nt: 650

ALIGNMENTS

Identities = 650/650 (100%), Gaps = 0/650 (0%)

Query	1	GGAGGATGGAGCAGTGAGCGGGTCTGGGCGGCTGCTGGCAGCGCCATGGAGACGGTACAG	60
Sbjct	1	GGAGGATGGAGCAGTGAGCGGGTCTGGGCGGCTGCTGGCAGCGCCATGGAGACGGTACAG	60
Query	61	CTGAGGAACCCGCCGCGCCGGCAGCTGAAAAAGTTGGATGAAGATAGTTTAACCAAACAA	120
Sbjct	61	CTGAGGAACCCGCCGCGCCGGCAGCTGAAAAAGTTGGATGAAGATAGTTTAACCAAACAA	120
Query	121	CCAGAAGAAGTATTTGATGTCTTAGAGAAACTTGGAGAAGGGTGAGTGTAAGAAACTAT	180
Sbjct	121	CCAGAAGAAGTATTTGATGTCTTAGAGAAACTTGGAGAAGGGTGAGTGTAAGAAACTAT	180
Query	181	AGGTAGGTCATTGGGTCCCAGTCTTTTTCCTGCCCCAGAAGAAGCAGAAGGATATGAACC	240
Sbjct	181	AGGTAGGTCATTGGGTCCCAGTCTTTTTCCTGCCCCAGAAGAAGCAGAAGGATATGAACC	240
Query	241	TTTCAGCATTGTTCTAGGTGGGGTGGAAGGTAAATTTACAGCTTGTGATGTCCTTCTTCG	300
Sbjct	241	TTTCAGCATTGTTCTAGGTGGGGTGGAAGGTAAATTTACAGCTTGTGATGTCCTTCTTCG	300
Query	301	CTTTACTCCAATCCCTATTATAGACAGATTTAGTGATTCCTGGTCTTTTAAACACGAAGA	360
Sbjct	301	CTTTACTCCAATCCCTATTATAGACAGATTTAGTGATTCCTGGTCTTTTAAACACGAAGA	360
Query	361	ATATCTATTGTTTTCTCTTTGTAGGATCTGTATGATTTTATCTACTTAACAGATAGCAC	420
Sbjct	361	ATATCTATTGTTTTCTCTTTGTAGGATCTGTATGATTTTATCTACTTAACAGATAGCAC	420
Query	421	TAATTAGATTAAAATTCTATAAGAAACTTTTTAATTTGCTGTTTCATAATTTCTGATTGGT	480
Sbjct	421	TAATTAGATTAAAATTCTATAAGAAACTTTTTAATTTGCTGTTTCATAATTTCTGATTGGT	480

Sequence 1165 matched with Sequence 395

Query= Sequence ID - 1165 nt: 502
Length=502

SEQ ID NO: 395 nt: 502

ALIGNMENTS

Identities = 502/502 (100%), Gaps = 0/502 (0%)

Query	1	CTCAAGTGAATCCTGGCTTCTTGAAGCGCTTGCCTAGACGAGACACAGTGCATAAAAAAC	60
Sbjct	1	CTCAAGTGAATCCTGGCTTCTTGAAGCGCTTGCCTAGACGAGACACAGTGCATAAAAAAC	60
Query	61	AACTTTTGGGGGACAGGTATGTTTTCTTGCAGCTGCGGTTGTAAGGTCTTGGCAAGACAA	120
Sbjct	61	AACTTTTGGGGGACAGGTATGTTTTCTTGCAGCTGCGGTTGTAAGGTCTTGGCAAGACAA	120
Query	121	GCAGTGTGGCCAGAATTTTGAACCTTCTGATGAATGTGTAATGCAAAGGACCTTGTACAtt	180
Sbjct	121	GCAGTGTGGCCAGAATTTTGAACCTTCTGATGAATGTGTAATGCAAAGGACCTTGTACATT	180
Query	181	tttttGTTTCAAGGTCCTCAAAATGAGCACATGAAGAGGTTGCTGTGAAACTTTAAGTGG	240
Sbjct	181	TTTTTGTTTCAAGGTCCTCAAAATGAGCACATGAAGAGGTTGCTGTGAAACTTTAAGTGG	240
Query	241	CCCTACTGCGCAGAAGCATTTCAGATGTCACTTGATGATCTGTAAGGGAACCTTGCTGATTT	300
Sbjct	241	CCCTACTGCGCAGAAGCATTTCAGATGTCACTTGATGATCTGTAAGGGAACCTTGCTGATTT	300
Query	301	GGGAATGTGCTTAGGGAACACACATTCCTTTTGACAGGGTCTGTCACTGGGTGGGTGATG	360
Sbjct	301	GGGAATGTGCTTAGGGAACACACATTCCTTTTGACAGGGTCTGTCACTGGGTGGGTGATG	360
Query	361	AATTATACAGATGACATGTGCTttttttttcttttttCAACCTCAATGGTATTCCTACAGG	420
Sbjct	361	AATTATACAGATGACATGTGCTTTTTTTTCTTTTTTCAACCTCAATGGTATTCCTACAGG	420
Query	421	AAATGGATAACCATTTTAACTGTATTTTTTGCAGCCCGTACCTTCTTGGAATACAATTG	480
Sbjct	421	AAATGGATAACCATTTTAACTGTATTTTTTGCAGCCCGTACCTTCTTGGAATACAATTG	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCTAACTTTTATTTTGGTCT	502
Sbjct	481	TCTAACTTTTATTTTGGTCT	502

Sequence 1172 matched with Sequence 396

Query= Sequence ID - 1172
Length=648

nt: 648

SEQ ID NO: 396

nt: 648

ALIGNMENTS

Identities = 648/648 (100%), Gaps = 0/648 (0%)

Query	1	CCACAATAATAAGAGAAAAACAGGAGCAAAAGGATATACAAAACCACCAGAAAACAAATA	60
Sbjct	1	CCACAATAATAAGAGAAAAACAGGAGCAAAAGGATATACAAAACCACCAGAAAACAAATA	60
Query	61	ACAAAGTGACAGGAGTAAGTCCTTAACTGGCAATAATAACCATGAATCTAAATGGATTCC	120
Sbjct	61	ACAAAGTGACAGGAGTAAGTCCTTAACTGGCAATAATAACCATGAATCTAAATGGATTCC	120
Query	121	ATTTCCCACTTAAAAGATAAAGACATGCTGAATGGATAAAAAGCTGTCACCCAGTTATAT	180
Sbjct	121	ATTTCCCACTTAAAAGATAAAGACATGCTGAATGGATAAAAAGCTGTCACCCAGTTATAT	180
Query	181	GCTGCCTACAACAACTCACTTCACCTGTAAACATACATATGGATGGAAAGAGAAGGCAT	240
Sbjct	181	GCTGCCTACAACAACTCACTTCACCTGTAAACATACATATGGATGGAAAGAGAAGGCAT	240
Query	241	GGGAAAAGATACTCTACTCAAATGAAAACAAAAACCAAACAAAGGTGGCTATTCTTATAT	300
Sbjct	241	GGGAAAAGATACTCTACTCAAATGAAAACAAAAACCAAACAAAGGTGGCTATTCTTATAT	300
Query	301	GAGATAATACAGACATTAAATCAAAAACTGGAAACAAACACAAAGTCATTGTATAATGAT	360
Sbjct	301	GAGATAATACAGACATTAAATCAAAAACTGGAAACAAACACAAAGTCATTGTATAATGAT	360
Query	361	GAATTCAATTATATCATGATGAATTCAATTATATCCTCCTTCCTGATCAATTCAGAAAGG	420
Sbjct	361	GAATTCAATTATATCATGATGAATTCAATTATATCCTCCTTCCTGATCAATTCAGAAAGG	420
Query	421	AGGATATAATCTTTTTAAATATATATACACCCAACACCAGAGCATATAAATATGTAAAGG	480
Sbjct	421	AGGATATAATCTTTTTAAATATATATACACCCAACACCAGAGCATATAAATATGTAAAGG	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 AAGATAAAGGGAGTCCTGTGATCAAGAATAAATATAACAATTATAAATATTTTATCTAAA 540
          |||
Sbjct 481 AAGATAAAGGGAGTCCTGTGATCAAGAATAAATATAACAATTATAAATATTTTATCTAAA 540

Query 541 GTGATAGATAGACTGTAATACAATAATAGGGTGGTGACATTAACACCCCCTCTCACATTG 600
          |||
Sbjct 541 GTGATAGATAGACTGTAATACAATAATAGGGTGGTGACATTAACACCCCCTCTCACATTG 600

Query 601 GACTGATCATCTAGAAAGGGAGAAAAAGCTTTATGATTGGAAAAGCCAT 648
          |||
Sbjct 601 GACTGATCATCTAGAAAGGGAGAAAAAGCTTTATGATTGGAAAAGCCAT 648
```

Sequence 1178 matched with Sequence 397

Query= Sequence ID 1178
Length=705

SEQ ID NO: 397

ALIGNMENTS

Identities = 705/705 (100%), Gaps = 0/705 (0%)

Query	1	ATTGTGTTGGCCACCCGGAATTGCGGCCGCGTCGACCTACGCACACGAGAACATGCCT	60
Sbjct	1	ATTGTGTTGGCCACCCGGAATTGCGGCCGCGTCGACCTACGCACACGAGAACATGCCT	60
Query	61	CTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGAGGAGAAGAGGAAACACAAGAAGAAA	120
Sbjct	61	CTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGAGGAGAAGAGGAAACACAAGAAGAAA	120
Query	121	CGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTGAAATGCCCAGGTGAGGAGACG	180
Sbjct	121	CGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTGAAATGCCCAGGTGAGGAGACG	180
Query	181	GCTTGCTGTAGTGGGGAAAGCACTGGACCTCAACAGTTGGAAAATGTTGTAGTGTTAGCT	240
Sbjct	181	GCTTGCTGTAGTGGGGAAAGCACTGGACCTCAACAGTTGGAAAATGTTGTAGTGTTAGCT	240
Query	241	GTCTCGTATCCTTGAAGCTGTGCAGCAGCTTCAGTTTCTTCGCCTGTGGAAAATATTTTC	300
Sbjct	241	GTCTCGTATCCTTGAAGCTGTGCAGCAGCTTCAGTTTCTTCGCCTGTGGAAAATATTTTC	300
Query	301	CCTGATACTCTTAAATTTGAATGTATGAGACTGGCAAAGTTTTGCATCTTAGGAGGAGT	360
Sbjct	301	CCTGATACTCTTAAATTTGAATGTATGAGACTGGCAAAGTTTTGCATCTTAGGAGGAGT	360
Query	361	GATTCATTTACCGTGATCTCTCATCACATTTACATACAACCCCTACGtttttttGTGT	420
Sbjct	361	GATTCATTTACCGTGATCTCTCATCACATTTACATACAACCCCTACGTTTTTTTGTGT	420
Query	421	TGGGAAACAATGTAATGGATGATGAGTTGGGCATAAGTGCAGGAAAGACGGGTGTAATAG	480
Sbjct	421	TGGGAAACAATGTAATGGATGATGAGTTGGGCATAAGTGCAGGAAAGACGGGTGTAATAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGGaaaaaaaTGTTATCTGCTTTTCTTTCAGGATGCTATAAAATCACCACGGTCTTTAGC	540
Sbjct	481	AGGAAAAAAATGTTATCTGCTTTTCTTTCAGGATGCTATAAAATCACCACGGTCTTTAGC	540
Query	541	CATGCACAAACGGTAGTTTTGTGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGA	600
Sbjct	541	CATGCACAAACGGTAGTTTTGTGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGA	600
Query	601	GGAAAAGCAAGGCTTACAGAAGGATG TTCCTTCAGGAGGAAGCAGCACTAAAAGCACTCT	660
Sbjct	601	GGAAAAGCAAGGCTTACAGAAGGATG TTCCTTCAGGAGGAAGCAGCACTAAAAGCACTCT	660
Query	661	GAGTCAANATGAGTGGGAAACCATCTCAATAAACACATTTTGGAT	705
Sbjct	661	GAGTCAANATGAGTGGGAAACCATCTCAATAAACACATTTTGGAT	705

Sequence 1180 matched with Sequence 398

Query= Sequence ID - 1180
Length=622

nt: 622

SEQ ID NO: 398

nt: 622

ALIGNMENTS

Identities = 622/622 (100%), Gaps = 0/622 (0%)

Query	1	CTTTTCCTCCCGCTGTCCCCACGGGAGGGGACTGCTCTCCCCGCTGCATCCTTTCTGT	60
Sbjct	1	CTTTTCCTCCCGCTGTCCCCACGGGAGGGGACTGCTCTCCCCGCTGCATCCTTTCTGT	60
Query	61	GAGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTC	120
Sbjct	61	GAGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTC	120
Query	121	GGGAAGTGTTTTTGAGAAGTCTCGGTTCGGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACT	180
Sbjct	121	GGGAAGTGTTTTTGAGAAGTCTCGGTTCGGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACT	180
Query	181	AACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGT	240
Sbjct	181	AACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGT	240
Query	241	CAAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGG	300
Sbjct	241	CAAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGG	300
Query	301	AAACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACT	360
Sbjct	301	AAACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACT	360
Query	361	ATTTGCTTCCAAAGGATCAGGCCCTGAGAACAAATGACCTTATTTCTACAACAGTGTCTG	420
Sbjct	361	ATTTGCTTCCAAAGGATCAGGCCCTGAGAACAAATGACCTTATTTCTACAACAGTGTCTG	420
Query	421	GGTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGAT	480
Sbjct	421	GGTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGAT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGA	540
Sbjct	481	GCTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGA	540
Query	541	AGAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACCTCTGACANCCA	600
Sbjct	541	AGAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACCTCTGACANCCA	600
Query	601	CAATCATGAGGATGATGTGTTG	622
Sbjct	601	CAATCATGAGGATGATGTGTTG	622

Sequence 1181 matched with Sequence 399

Query= Sequence ID - 1181 nt: 155
Length=155

SEQ ID NO: 399 nt: 155

ALIGNMENTS

Identities = 155/155 (100%), Gaps = 0/155 (0%)

```
Query 1 CGCCACTTATCCAGTGAACCACTATCACGaaaaaaCTCTACCTCTCTATACTAATCTCC 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 CGCCACTTATCCAGTGAACCACTATCACGAAAAAACTCTACCTCTCTATACTAATCTCC 60

Query 61 CTACAAATCTCCTTAATTATAACATTACAGCCACAGAACTAATCATATTaaaaaaaaa 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 CTACAAATCTCCTTAATTATAACATTACAGCCACAGAACTAATCATATTAAAAAAAAAAA 120

Query 121 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 155
      ||||||||||||||||||||||||||||||||
Sbjct 121 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 155
```

Sequence 1182 matched with Sequence 400

Query= Sequence ID 1182

Length=700

SEQ ID NO: 400

ALIGNMENTS

Identities = 700/700 (100%), Gaps = 0/700 (0%)

Query	1	CATTGTGTTGGCNC	CGGAATTCGCGGCCGCGTCGACTTTTTGTGTTGTTTGGAGCAGA	60
Sbjct	1	CATTGTGTTGGCNC	CGGAATTCGCGGCCGCGTCGACTTTTTGTGTTGTTTGGAGCAGA	60
Query	61	AATACTAAAGAAGATTCCGGG	CCGAGTATCCACAGAAGTGGACGCAAGGCTCTCCTTTGA	120
Sbjct	61	AATACTAAAGAAGATTCCGGG	CCGAGTATCCACAGAAGTGGACGCAAGGCTCTCCTTTGA	120
Query	121	TAAAGATGCGATGGTGGCCAGAGCCAGGCGGCTCATCGAGCTCTACAAGGAAGCTGGGAT	180	
Sbjct	121	TAAAGATGCGATGGTGGCCAGAGCCAGGCGGCTCATCGAGCTCTACAAGGAAGCTGGGAT	180	
Query	181	CAGCAAGGACCGAATTCTTATAAAAGCTGTCATCAACCTGGGAAGGAATTCAGGCTGGAAA	240	
Sbjct	181	CAGCAAGGACCGAATTCTTATAAAAGCTGTCATCAACCTGGGAAGGAATTCAGGCTGGAAA	240	
Query	241	GGAGCTCGAGGAGCAGCACGGCATCCACTGCAACATGACGTTACTCTTCTCCTTCGCCCA	300	
Sbjct	241	GGAGCTCGAGGAGCAGCACGGCATCCACTGCAACATGACGTTACTCTTCTCCTTCGCCCA	300	
Query	301	GGCTGTGGCCTGTGCCGAGGCGGGTGTGACCCTCATCTCCCCATTTGTTGGGCGCATCCT	360	
Sbjct	301	GGCTGTGGCCTGTGCCGAGGCGGGTGTGACCCTCATCTCCCCATTTGTTGGGCGCATCCT	360	
Query	361	TGATTGGCATGTGGCAAACACCGACAAGAAATCCTATGAGCCCCTGGAAGACCCTGGGGT	420	
Sbjct	361	TGATTGGCATGTGGCAAACACCGACAAGAAATCCTATGAGCCCCTGGAAGACCCTGGGGT	420	
Query	421	AAAGAGTGTCACTAAAATCTACA	ACTACTACAAGAAGTTTAGCTACAAAACCATTGTCAT	480
Sbjct	421	AAAGAGTGTCACTAAAATCTACA	ACTACTACAAGAAGTTTAGCTACAAAACCATTGTCAT	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 GGGCGCCTCCTTCCGCAACACGGGCGAGATCAAAGCACTGGCCGGCTGTGACTTCCTCAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 GGGCGCCTCCTTCCGCAACACGGGCGAGATCAAAGCACTGGCCGGCTGTGACTTCCTCAC 540

Query 541 CATCTCACCCAAGCTCCTGGGAGAGCTGCTGCAGGACAACGCCAAGCTGGTGCCTGTGCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 CATCTCACCCAAGCTCCTGGGAGAGCTGCTGCAGGACAACGCCAAGCTGGTGCCTGTGCT 600

Query 601 CTCAGCCAAGGCGGCCCAAGCCAGTGACCTGGAAAAAATCCACCTGGATGAGAAGTCTTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 CTCAGCCAAGGCGGCCCAAGCCAGTGACCTGGAAAAAATCCACCTGGATGAGAAGTCTTT 660

Query 661 CCGTTGGTTGCACAACGAGGACCAGATGGCTGTGGAGAAG 700
          ||||||||||||||||||||||||||||||||||||
Sbjct 661 CCGTTGGTTGCACAACGAGGACCAGATGGCTGTGGAGAAG 700
```

Sequence 1183 matched with Sequence 401

Query= Sequence ID - 1183
Length=479

nt: 479

SEQ ID NO: 401

nt: 479

ALIGNMENTS

Identities = 479/479 (100%), Gaps = 0/479 (0%)

Query	1	CGTGGCAGCCATCTCCTTCTCGGCATCATGGCCGCCCTCAGACCCCTTGTGAAGCCCAAG	60
Sbjct	1	CGTGGCAGCCATCTCCTTCTCGGCATCATGGCCGCCCTCAGACCCCTTGTGAAGCCCAAG	60
Query	61	ATCGTCAAAAAGAGAACCAAGAAGTTCATCCGGCACCAGTCAGACCGATATGTCAAAATT	120
Sbjct	61	ATCGTCAAAAAGAGAACCAAGAAGTTCATCCGGCACCAGTCAGACCGATATGTCAAAATT	120
Query	121	AAGCGTAACTGGCGGAAACCCAGAGGCATTGACAACAGGGTTCGTAGAAGATTCAAGGGC	180
Sbjct	121	AAGCGTAACTGGCGGAAACCCAGAGGCATTGACAACAGGGTTCGTAGAAGATTCAAGGGC	180
Query	181	CAGATCTTGATGCCCAACATTGGTTATGGAAGCAACaaaaaaaaCAAAGCACATGCTGCCC	240
Sbjct	181	CAGATCTTGATGCCCAACATTGGTTATGGAAGCAACAAAAAAAACAAAGCACATGCTGCCC	240
Query	241	AGTGGCTTCCGGAAGTTCCTGGTCCACAACGTCAAGGAGCTGGAAGTGCTGCTGATGTGC	300
Sbjct	241	AGTGGCTTCCGGAAGTTCCTGGTCCACAACGTCAAGGAGCTGGAAGTGCTGCTGATGTGC	300
Query	301	AACAAATCTTACTGTGCCGAGATCGCTCACAATGTTTCCTCCAAGAACCGCAAAGCCATC	360
Sbjct	301	AACAAATCTTACTGTGCCGAGATCGCTCACAATGTTTCCTCCAAGAACCGCAAAGCCATC	360
Query	361	GTGGAAAGAGCTGCCCAACTGGCCATCAGAGTCACCAACCCCAATGCCAGGCTGCGCAGT	420
Sbjct	361	GTGGAAAGAGCTGCCCAACTGGCCATCAGAGTCACCAACCCCAATGCCAGGCTGCGCAGT	420
Query	421	GAAGAAAAATGAGTAGGCAGCTCATGTGCACGTTTTCTGTTTAAATAAATGTAAAAACTG	479
Sbjct	421	GAAGAAAAATGAGTAGGCAGCTCATGTGCACGTTTTCTGTTTAAATAAATGTAAAAACTG	479

Sequence 1185 matched with Sequence 402

Query= Sequence ID - 1185
Length=628

nt: 628

SEQ ID NO: 402

nt: 628

ALIGNMENTS

Identities = 628/628 (100%), Gaps = 0/628 (0%)

Query	1	CTTTGATTACCTTTGAGTATTAGGTTGAAAGCTTCTCTGTGCTTGATTGAACATTGTGAT	60
Sbjct	1	CTTTGATTACCTTTGAGTATTAGGTTGAAAGCTTCTCTGTGCTTGATTGAACATTGTGAT	60
Query	61	GATGTTGATTGGGTCATGTCAGATTTAGACAGTGTTGTGTTTAAGATAAATGTTTAATGG	120
Sbjct	61	GATGTTGATTGGGTCATGTCAGATTTAGACAGTGTTGTGTTTAAGATAAATGTTTAATGG	120
Query	121	CTCTTAGCAGTGTTTCATGCCTCCCCTTTTCCCCTGATACTTTAAAAACAGAATATACAGA	180
Sbjct	121	CTCTTAGCAGTGTTTCATGCCTCCCCTTTTCCCCTGATACTTTAAAAACAGAATATACAGA	180
Query	181	AAAGGGGAGTTGGGTGAAGAATCACCATATTCTCATTACCAGAGTAGTGTCTACCAGCTG	240
Sbjct	181	AAAGGGGAGTTGGGTGAAGAATCACCATATTCTCATTACCAGAGTAGTGTCTACCAGCTG	240
Query	241	TTTTCACATTTTCTGTTTCCTTCTGTCCTTGGAATCCTtttttttAGATCCTTGTAATAC	300
Sbjct	241	TTTTCACATTTTCTGTTTCCTTCTGTCCTTGGAATCCTTTTTTTTAGATCCTTGTAATAC	300
Query	301	TAGTAAAGATATTCCACTCTGTGTTGTAAGCATTTTTCCATTTTGCTCCATGGTCTTCAT	360
Sbjct	301	TAGTAAAGATATTCCACTCTGTGTTGTAAGCATTTTTCCATTTTGCTCCATGGTCTTCAT	360
Query	361	AATGCCCTGTGGTCCTTTATTAAGGGGATGCACCATGTAGAGGTGAAAGGCTTTCCTTGA	420
Sbjct	361	AATGCCCTGTGGTCCTTTATTAAGGGGATGCACCATGTAGAGGTGAAAGGCTTTCCTTGA	420
Query	421	CTTGGCCACCATTTCTGTATTTTCCTTAGAGGAGGAGGTTTCCAACATTTCTTTTTTAGA	480
Sbjct	421	CTTGGCCACCATTTCTGTATTTTCCTTAGAGGAGGAGGTTTCCAACATTTCTTTTTTAGA	480

PATENT SEQUENCE ALIGNMENT

Query	481	GACAGAGTCTCGTTCTGACACGCAGGCAGGAGTGCAGTGGCATGATAACAGCTCACTGCA	540
Sbjct	481	GACAGAGTCTCGTTCTGACACGCAGGCAGGAGTGCAGTGGCATGATAACAGCTCACTGCA	540
Query	541	GCCTCGAACTCCTGGGCTCAAGTTATCCTCCCACCTCAGCTTCCTGAGTAGCTAGGACTG	600
Sbjct	541	GCCTCGAACTCCTGGGCTCAAGTTATCCTCCCACCTCAGCTTCCTGAGTAGCTAGGACTG	600
Query	601	CAGGTGCCTGCCACCACACCCAGCTAAT	628
Sbjct	601	CAGGTGCCTGCCACCACACCCAGCTAAT	628

Sequence 1186 matched with Sequence 403

Query= Sequence ID - 1186
Length=494

nt: 494

SEQ ID NO: 403

nt: 494

ALIGNMENTS

Identities = 494/494 (100%), Gaps = 0/494 (0%)

Query	1	CAGCCCTCCGTCACCTCTTCACCGCACCCCTCGGACTgcccccaaggcccccgccgcgcct	60
Sbjct	1	CAGCCCTCCGTCACCTCTTCACCGCACCCCTCGGACTGCCCCAAGGCCCCCGCCGCCGCT	60
Query	61	ccagcgccgcgcagccaccgcccgcgcgcgcctctccttagtcgcccATGACGACC	120
Sbjct	61	CCAGCGCCGCGCAGCCACCGCCGCCGCCGCCCTCTCCTTAGTCGCCGCCATGACGACC	120
Query	121	GCGTCCACCTCGCAGGTGCGCCAGAACTACCACCAGGACTCAGAGGCCGCCATCAACCGC	180
Sbjct	121	GCGTCCACCTCGCAGGTGCGCCAGAACTACCACCAGGACTCAGAGGCCGCCATCAACCGC	180
Query	181	CAGATCAACCTGGAGCTCTACGCCTCCTACGTTTACCTGTCCATGTCTTACTACTTTGAC	240
Sbjct	181	CAGATCAACCTGGAGCTCTACGCCTCCTACGTTTACCTGTCCATGTCTTACTACTTTGAC	240
Query	241	CGCGATGATGTGGCTTTGAAGAACTTTGCCAAATACTTTCTTCACCAATCTCATGAGGAG	300
Sbjct	241	CGCGATGATGTGGCTTTGAAGAACTTTGCCAAATACTTTCTTCACCAATCTCATGAGGAG	300
Query	301	AGGGGAACATGCTGAGAACTGATGAAGCTGCAGAACCAACGAGGGTGGCCGAATCTTCC	360
Sbjct	301	AGGGGAACATGCTGAGAACTGATGAAGCTGCAGAACCAACGAGGGTGGCCGAATCTTCC	360
Query	361	TTCAGGATATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGT	420
Sbjct	361	TTCAGGATATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGT	420
Query	421	GTGCATTACATTTGGGaaaaaaTGTGAATCAGTCACTACTGGAAGTGCACAACTGGCCA	480
Sbjct	421	GTGCATTACATTTGGAAAAAATGTGAATCAGTCACTACTGGAAGTGCACAACTGGCCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CTGACAAAAATGAC	494
Sbjct	481	CTGACAAAAATGAC	494

nt: 599

nt: 599

Identities = 599/599 (100%), Gaps = 0/599 (0%)

Query	1	GGGAGACAAGCCCAGCCTTTTCGGCGAGNATACGTCTAACCCCTGTGCAACAGCCACTACAT 	60
Sbjct	1	GGGAGACAAGCCCAGCCTTTTCGGCGAGNATACGTCTAACCCCTGTGCAACAGCCACTACAT 	60
Query	61	TACTTCAAACCTGAGATCCTTCCTTTTGAGGGAGCAAGTCCTTCCCTTTTCATTTTTTCCAG 	120
Sbjct	61	TACTTCAAACCTGAGATCCTTCCTTTTGAGGGAGCAAGTCCTTCCCTTTTCATTTTTTCCAG 	120
Query	121	TCTTCCTCCCTGTGTATTCAATTCTCATGATTATTATTTTAGTGGGGGCGGGGTGGGAAAG 	180
Sbjct	121	TCTTCCTCCCTGTGTATTCAATTCTCATGATTATTATTTTAGTGGGGGCGGGGTGGGAAAG 	180
Query	181	ATTACTTTTTCTTTATGTGTTTGACGGGAACAAAACCTAGGTAAAATCTACAGTACACCA 	240
Sbjct	181	ATTACTTTTTCTTTATGTGTTTGACGGGAACAAAACCTAGGTAAAATCTACAGTACACCA 	240
Query	241	CAAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCGTGGAAAGGGGCAGGCCANA 	300
Sbjct	241	CAAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCGTGGAAAGGGGCAGGCCANA 	300
Query	301	GCTACCCGCAGAGTTCTCAGAATCATGCTGAGAGAGCTGGAGGCACCCATGCCATCTCAA 	360
Sbjct	301	GCTACCCGCAGAGTTCTCAGAATCATGCTGAGAGAGCTGGAGGCACCCATGCCATCTCAA 	360
Query	361	CCTCTTCCCCGCCCGTTTTTACAAAGGGGGAGGCTAAAGCCCAGAGACAGCTTGATCAAAG 	420
Sbjct	361	CCTCTTCCCCGCCCGTTTTTACAAAGGGGGAGGCTAAAGCCCAGAGACAGCTTGATCAAAG 	420
Query	421	GCACACAGCAAGTCAGGGTTGGAGCAGTAGCTGGAGGGACCTTGTCTCCCAGCTCAGGGC 	480
Sbjct	421	GCACACAGCAAGTCAGGGTTGGAGCAGTAGCTGGAGGGACCTTGTCTCCCAGCTCAGGGC 	480

Sequence 1189 matched with Sequence 405

Query= Sequence ID 1189

Length=610

SEQ ID NO: 405

ALIGNMENTS

Identities = 610/610 (100%), Gaps = 0/610 (0%)

Query	1	GGGAGACAAGCCCAGCCTTTTCGGCGAGATACGTCTAACCCCTGTGCAACAGCCACTACATT	60
Sbjct	1	GGGAGACAAGCCCAGCCTTTTCGGCGAGATACGTCTAACCCCTGTGCAACAGCCACTACATT	60
Query	61	ACTTCAAACCTGAGATCCTTCCTTTTGAGGGAGCAAGTCCTTCCCTTTCATTTTTTCCAGT	120
Sbjct	61	ACTTCAAACCTGAGATCCTTCCTTTTGAGGGAGCAAGTCCTTCCCTTTCATTTTTTCCAGT	120
Query	121	CTTCCTCCCTGTGTATTTCATTCTCATGATTATTATTTTAGTGGGGGCGGGGTGGGAAAGA	180
Sbjct	121	CTTCCTCCCTGTGTATTTCATTCTCATGATTATTATTTTAGTGGGGGCGGGGTGGGAAAGA	180
Query	181	TTACTTTTTCTTTATGTGTTTGACGGGAAACAAAACCTAGGTAAAATCTACAGTACACCAC	240
Sbjct	181	TTACTTTTTCTTTATGTGTTTGACGGGAAACAAAACCTAGGTAAAATCTACAGTACACCAC	240
Query	241	AAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCGTGGAAGGGGCAGGCCAGAG	300
Sbjct	241	AAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCGTGGAAGGGGCAGGCCAGAG	300
Query	301	CTACCCGCAGAGTTCTCAGAATCATGCTGAGAGAGCTGGAGGCACCCATGCCATCTCAAC	360
Sbjct	301	CTACCCGCAGAGTTCTCAGAATCATGCTGAGAGAGCTGGAGGCACCCATGCCATCTCAAC	360
Query	361	CTCTTCCCCGCCCCTTTTACAAAGGGGGAGGCTAAAGCCCAGAGACAGCTTGATCAAAGG	420
Sbjct	361	CTCTTCCCCGCCCCTTTTACAAAGGGGGAGGCTAAAGCCCAGAGACAGCTTGATCAAAGG	420
Query	421	CACACAGCAAGTCAGGGTTGGAGCAGTAGCTGGAGGGACCTTGTCTCCAGCTCAGGGCT	480
Sbjct	421	CACACAGCAAGTCAGGGTTGGAGCAGTAGCTGGAGGGACCTTGTCTCCAGCTCAGGGCT	480

Sequence 1190 matched with Sequence 406

Query= Sequence ID 1190
Length=644

SEQ ID NO: 406

ALIGNMENTS

Identities = 644/644 (100%), Gaps = 0/644 (0%)

Query	1	GTTTAAATTTGACAACTAAAGCTNATNACTGCTATAAGAGTAATAACTGCTCATTTTCC	60
Sbjct	1	GTTTAAATTTGACAACTAAAGCTNATNACTGCTATAAGAGTAATAACTGCTCATTTTCC	60
Query	61	ATAACTCATTCTTAAAGTTTTAGTAATGTAAAAGTTAAttttttGCAGTAAGTTATAATG	120
Sbjct	61	ATAACTCATTCTTAAAGTTTTAGTAATGTAAAAGTTATTTTTTTGCAGTAAGTTATAATG	120
Query	121	ATAGAAGCTTACATGTTTTTTCATGCCTCATCTGTTTCCCCTTAAAACTATAATTATCAG	180
Sbjct	121	ATAGAAGCTTACATGTTTTTTCATGCCTCATCTGTTTCCCCTTAAAACTATAATTATCAG	180
Query	181	TAAAGTCCTGTGGTATTTTTCAATTTGTAAGAACTAGGCTATATATACATTGGGAAAAA	240
Sbjct	181	TAAAGTCCTGTGGTATTTTTCAATTTGTAAGAACTAGGCTATATATACATTGGGAAAAA	240
Query	241	CAGCCTTCATTTGTCAATGCACTAGTGTCCAAAGGTTTCTGGTAATTGTGTGCTATTGC	300
Sbjct	241	CAGCCTTCATTTGTCAATGCACTAGTGTCCAAAGGTTTCTGGTAATTGTGTGCTATTGC	300
Query	301	TTTTTGTTGACTTGCaaaaaaaaaaaaaaaaaTTACTATGACTTGNGGTAGCCCTGCA	360
Sbjct	301	TTTTTGTTGACTTGCaaaaaaaaaaaaaaaaaTTACTATGACTTGNGGTAGCCCTGCA	360
Query	361	ACCTTCGGAAGTGCTTAGCCCAGTCTGACCATACATTTATATTTANAATGCTTAGGTAAA	420
Sbjct	361	ACCTTCGGAAGTGCTTAGCCCAGTCTGACCATACATTTATATTTANAATGCTTAGGTAAA	420
Query	421	TAAATAATATGCCTAAACCCAATGCTATAAGATACTATATAATATCTCATAATTTTAAAA	480
Sbjct	421	TAAATAATATGCCTAAACCCAATGCTATAAGATACTATATAATATCTCATAATTTTAAAA	480

PATENT SEQUENCE ALIGNMENT

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Query  481  ATCACTGTTTTGTATAATAATAAAACAAGGCAGGCAAGCTGTTCTACAATGACTGTTGGT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATCACTGTTTTGTATAATAATAAAACAAGGCAGGCAAGCTGTTCTACAATGACTGTTGGT  540

Query  541  AAGGGTGCTGAGGAAGAAAAACAAACAATCTTGATTGAGGATAGTGAATAGACAAAAAA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAGGGTGCTGAGGAAGAAAAACAAACAATCTTGATTGAGGATAGTGAATAGACAAAAAA  600

Query  601  TGTCTAATCAATGAAGCTGTGTGATGATTCTGATTGACAGAGA  644
          |||||||||||||||||||||||||||||||||||||||
Sbjct  601  TGTCTAATCAATGAAGCTGTGTGATGATTCTGATTGACAGAGA  644
```

Sequence 1191 matched with Sequence 407

Query= Sequence ID 1191

Length=653

SEQ ID NO: 407

ALIGNMENTS

Identities = 653/653 (100%), Gaps = 0/653 (0%)

Query	1	GTGCAAAGTGTTATATCCACTTTCAACAAAGAGAGAAGCTGAAAAGCTAACCCAATGTTA	60
Sbjct	1	GTGCAAAGTGTTATATCCACTTTCAACAAAGAGAGAAGCTGAAAAGCTAACCCAATGTTA	60
Query	61	ATTTTGGATCACACACATTTCAGTGTAGACTTTAAGATTTTACTTCTGTTGGAGTAGCTAT	120
Sbjct	61	ATTTTGGATCACACACATTTCAGTGTAGACTTTAAGATTTTACTTCTGTTGGAGTAGCTAT	120
Query	121	ATTATTTCTAGTTAAAAAACTCTCTATATACATATTTATTTGTTTTTCTACTTGTTTAAAT	180
Sbjct	121	ATTATTTCTAGTTAAAAAACTCTCTATATACATATTTATTTGTTTTTCTACTTGTTTAAAT	180
Query	181	ATTTTCTCTTCCAATTAGGAACTCAATATGGAATAAAAAATATTTAAATGTATTTTACT	240
Sbjct	181	ATTTTCTCTTCCAATTAGGAACTCAATATGGAATAAAAAATATTTAAATGTATTTTACT	240
Query	241	CAAACGTGTGTGTATATATGTTTGTGTGCATGATAAGgagagtgagagcaagagtaagag	300
Sbjct	241	CAAACGTGTGTGTATATATGTTTGTGTGCATGATAAGGAGAGTGAGAGCAAGAGTAAGAG	300
Query	301	agagagagCACGCATAGATGGAAGCACACATTTAATGTCTATGAAATGAGAAAACATTAA	360
Sbjct	301	AGAGAGAGCACGCATAGATGGAAGCACACATTTAATGTCTATGAAATGAGAAAACATTAA	360
Query	361	GGCTAAGATATTTTTCCTTCTGAACTAGCAGATTGTATCAATGGCTGGTCACTTAAATTA	420
Sbjct	361	GGCTAAGATATTTTTCCTTCTGAACTAGCAGATTGTATCAATGGCTGGTCACTTAAATTA	420
Query	421	ATCAGTTTGTAAGATATTTAAAGGTATGTCTACCTTCTTGCAATTAATTTGATTATGT	480
Sbjct	421	ATCAGTTTGTAAGATATTTAAAGGTATGTCTACCTTCTTGCAATTAATTTGATTATGT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCTAATGGCATGGCAAGAGAAAATGAAAGAAGATAACTAAAAGTTAAAAGTCGTTGCATGT	540
Sbjct	481	TCTAATGGCATGGCAAGAGAAAATGAAAGAAGATAACTAAAAGTTAAAAGTCGTTGCATGT	540
Query	541	TTTTGTTGCAGCATACCCTTCTTTCAGGCTACCGAATAACCTTGATTGACATTGGATTAG	600
Sbjct	541	TTTTGTTGCAGCATACCCTTCTTTCAGGCTACCGAATAACCTTGATTGACATTGGATTAG	600
Query	601	TAGTAGAATACCTCATTGGTAGAGCATATCGCAGCANCTACACTAGAAAACAT	653
Sbjct	601	TAGTAGAATACCTCATTGGTAGAGCATATCGCAGCANCTACACTAGAAAACAT	653

Sequence 1192 matched with Sequence 408

Query= Sequence ID 1192

Length=452

SEQ ID NO: 408

ALIGNMENTS

Identities = 452/452 (100%), Gaps = 0/452 (0%)

Query	1	GTCTGGAACCTCCAGACCTCAGGTGATACCCCTGCCTCAGCCTCCCAATGTGCTGGGATTA	60
Sbjct	1	GTCTGGAACCTCCAGACCTCAGGTGATACCCCTGCCTCAGCCTCCCAATGTGCTGGGATTA	60
Query	61	CAGCTGTGAAGCCACCGCGCCCGGCTGCTGTGATAGTTGAGATGTAAACCAAAAATAAAA	120
Sbjct	61	CAGCTGTGAAGCCACCGCGCCCGGCTGCTGTGATAGTTGAGATGTAAACCAAAAATAAAA	120
Query	121	TTCTAAGCCACCCAATCCGACTGAATGGACCCTTCCTGTTGAGCAAGGACATTCCAAAGT	180
Sbjct	121	TTCTAAGCCACCCAATCCGACTGAATGGACCCTTCCTGTTGAGCAAGGACATTCCAAAGT	180
Query	181	AAACTGAAAAGACCAGCTTAGGCCATGATGGGAAGGGGAGGTGTCAACATGCCTCATTCT	240
Sbjct	181	AAACTGAAAAGACCAGCTTAGGCCATGATGGGAAGGGGAGGTGTCAACATGCCTCATTCT	240
Query	241	ACCTTCCTCCCTCTGGAATCCAGACACAACCTGACCAGCATTAACATTAAAACAGAGATCT	300
Sbjct	241	ACCTTCCTCCCTCTGGAATCCAGACACAACCTGACCAGCATTAACATTAAAACAGAGATCT	300
Query	301	TAAGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGAT	360
Sbjct	301	TAAGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGAT	360
Query	361	CACCTGAGGTCGGAAGTTCAAGACCAGCCTGGCCGGTATGGTGAAGCCATGTCTCTACTG	420
Sbjct	361	CACCTGAGGTCGGAAGTTCAAGACCAGCCTGGCCGGTATGGTGAAGCCATGTCTCTACTG	420
Query	421	AAAATGCAAAAATTGGCCGGACATTGTGGTGCA	452
Sbjct	421	AAAATGCAAAAATTGGCCGGACATTGTGGTGCA	452

Sequence 1193 matched with Sequence 409

Query= Sequence ID 1193
Length=900

SEQ ID NO: 409

ALIGNMENTS

Identities = 896/896 (100%), Gaps = 0/896 (0%)

Query	5	tttttttttCCCNCGGGAAAGCGCGCCATTGTGTTGGTCCCCGGGAATTCGCGGCCGCGTC	64
Sbjct	5	TTTTTTTTTCCCNCGGGAAAGCGCGCCATTGTGTTGGTCCCCGGGAATTCGCGGCCGCGTC	64
Query	65	GACGAGAAATGGCTTGAACCCAGTAGGCAGAGGTTGTAGTGAGCCCAGAATNGGNCACCT	124
Sbjct	65	GACGAGAAATGGCTTGAACCCAGTAGGCAGAGGTTGTAGTGAGCCCAGAATNGGNCACCT	124
Query	125	GCACNTTANCCNTGGGTGACAAAANTGAAAACCTTGTCTnaaaaaaaaaaaaaaaaaaat	184
Sbjct	125	GCACNTTANCCNTGGGTGACAAAANTGAAAACCTTGTCTNAAAAAAAAAAAAAAAAAAAT	184
Query	185	tttaantnaaatnaaaaancctttncnttntttttnaaannggggggggNNTTTTTNNGGG	244
Sbjct	185	TTTAANTNAAATNAAAAANCCTTTNCNTTNTTTTTNAAANNGGGGGGGGNNTTTTTNNGGG	244
Query	245	NTTNGNNNTGGTAAAAANTNNNTtttttttttttaggggccnanncccnttttanaaa	304
Sbjct	245	NTTNGNNNTGGTAAAAANTNNNTTTTTTTTTTTTTTAGGGGCCNANNCCCCNTTTTANAAA	304
Query	305	anccngnttttnaaaaaanttttttNCCNCNNTTNggggggggggNTTTTNANCNNTNT	364
Sbjct	305	ANCCNGNTTTTNAAAAAANTTTTTTNCCNCNNTTNNGGGGGGGGGNTTTTNANCNNTNT	364
Query	365	TNggggggggNCCCCCTNTTANNACCNNCaaantttttanttttttgnnnaannnccccct	424
Sbjct	365	TNGGGGGGGNCCCCCTNTTANNACCNNCAAANTTTTTANTTTTTTGNNAANNNCCCCCT	424
Query	425	tttttnnttttttttGNggggggggggNNGCCCCCNCCTTTNGggggggggggNTTNNGN	484
Sbjct	425	TTTTTNNTTTTTTTTGNNGGGGGGGGGNNGCCCCCNCCTTTNGGGGGGGGGGNTTNNGN	484

PATENT SEQUENCE ALIGNMENT

Sequence 1195 matched with Sequence 410

Query= Sequence ID 1195
Length=271

SEQ ID NO: 410

ALIGNMENTS

Identities = 271/271 (100%), Gaps = 0/271 (0%)

Query	1	GTTCGTGACNTTCGGAGCTACCTGACAGAGCAGAGTCAACCAGGNTCTGCCCAAAGAGAG	60
Sbjct	1	GTTCGTGACNTTCGGAGCTACCTGACAGAGCAGAGTCAACCAGGNTCTGCCCAAAGAGAG	60
Query	61	TGTTAGGCCTGAGCTTGAGAGCCCTGGAGAGACGTGTGCACAAAATGTGACCTGAGGCCC	120
Sbjct	61	TGTTAGGCCTGAGCTTGAGAGCCCTGGAGAGACGTGTGCACAAAATGTGACCTGAGGCCC	120
Query	121	TAGTCTAGCAAGAGGACATAGCACCCCTCATCTGGGAATAGGGAAGGCACCTTGCAGAAAA	180
Sbjct	121	TAGTCTAGCAAGAGGACATAGCACCCCTCATCTGGGAATAGGGAAGGCACCTTGCAGAAAA	180
Query	181	TATGAGCAATTTGATATTAATAACATCTTCAATGTGCCATAGACCTTCCCACAAAGACT	240
Sbjct	181	TATGAGCAATTTGATATTAATAACATCTTCAATGTGCCATAGACCTTCCCACAAAGACT	240
Query	241	GTCCAATAATAAGAGATGCTTATCTATTTTA	271
Sbjct	241	GTCCAATAATAAGAGATGCTTATCTATTTTA	271

Sequence 1196 matched with Sequence 411

Query= Sequence ID - 1196 nt: 412
Length=412

SEQ ID NO: 411 nt: 412

ALIGNMENTS

Identities = 412/412 (100%), Gaps = 0/412 (0%)

Query	1	GTCGACGCGGCCGCGGTCGCTGGAGNCGATCAACTCTAGGCTCCAACTCGTTATGAAAAG	60
Sbjct	1	GTCGACGCGGCCGCGGTCGCTGGAGNCGATCAACTCTAGGCTCCAACTCGTTATGAAAAG	60
Query	61	TGGGAAGTACGTCCTGGGGTACAAGCAGACTCTGAAGATGATCAGACAAGGCAAAGCGAA	120
Sbjct	61	TGGGAAGTACGTCCTGGGGTACAAGCAGACTCTGAAGATGATCAGACAAGGCAAAGCGAA	120
Query	121	ATTGGTCATTCTCGCTAACAACTGCCAGCTTTGAGGAAATCTGAAATAGAGTACTATGC	180
Sbjct	121	ATTGGTCATTCTCGCTAACAACTGCCAGCTTTGAGGAAATCTGAAATAGAGTACTATGC	180
Query	181	TATGTTGGCTAAAACTGGTGTCCATCACTACAGTGGCAATAATATTGAACTGGGCACAGC	240
Sbjct	181	TATGTTGGCTAAAACTGGTGTCCATCACTACAGTGGCAATAATATTGAACTGGGCACAGC	240
Query	241	ATGCGGAAAATACTACAGAGTGTGCACACTGGCTATCATTGATCCAGGTGACTCTGACAT	300
Sbjct	241	ATGCGGAAAATACTACAGAGTGTGCACACTGGCTATCATTGATCCAGGTGACTCTGACAT	300
Query	301	CATTAGAAGCATGCCAGAACAGACTGGTGAAAAGTAAACCTTTTCACCTACAAAATTTCA	360
Sbjct	301	CATTAGAAGCATGCCAGAACAGACTGGTGAAAAGTAAACCTTTTCACCTACAAAATTTCA	360
Query	361	CCTGCAAACCTTAAACCTGCAAAATTTTCCTTTAATAAAATTTGCTTGTTTT	412
Sbjct	361	CCTGCAAACCTTAAACCTGCAAAATTTTCCTTTAATAAAATTTGCTTGTTTT	412

Sequence 1198 matched with Sequence 413

Query= Sequence ID 1198
Length=245

SEQ ID NO: 413

ALIGNMENTS

Identities = 245/245 (100%), Gaps = 0/245 (0%)

Query	1	CAGAGGTGGGAGGATTGCTTCAGTTCAAGAGTTTGAGACCAGCCTGGGTAACATGGCGAA	60
Sbjct	1	CAGAGGTGGGAGGATTGCTTCAGTTCAAGAGTTTGAGACCAGCCTGGGTAACATGGCGAA	60
Query	61	ACCCTGTCTTTACAAAAAATGCAAACCTTTGCCGCATGTGTTGGGGTGCGCCTGTAGTCC	120
Sbjct	61	ACCCTGTCTTTACAAAAAATGCAAACCTTTGCCGCATGTGTTGGGGTGCGCCTGTAGTCC	120
Query	121	CAGCTTCTCGGGAGGCTGAGGTGGGGGGACCACCTGAGCCATGGAGGTTGAGGCTGCAGT	180
Sbjct	121	CAGCTTCTCGGGAGGCTGAGGTGGGGGGACCACCTGAGCCATGGAGGTTGAGGCTGCAGT	180
Query	181	GAGCCGTGATACCACCACTGTACTCTAGCCTGGGCCATAGAGTGAGACACCCTGCCTCAG	240
Sbjct	181	GAGCCGTGATACCACCACTGTACTCTAGCCTGGGCCATAGAGTGAGACACCCTGCCTCAG	240
Query	241	AAATA	245
Sbjct	241	AAATA	245

Sequence 1199 matched with Sequence 414

Query= Sequence ID - 1199 nt: 439
Length=439

SEQ ID NO: 414 nt: 439

ALIGNMENTS

Identities = 439/439 (100%), Gaps = 0/439 (0%)

Query	1	CCCATCCCCTCGACCGCTCGCGTCGCATTGCGCCGCTCCCTACCGCTCCAAGCCCAGCC	60
Sbjct	1	CCCATCCCCTCGACCGCTCGCGTCGCATTGCGCCGCTCCCTACCGCTCCAAGCCCAGCC	60
Query	61	CTCAGCCATGGCATGCCCCCTGGATCAGGCCATTGGCCTCCTCGTGGCCATCTTCCACAA	120
Sbjct	61	CTCAGCCATGGCATGCCCCCTGGATCAGGCCATTGGCCTCCTCGTGGCCATCTTCCACAA	120
Query	121	GTACTCCGGCAGGGAGGGTGACAAGCACACCCTGAGCAAGAAGGAGCTGAAGGAGCTGAT	180
Sbjct	121	GTACTCCGGCAGGGAGGGTGACAAGCACACCCTGAGCAAGAAGGAGCTGAAGGAGCTGAT	180
Query	181	CCAGAAGGAGCTCACCATTGGCTCGAAGCTGCAGGATGCTGAAATTGCAAGGCTGATGGA	240
Sbjct	181	CCAGAAGGAGCTCACCATTGGCTCGAAGCTGCAGGATGCTGAAATTGCAAGGCTGATGGA	240
Query	241	AGACTTGGACCGGAACAAGGACCAGGAGGTGAACTTCAGGAGTATGTCACCTTCCTGGG	300
Sbjct	241	AGACTTGGACCGGAACAAGGACCAGGAGGTGAACTTCAGGAGTATGTCACCTTCCTGGG	300
Query	301	GGCCTTGGCTTTGATCTACAATGAAGCCCTCAAGGGCTGAAAATAAATAGGGAAGATGGA	360
Sbjct	301	GGCCTTGGCTTTGATCTACAATGAAGCCCTCAAGGGCTGAAAATAAATAGGGAAGATGGA	360
Query	361	GACACCCTCTGGGGTCTCTCTGAGTCAAATCCAGTGGTGGGTAATTGTACAATAAAtt	420
Sbjct	361	GACACCCTCTGGGGTCTCTCTGAGTCAAATCCAGTGGTGGGTAATTGTACAATAAATT	420
Query	421	tttttttGGTCAAATTTAA	439
Sbjct	421	TTTTTTTGGTCAAATTTAA	439

Sequence 1200 matched with Sequence 415

Query= Sequence ID - 1200
Length=526

nt: 526

SEQ ID NO: 415

nt: 526

ALIGNMENTS

Identities = 526/526 (100%), Gaps = 0/526 (0%)

Query	1	CTGGAGACGACGTGCAGAAATGGCACCTCGAAAGGGGAAGGAAAAGAAGGAAGAACAGGT	60
Sbjct	1	CTGGAGACGACGTGCAGAAATGGCACCTCGAAAGGGGAAGGAAAAGAAGGAAGAACAGGT	60
Query	61	CATCAGCCTCGGACCTCAGGTGGCTGAAGGAGAGAATGTATTTGGTGTCTGCCATATCTT	120
Sbjct	61	CATCAGCCTCGGACCTCAGGTGGCTGAAGGAGAGAATGTATTTGGTGTCTGCCATATCTT	120
Query	121	TGCATCCTTCAATGACACTTTTGTCCATGTCACTGATCTTTCTGGCAAGGAAACCATCTG	180
Sbjct	121	TGCATCCTTCAATGACACTTTTGTCCATGTCACTGATCTTTCTGGCAAGGAAACCATCTG	180
Query	181	CCGTGTGACTGGTGGGATGAAGGTAAAGGCAGACCGAGATGAATCCTCACCATATGCTGC	240
Sbjct	181	CCGTGTGACTGGTGGGATGAAGGTAAAGGCAGACCGAGATGAATCCTCACCATATGCTGC	240
Query	241	TATGTTGGCTGCCCAGGATGTGGCCCAGAGGTGCAAGGAGCTGGGTATCACCGCCCTACA	300
Sbjct	241	TATGTTGGCTGCCCAGGATGTGGCCCAGAGGTGCAAGGAGCTGGGTATCACCGCCCTACA	300
Query	301	CATCAAACCTCCGGGCCACAGGAGGAAATAGGACCAAGACCCCTGGACCTGGGGCCCAGTC	360
Sbjct	301	CATCAAACCTCCGGGCCACAGGAGGAAATAGGACCAAGACCCCTGGACCTGGGGCCCAGTC	360
Query	361	GGCCCTCANAGCCCTTGCCCGCTCGGGTATGAAGATCGGGCGGATTGAGGATGTCACCCC	420
Sbjct	361	GGCCCTCANAGCCCTTGCCCGCTCGGGTATGAAGATCGGGCGGATTGAGGATGTCACCCC	420
Query	421	CATCCCTCTGACAGCACTCGCAGGAAGGGGGGTGCGCGTGGTCGCCGTCTGTGAACAAG	480
Sbjct	421	CATCCCTCTGACAGCACTCGCAGGAAGGGGGGTGCGCGTGGTCGCCGTCTGTGAACAAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	ATTCTCAAAATATTTTCTGTAAATAAATTGCCTTCATGTAAACTG	526
Sbjct	481	ATTCTCAAAATATTTTCTGTAAATAAATTGCCTTCATGTAAACTG	526

Sequence 1201 matched with Sequence 416

Query= Sequence ID - 1201 nt: 613
Length=613

SEQ ID NO: 416 nt: 613

ALIGNMENTS

Identities = 613/613 (100%), Gaps = 0/613 (0%)

Query	1	CTTAAGTATGCCCTGACAGGAGNATGAAGTAAAGAAGATTTGCATGCAGCGGTTCA	60
Sbjct	1	CTTAAGTATGCCCTGACAGGAGNATGAAGTAAAGAAGATTTGCATGCAGCGGTTCA	60
Query	61	AATCGATGGCAAGGTCCGAAGTATATAACCTACCCTGCTGGATTCATGGATGTCATCAG	120
Sbjct	61	AATCGATGGCAAGGTCCGAAGTATATAACCTACCCTGCTGGATTCATGGATGTCATCAG	120
Query	121	CATTGACAAGACGGGAGAGAATTTCCGTCTGATCTATGACACCAAGGGTCGCTTTGCTGT	180
Sbjct	121	CATTGACAAGACGGGAGAGAATTTCCGTCTGATCTATGACACCAAGGGTCGCTTTGCTGT	180
Query	181	ACATCGTATTACACCTGAGGAGGCCAAGTACAAGTTGTGCAAAGTGAGAAAGATCTTTGT	240
Sbjct	181	ACATCGTATTACACCTGAGGAGGCCAAGTACAAGTTGTGCAAAGTGAGAAAGATCTTTGT	240
Query	241	GGGCACAAAAGGAATCCCTCATCTGGTGACTCATGATGCCCCGACCATCCGCTACCCCGA	300
Sbjct	241	GGGCACAAAAGGAATCCCTCATCTGGTGACTCATGATGCCCCGACCATCCGCTACCCCGA	300
Query	301	TCCCCTCATCAAGGTGAATGATACCATTCAGATTGATTTAGAGACTGGCAAGATTACTGA	360
Sbjct	301	TCCCCTCATCAAGGTGAATGATACCATTCAGATTGATTTAGAGACTGGCAAGATTACTGA	360
Query	361	TTTCATCAAGTTCGACACTGGTAACCTGTGTATGGTGACTGGAGGTGCTAACCTAGGAAG	420
Sbjct	361	TTTCATCAAGTTCGACACTGGTAACCTGTGTATGGTGACTGGAGGTGCTAACCTAGGAAG	420
Query	421	AATTGGTGTGATCACCAACAGAGAGAGGGACCCTGGATCTTTTGACGTGGTTCACGTGAA	480
Sbjct	421	AATTGGTGTGATCACCAACAGAGAGAGGGACCCTGGATCTTTTGACGTGGTTCACGTGAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGATGCCAATGGCAACAGCTTTGCCACTCGACTTTCCAACATTTTGTATTGGCAAGGG	540
Sbjct	481	AGATGCCAATGGCAACAGCTTTGCCACTCGACTTTCCAACATTTTGTATTGGCAAGGG	540
Query	541	CAACAAACCATGGATTTCTCTTCCCCGAGGAAAGGGTATCCGCCTCACCATTGCTGAAGA	600
Sbjct	541	CAACAAACCATGGATTTCTCTTCCCCGAGGAAAGGGTATCCGCCTCACCATTGCTGAAGA	600
Query	601	GAGAGACAAAAGA	613
Sbjct	601	GAGAGACAAAAGA	613

Sequence 1202 matched with Sequence 417

Query= Sequence ID 1202
Length=663

SEQ ID NO: 417

ALIGNMENTS

Identities = 663/663 (100%), Gaps = 0/663 (0%)

Query	1	GGAATTCGCGGCCGCGTCGACCTCTGCTCGAATTGACAGAAAAGGATTCTGTGAAGAGTG	60
Sbjct	1	GGAATTCGCGGCCGCGTCGACCTCTGCTCGAATTGACAGAAAAGGATTCTGTGAAGAGTG	60
Query	61	ATGAGATTTCCATCCATGCTGACTTTGAGAATACATGTTCCCGAATTGTGGTCCCCAAAG	120
Sbjct	61	ATGAGATTTCCATCCATGCTGACTTTGAGAATACATGTTCCCGAATTGTGGTCCCCAAAG	120
Query	121	CTGCCATTGTGGCCCGCCACACTTACCTTGCCAATGGCCAGACCAAGGTGCTGACTCAGA	180
Sbjct	121	CTGCCATTGTGGCCCGCCACACTTACCTTGCCAATGGCCAGACCAAGGTGCTGACTCAGA	180
Query	181	AGTTGTCATCAGTCAGAGGCAATCATATTATCTCAGGGACATGCGCATCATGGCGTGGCA	240
Sbjct	181	AGTTGTCATCAGTCAGAGGCAATCATATTATCTCAGGGACATGCGCATCATGGCGTGGCA	240
Query	241	AGAGCCTTCGGGTTTCTGAGATCAGGCCTTCTATCCTGGGCTGCAACATCCTTCGAGTTG	300
Sbjct	241	AGAGCCTTCGGGTTTCTGAGATCAGGCCTTCTATCCTGGGCTGCAACATCCTTCGAGTTG	300
Query	301	AATATTCCTTACTGATCTATGTTAGCGTTCCTGGATCCAAGAAGGTCATCCTTGACCTGC	360
Sbjct	301	AATATTCCTTACTGATCTATGTTAGCGTTCCTGGATCCAAGAAGGTCATCCTTGACCTGC	360
Query	361	CCCTGGTAATTGGCAGCAGATCAGGTCTAAGCAGCAGAACATCCAGCATGGCCAGCCGAA	420
Sbjct	361	CCCTGGTAATTGGCAGCAGATCAGGTCTAAGCAGCAGAACATCCAGCATGGCCAGCCGAA	420
Query	421	CCAGCTCTGAGATGAGTTGGGTAGATCTGAACATCCCTGATACCCAGAAGCTCCTCCCT	480
Sbjct	421	CCAGCTCTGAGATGAGTTGGGTAGATCTGAACATCCCTGATACCCAGAAGCTCCTCCCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCTATATGGATGTCATTCTGAAGATCACCGATTGGAGAGCCCAACCACTCCTCTGCTAG	540
Sbjct	481	GCTATATGGATGTCATTCTGAAGATCACCGATTGGAGAGCCCAACCACTCCTCTGCTAG	540
Query	541	ATGACATGGATGGCTCTCAAGACAGCCCTATCTTTATGTATGCCCCTGAGTTCAAGTTCA	600
Sbjct	541	ATGACATGGATGGCTCTCAAGACAGCCCTATCTTTATGTATGCCCCTGAGTTCAAGTTCA	600
Query	601	TGCCACCACCGACTTATACTGAGGTGGATCCCTGCATCCTCAACAACAATGTGCAGTGAG	660
Sbjct	601	TGCCACCACCGACTTATACTGAGGTGGATCCCTGCATCCTCAACAACAATGTGCAGTGAG	660
Query	661	CAT	663
Sbjct	661	CAT	663

Sequence 1203 matched with Sequence 418

Query= Sequence ID - 1203
Length=692

nt: 692

SEQ ID NO: 418

nt: 692

ALIGNMENTS

Identities = 692/692 (100%), Gaps = 0/692 (0%)

Query	1	TGCAGAGGGGTCCATACGGCGTTGTTCTGGATTCCCGTCGTAACCTAAAGGGAACTTTC	60
Sbjct	1	TGCAGAGGGGTCCATACGGCGTTGTTCTGGATTCCCGTCGTAACCTAAAGGGAACTTTC	60
Query	61	ACAATGTCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTT	120
Sbjct	61	ACAATGTCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTT	120
Query	121	GCAGCAGGAACCCACTTAGGTGGCACCAATCTTGACTTCCAGATGGAACAGTACATCTAT	180
Sbjct	121	GCAGCAGGAACCCACTTAGGTGGCACCAATCTTGACTTCCAGATGGAACAGTACATCTAT	180
Query	181	AAAAGGAAAAGTGATGGCATCTATATCATAAATCTCAAGAGGACCTGGGAGAAGCTTCTG	240
Sbjct	181	AAAAGGAAAAGTGATGGCATCTATATCATAAATCTCAAGAGGACCTGGGAGAAGCTTCTG	240
Query	241	CTGGCAGCTCGTGCAATTGTTGCCATTGAAAACCCTGCTGATGTCAGTGTTATATCCTCC	300
Sbjct	241	CTGGCAGCTCGTGCAATTGTTGCCATTGAAAACCCTGCTGATGTCAGTGTTATATCCTCC	300
Query	301	AGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATT	360
Sbjct	301	AGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATT	360
Query	361	GCTGGCCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCCA	420
Sbjct	361	GCTGGCCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCCA	420
Query	421	CGGCTTCTTGTTGTTACTGACCCAGGGCTGACCACCAGCCTCTCACGGAGGCATCTTAT	480
Sbjct	421	CGGCTTCTTGTTGTTACTGACCCAGGGCTGACCACCAGCCTCTCACGGAGGCATCTTAT	480

Query	481	GTTAACCTACCTACCATTGCGCTGTGTAACACAGATTCTCCTCTGCGCTATGTGGACATT	540
Sbjct	481	GTTAACCTACCTACCATTGCGCTGTGTAACACAGATTCTCCTCTGCGCTATGTGGACATT	540
Query	541	GCCATCCCATGCAACAACAAGGGAGCTCACTCAGTGGGTTTAATGTGGTGGATGCTGGCT	600
Sbjct	541	GCCATCCCATGCAACAACAAGGGAGCTCACTCAGTGGGTTTAATGTGGTGGATGCTGGCT	600
Query	601	CGGGAAGTTCTGCGCATGCGTGGCACCATTTCCCGTGAACACCCATGGGAGGTCATGCCT	660
Sbjct	601	CGGGAAGTTCTGCGCATGCGTGGCACCATTTCCCGTGAACACCCATGGGAGGTCATGCCT	660
Query	661	GATCTGTACTTCTACAGAGATCCTGAAGAGAT	692
Sbjct	661	GATCTGTACTTCTACAGAGATCCTGAAGAGAT	692

Sequence 1204 matched with Sequence 419

Query= Sequence ID 1204
Length=365

SEQ ID NO: 419

ALIGNMENTS

Identities = 213/213 (100%), Gaps = 0/213 (0%)

Query	1	tttttttttttttCCTGCGGGAAAGCGCGCCATTGTGTTGGTACCCGGGAAATTCGCGGC	60
Sbjct	1	TTTTTTTTTTTTCCTGCGGGAAAGCGCGCCATTGTGTTGGTACCCGGGAAATTCGCGGC	60
Query	61	CGCGTCGACACAGGCCCCAGCATCAAGATCTGGGATTTAGAGAGGAAAGATCATTGTAGA	120
Sbjct	61	CGCGTCGACACAGGCCCCAGCATCAAGATCTGGGATTTAGAGAGGAAAGATCATTGTAGA	120
Query	121	TGAACTGAAGCAAGAAGTTATCAGTACCAGCAGCAAGGCAGAACCACCCCAGTGCACCTC	180
Sbjct	121	TGAACTGAAGCAAGAAGTTATCAGTACCAGCAGCAAGGCAGAACCACCCCAGTGCACCTC	180
Query	181	CCTGGCCTGGTCTGCTGATGACACAGGTGGGC	213
Sbjct	181	CCTGGCCTGGTCTGCTGATGACACAGGTGGGC	213

Sequence 1205 matched with Sequence 420

Query= Sequence ID 1205
Length=299

SEQ ID NO: 420

ALIGNMENTS

Identities = 241/241 (100%), Gaps = 0/241 (0%)

Query	1	CAGACTCTGACCCAGCCTCAGTCCTAACTCCTGGGGCTGGGCTGAGGGGAACAAGCATTT	60
Sbjct	1	CAGACTCTGACCCAGCCTCAGTCCTAACTCCTGGGGCTGGGCTGAGGGGAACAAGCATTT	60
Query	61	GCTGAAACTTGaaaaaacaagcaaatcaaaaacaggaaaaaattgtacctggtactttt	120
Sbjct	61	GCTGAAACTTGAAAAAACAAGCAAATCAAAAACAGGAAAAAATTGTACCTGGTACTTTT	120
Query	121	ttttagaaaaaaagattaaaaaagaaagaataaattcttgtttggaaacttgaaaaaaa	180
Sbjct	121	TTTTAGAAAAAAAGATTAAAAAAGAAAGAATAAATTCTTGTTTGAAACTTGAAAAAAA	180
Query	181	aaatttttaactc	240
Sbjct	181	AATTTTAACTC	240
Query	241	t 241	
Sbjct	241	T 241	

Sequence 1207 matched with Sequence 421

Query= Sequence ID - 1207
Length=642

nt: 642

SEQ ID NO: 421

nt: 642

ALIGNMENTS

Identities = 642/642 (100%), Gaps = 0/642 (0%)

Query	1	ACGAGAAGCCAGATACTAAAGAGAAGAANCCCGAAGCCAAGAAGGTTGATGCTGGTGGCA	60
Sbjct	1	ACGAGAAGCCAGATACTAAAGAGAAGAANCCCGAAGCCAAGAAGGTTGATGCTGGTGGCA	60
Query	61	AGGTGAAAAAGGGTAACCTCAAAGCTAAAAAGCCCAAGAAGGGGAAGCCCCATTGCAGCC	120
Sbjct	61	AGGTGAAAAAGGGTAACCTCAAAGCTAAAAAGCCCAAGAAGGGGAAGCCCCATTGCAGCC	120
Query	121	GCAACCCTGTCCTTGTCTAGAGGAATTGGCAGGTATTCCCGATCTGCCATGTATTCCANAA	180
Sbjct	121	GCAACCCTGTCCTTGTCTAGAGGAATTGGCAGGTATTCCCGATCTGCCATGTATTCCANAA	180
Query	181	AGGCCATGTACAAGAGGAAGTACTCAGCCGCTAAATCCAAGGTTGAAAAAGAAAAAGAAGG	240
Sbjct	181	AGGCCATGTACAAGAGGAAGTACTCAGCCGCTAAATCCAAGGTTGAAAAAGAAAAAGAAGG	240
Query	241	AGAAGGTTCTCGCAACTGTTACAAAACCAAGTTGGTGGTGACAAGAACGGCGGTACCCGGG	300
Sbjct	241	AGAAGGTTCTCGCAACTGTTACAAAACCAAGTTGGTGGTGACAAGAACGGCGGTACCCGGG	300
Query	301	TGGTTAAACTTCGCAAAATGCCTAGATATTATCCTACTGAAGATGTGCCTCGAAAGCTGT	360
Sbjct	301	TGGTTAAACTTCGCAAAATGCCTAGATATTATCCTACTGAAGATGTGCCTCGAAAGCTGT	360
Query	361	TGAGCCACGGCAAAAAACCCTTCAGTCAGCACGTGAGAAAAGTGCAGCCAGCATTACCC	420
Sbjct	361	TGAGCCACGGCAAAAAACCCTTCAGTCAGCACGTGAGAAAAGTGCAGCCAGCATTACCC	420
Query	421	CCGGGACCATTTCTGATCATCCTCACTGGACGCCACAGGGGCAAGAGGGTGGTTTTCTGA	480
Sbjct	421	CCGGGACCATTTCTGATCATCCTCACTGGACGCCACAGGGGCAAGAGGGTGGTTTTCTGA	480

Sequence 1208 matched with Sequence 422

Query= Sequence ID 1208
Length=503

SEQ ID NO: 422

ALIGNMENTS

Identities = 503/503 (100%), Gaps = 0/503 (0%)

Query	1	CCCTATACCTTCTGCATAATGAATTANCTAGAAATAACTTTGCAAGGGAGAGCCAAAGCT	60
Sbjct	1	CCCTATACCTTCTGCATAATGAATTANCTAGAAATAACTTTGCAAGGGAGAGCCAAAGCT	60
Query	61	AAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCCGTCTATGT	120
Sbjct	61	AAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCCGTCTATGT	120
Query	121	AGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGTGATAGC	180
Sbjct	121	AGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGTGATAGC	180
Query	181	TGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAACCCCTCTAAATC	240
Sbjct	181	TGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAACCCCTCTAAATC	240
Query	241	CCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAAC	300
Sbjct	241	CCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAAC	300
Query	301	CTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTAA	360
Sbjct	301	CTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTAA	360
Query	361	GAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATAACTGAACTCCT	420
Sbjct	361	GAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATAACTGAACTCCT	420
Query	421	CACACCCAATTGGACCAATCTATCACCCCTATAGAAGAACTAATGTTAGTATAAGTAACAT	480
Sbjct	421	CACACCCAATTGGACCAATCTATCACCCCTATAGAAGAACTAATGTTAGTATAAGTAACAT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GAAAACATTCTCCTCCGCATAAG	503
Sbjct	481	GAAAACATTCTCCTCCGCATAAG	503

Sequence 1209 matched with Sequence 423

Query= Sequence ID - 1209 nt: 620
Length=620

SEQ ID NO: 423 nt: 620

ALIGNMENTS

Identities = 620/620 (100%), Gaps = 0/620 (0%)

Query	1	CTCTCCTGTCAACAGCGGCCAGCCTCCCAACTACGAGAATGCTCAAGGAGGAGCAGGAAG	60
Sbjct	1	CTCTCCTGTCAACAGCGGCCAGCCTCCCAACTACGAGAATGCTCAAGGAGGAGCAGGAAG	60
Query	61	TGGCTATGCTGGGGGCGCCCCACAACCCTGCTCCCCCGACGTCCACCGTGATCCACATCC	120
Sbjct	61	TGGCTATGCTGGGGGCGCCCCACAACCCTGCTCCCCCGACGTCCACCGTGATCCACATCC	120
Query	121	GCAGCGAGACCTCCGTGCCCCGACCATGTCGTCTGGTCCCTGTTCAACACCCTCTTCATGA	180
Sbjct	121	GCAGCGAGACCTCCGTGCCCCGACCATGTCGTCTGGTCCCTGTTCAACACCCTCTTCATGA	180
Query	181	ACACCTGCTGCCTGGGCTTCATAGCATTGCGCTACTCCGTGAAGTCTAGGGACAGGAAGA	240
Sbjct	181	ACACCTGCTGCCTGGGCTTCATAGCATTGCGCTACTCCGTGAAGTCTAGGGACAGGAAGA	240
Query	241	TGGTTGGCGACGTGACCGGGGCCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCT	300
Sbjct	241	TGGTTGGCGACGTGACCGGGGCCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCT	300
Query	301	GGGCCCTGATTTTGGGCATCTTCATGACCATTCTGCTCGTCATCATCCCAGTGTTGGTCG	360
Sbjct	301	GGGCCCTGATTTTGGGCATCTTCATGACCATTCTGCTCGTCATCATCCCAGTGTTGGTCG	360
Query	361	TCCAGGCCCAGCGATAGATCAGGAGGCATCATTGAGGCCAGGAGCTCTGCCCCTGACCTG	420
Sbjct	361	TCCAGGCCCAGCGATAGATCAGGAGGCATCATTGAGGCCAGGAGCTCTGCCCCTGACCTG	420
Query	421	TATCCCACGTACTCTATCTTCCATTCCCTCGCCCTGCCCCCAGAGGCCAGGAGCTCTGCCC	480
Sbjct	421	TATCCCACGTACTCTATCTTCCATTCCCTCGCCCTGCCCCCAGAGGCCAGGAGCTCTGCCC	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTGACCTGTATTCCACTTACTCCACCTTCCATTCCCTCGCCCTGTCCCCACAGCCGAGTCC	540
Sbjct	481	TTGACCTGTATTCCACTTACTCCACCTTCCATTCCCTCGCCCTGTCCCCACAGCCGAGTCC	540
Query	541	TGCATCAGCCCTTTATCCTCACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGT	600
Sbjct	541	TGCATCAGCCCTTTATCCTCACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGT	600
Query	601	TTCTGGTGCTGCTGTGACTT	620
Sbjct	601	TTCTGGTGCTGCTGTGACTT	620

Sequence 1210 matched with Sequence 424

Query= Sequence ID 1210
Length=702

SEQ ID NO: 424

ALIGNMENTS

Identities = 68/68 (100%), Gaps = 0/68 (0%)

Query	497	TAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTTAGGTGTTTTCACTTGC	556
Sbjct	565	TAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTTAGGTGTTTTCACTTGC	624
Query	557	ATTTCCTT	564
Sbjct	625	ATTTCCTT	632

Sequence 1211 matched with Sequence 425

Query= Sequence ID 1211

Length=632

SEQ ID NO: 425

ALIGNMENTS

Identities = 632/632 (100%), Gaps = 0/632 (0%)

Query	1	CCATTGTGTTGGNACCCGGAATTCGCGGCCGCGTCGACGGAGTTTACCTTATTACACT	60
Sbjct	1	CCATTGTGTTGGNACCCGGAATTCGCGGCCGCGTCGACGGAGTTTACCTTATTACACT	60
Query	61	TTAATCTCTGGATTTACCCCATCTCATTCTCTTTTAGGAAAAGTGTGTATGTGGTGG	120
Sbjct	61	TTAATCTCTGGATTTACCCCATCTCATTCTCTTTTAGGAAAAGTGTGTATGTGGTGG	120
Query	121	CTTTGATGGTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAAGTAGAAATGAATG	180
Sbjct	121	CTTTGATGGTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAAGTAGAAATGAATG	180
Query	181	GAAGATGATGGGAAATATGACTTCACCAAGGAGCAATGCTGGGATTGCAACTGTAGGGAA	240
Sbjct	181	GAAGATGATGGGAAATATGACTTCACCAAGGAGCAATGCTGGGATTGCAACTGTAGGGAA	240
Query	241	CACCATTTATGCAGTGGGAGGATTCGATGGCAATGAATTTCTGAATACGGTGGAAGTCTA	300
Sbjct	241	CACCATTTATGCAGTGGGAGGATTCGATGGCAATGAATTTCTGAATACGGTGGAAGTCTA	300
Query	301	TAACCTTGAGTCAAATGAATGGAGCCCCTATACAAAGATTTTCCAGTTTAAACAAATTTA	360
Sbjct	301	TAACCTTGAGTCAAATGAATGGAGCCCCTATACAAAGATTTTCCAGTTTAAACAAATTTA	360
Query	361	AGACCCTCTCAAACAAAGGCTTAGTGATGTAATTATGGTTAGCAGAGGTACACTTGTG	420
Sbjct	361	AGACCCTCTCAAACAAAGGCTTAGTGATGTAATTATGGTTAGCAGAGGTACACTTGTG	420
Query	421	AATAAAGAGGGTGGGTGGGTATAGATGTTGCTAACAGCAACACAAAGCTTTTGCATATTG	480
Sbjct	421	AATAAAGAGGGTGGGTGGGTATAGATGTTGCTAACAGCAACACAAAGCTTTTGCATATTG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CATACTATTAAACATGCTGTACATACTTTTTGGGTTTATTTGGAAAGGAATGCAAAGATG	540
Sbjct	481	CATACTATTAAACATGCTGTACATACTTTTTGGGTTTATTTGGAAAGGAATGCAAAGATG	540
Query	541	AAGGTCTGTTTTGTGTACTTTTAAGACTTTGGTTATTTTACTTTTTGGAAAAGAATAAAC	600
Sbjct	541	AAGGTCTGTTTTGTGTACTTTTAAGACTTTGGTTATTTTACTTTTTGGAAAAGAATAAAC	600
Query	601	CAAGAATTGATTGGGCACATCATTTCAAGAAG	632
Sbjct	601	CAAGAATTGATTGGGCACATCATTTCAAGAAG	632

Sequence 1212 matched with Sequence 426

Query= Sequence ID - 1212 nt: 374
Length=374

SEQ ID NO: 426 nt: 374

ALIGNMENTS

Identities = 374/374 (100%), Gaps = 0/374 (0%)

Query	1	AGAGCAGCAGCCATGGCCCTACGCTACCCTATGGCCGTGGGCCTCAACAAGGGCCACAAA	60
Sbjct	1	AGAGCAGCAGCCATGGCCCTACGCTACCCTATGGCCGTGGGCCTCAACAAGGGCCACAAA	60
Query	61	GTGACCAAGAACGTGAGCAAGCCCAGGCACAGCCGACGCCGCGGGCGTCTGACCAAACAC	120
Sbjct	61	GTGACCAAGAACGTGAGCAAGCCCAGGCACAGCCGACGCCGCGGGCGTCTGACCAAACAC	120
Query	121	ACCAAGTTCGTGCGGGACATGATTCGGGAGGTGTGTGGCTTTGCCCCGTACGAGCGGCGC	180
Sbjct	121	ACCAAGTTCGTGCGGGACATGATTCGGGAGGTGTGTGGCTTTGCCCCGTACGAGCGGCGC	180
Query	181	GCCATGGAGTTACTGAAGGTCTCCAAGGACAAACGGGCCCTCAAATTTATCAAGAAAAGG	240
Sbjct	181	GCCATGGAGTTACTGAAGGTCTCCAAGGACAAACGGGCCCTCAAATTTATCAAGAAAAGG	240
Query	241	GTGGGGACGCACATCCGCGCCAAGAGGAAGCGGGAGGAGCTGAGCAACGTACTGGCCGCC	300
Sbjct	241	GTGGGGACGCACATCCGCGCCAAGAGGAAGCGGGAGGAGCTGAGCAACGTACTGGCCGCC	300
Query	301	ATGAGGAAAAGCTGCTGCCAAGAAAGACTGAGCCCCTCCCCTGCCCTCTCCCTGAAATAAA	360
Sbjct	301	ATGAGGAAAAGCTGCTGCCAAGAAAGACTGAGCCCCTCCCCTGCCCTCTCCCTGAAATAAA	360
Query	361	GAACAGCTTGACAG	374
Sbjct	361	GAACAGCTTGACAG	374

Sequence 1213 matched with Sequence 427

Query= Sequence ID - 1213
Length=567

nt: 567

SEQ ID NO: 427

nt: 567

ALIGNMENTS

Identities = 567/567 (100%), Gaps = 0/567 (0%)

Query	1	GAATTATTGACTTTGAATTGCATTTCACTACCATGAAGTCAAAGTCAGTGGTGTATTTGC	60
Sbjct	1	GAATTATTGACTTTGAATTGCATTTCACTACCATGAAGTCAAAGTCAGTGGTGTATTTGC	60
Query	61	TCATTTGTTCACTCTTTCTTTTCCACCAACATTACTGCCTGCAGAGCCAGAGGTGAGTGC	120
Sbjct	61	TCATTTGTTCACTCTTTCTTTTCCACCAACATTACTGCCTGCAGAGCCAGAGGTGAGTGC	120
Query	121	AGAAATCCTGTCAATTCGTCACTTGTGGACAACCTGCAGCTTGCCACAGCCTACAGTTCC	180
Sbjct	121	AGAAATCCTGTCAATTCGTCACTTGTGGACAACCTGCAGCTTGCCACAGCCTACAGTTCC	180
Query	181	ACCACTGTGACCTCTGAAAACCTCCTGAACAAAAGGAAGGAGACTTGGAATCCTGAATG	240
Sbjct	181	ACCACTGTGACCTCTGAAAACCTCCTGAACAAAAGGAAGGAGACTTGGAATCCTGAATG	240
Query	241	GGCTTGGAGACATTAAGGGAGAACTGCCTCCCTGGACCAAGGCAGAATTCAATAGAACCA	300
Sbjct	241	GGCTTGGAGACATTAAGGGAGAACTGCCTCCCTGGACCAAGGCAGAATTCAATAGAACCA	300
Query	301	GCAAGAAATTTTCCTATGAATGGGAAAGCAGGTGGCAGGGGGCAGGGGTGAAAAGCTTT	360
Sbjct	301	GCAAGAAATTTTCCTATGAATGGGAAAGCAGGTGGCAGGGGGCAGGGGTGAAAAGCTTT	360
Query	361	GTACAGGAATTGTGGAAAAGCTTTTGCATTATCTCTAGTCTGAAAGTCACATTTCTCAGT	420
Sbjct	361	GTACAGGAATTGTGGAAAAGCTTTTGCATTATCTCTAGTCTGAAAGTCACATTTCTCAGT	420
Query	421	TCCTTTCCACTCTCTTCTGTCAACTTGCTGTGAGTAAATGACATCTGTCACCTGTGACAC	480
Sbjct	421	TCCTTTCCACTCTCTTCTGTCAACTTGCTGTGAGTAAATGACATCTGTCACCTGTGACAC	480

PATENT SEQUENCE ALIGNMENT

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Query 481 GGGCCAGGGACTATCACCATATGGCCCCCACACATTATCTAGTACCAGCCTGCCTGGGCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 GGGCCAGGGACTATCACCATATGGCCCCCACACATTATCTAGTACCAGCCTGCCTGGGCC 540

Query 541 ATGCCTTTTCCAGTCACTGTACCAGCC 567
          ||||||||||||||||||||
Sbjct 541 ATGCCTTTTCCAGTCACTGTACCAGCC 567
```

Sequence 1214 matched with Sequence 428

Query= Sequence ID - 1214
Length=620

nt: 620

SEQ ID NO: 428

nt: 620

ALIGNMENTS

Identities = 620/620 (100%), Gaps = 0/620 (0%)

Query	1	CTCTCCTGTCAACAGCGGCCAGCCTCCCAACTACGAGAATGCTCAAGGAGGAGCAGGAAG	60
Sbjct	1	CTCTCCTGTCAACAGCGGCCAGCCTCCCAACTACGAGAATGCTCAAGGAGGAGCAGGAAG	60
Query	61	TGGCTATGCTGGGGGCGCCCCACAACCCTGCTCCCCCGACGTCCACCGTGATCCACATCC	120
Sbjct	61	TGGCTATGCTGGGGGCGCCCCACAACCCTGCTCCCCCGACGTCCACCGTGATCCACATCC	120
Query	121	GCAGCGAGACCTCCGTGCCCCGACCATGTCGTCTGGTCCCTGTTCAACACCCTCTTCATGA	180
Sbjct	121	GCAGCGAGACCTCCGTGCCCCGACCATGTCGTCTGGTCCCTGTTCAACACCCTCTTCATGA	180
Query	181	ACACCTGCTGCCTGGGCTTCATAGCATTGCGCTACTCCGTGAAGTCTAGGGACAGGAAGA	240
Sbjct	181	ACACCTGCTGCCTGGGCTTCATAGCATTGCGCTACTCCGTGAAGTCTAGGGACAGGAAGA	240
Query	241	TGGTTGGCGACGTGACCGGGGCCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCT	300
Sbjct	241	TGGTTGGCGACGTGACCGGGGCCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCT	300
Query	301	GGGCCCTGATTTTGGGCATCTTCATGACCATTCTGCTCGTCATCATCCCAGTGTTGGTCTG	360
Sbjct	301	GGGCCCTGATTTTGGGCATCTTCATGACCATTCTGCTCGTCATCATCCCAGTGTTGGTCTG	360
Query	361	TCCAGGCCCAGCGATAGATCAGGAGGCATCATTGAGGCCAGGAGCTCTGCCCCTGACCTG	420
Sbjct	361	TCCAGGCCCAGCGATAGATCAGGAGGCATCATTGAGGCCAGGAGCTCTGCCCCTGACCTG	420
Query	421	TATCCCACGTACTCTATCTTCCATTCCCTCGCCCTGCCCCAGAGGCCAGGAGCTCTGCCC	480
Sbjct	421	TATCCCACGTACTCTATCTTCCATTCCCTCGCCCTGCCCCAGAGGCCAGGAGCTCTGCCC	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTGACCTGTATTCCACTTACTCCACCTTCCATTCCCTCGCCCTGTCCCCACAGCCGAGTCC	540
Sbjct	481	TTGACCTGTATTCCACTTACTCCACCTTCCATTCCCTCGCCCTGTCCCCACAGCCGAGTCC	540
Query	541	TGCATCAGCCCTTTATCCTCACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGT	600
Sbjct	541	TGCATCAGCCCTTTATCCTCACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGT	600
Query	601	TTCTGGTGCTGCTGTGACTT	620
Sbjct	601	TTCTGGTGCTGCTGTGACTT	620

Sequence 1215 matched with Sequence 429

Query= Sequence ID 1215
Length=669

SEQ ID NO: 429

ALIGNMENTS

Identities = 669/669 (100%), Gaps = 0/669 (0%)

Query	1	CACAAGATAGAATGGTaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaTTTTAAGTGA	60
Sbjct	1	CACAAGATAGAATGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTTAAGTGA	60
Query	61	CAGTGCCATAGTTTGGACAGTACCTTTCAATGATTAATTTTAATAGCCTGTGAGTCCAAG	120
Sbjct	61	CAGTGCCATAGTTTGGACAGTACCTTTCAATGATTAATTTTAATAGCCTGTGAGTCCAAG	120
Query	121	TAAATGATCACTTTATTTGCTAGGGAGGGAAGTCCTAGGGTGGTTTCAGTTTCTCCCAGA	180
Sbjct	121	TAAATGATCACTTTATTTGCTAGGGAGGGAAGTCCTAGGGTGGTTTCAGTTTCTCCCAGA	180
Query	181	CATACCTAAATTTTTACATCAATCCTTTTAAAGAAAATCTGTATTTCAAAGAATCTTTCT	240
Sbjct	181	CATACCTAAATTTTTACATCAATCCTTTTAAAGAAAATCTGTATTTCAAAGAATCTTTCT	240
Query	241	CTGCAGTAAATCTCGCAGGGGAATTTGCACTATTACACTTGAAAGTTGTTATTGTAAACC	300
Sbjct	241	CTGCAGTAAATCTCGCAGGGGAATTTGCACTATTACACTTGAAAGTTGTTATTGTAAACC	300
Query	301	TTTTCGGCAGCTTTTAATAGGAAAGTTAAACGTTTTAAACATGGTAGTACTGGAAATTTT	360
Sbjct	301	TTTTCGGCAGCTTTTAATAGGAAAGTTAAACGTTTTAAACATGGTAGTACTGGAAATTTT	360
Query	361	ACAAGACTTTTACCTAGCACTTAAATATGTATAAATGTACATAAAGACAACTAGTAAGC	420
Sbjct	361	ACAAGACTTTTACCTAGCACTTAAATATGTATAAATGTACATAAAGACAACTAGTAAGC	420
Query	421	ATGACCTGGGGAAATGGTCAGACCTTGTATTGTGTTTTTGGCCTTGAAAGTAGCAAGTGA	480
Sbjct	421	ATGACCTGGGGAAATGGTCAGACCTTGTATTGTGTTTTTGGCCTTGAAAGTAGCAAGTGA	480

PATENT SEQUENCE ALIGNMENT

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Query 481 CCAGAATCTGCCATGGCAACAGGCTTTAAAAAAGACCCTTAAAAAGACACTGTCTCAACT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 CCAGAATCTGCCATGGCAACAGGCTTTAAAAAAGACCCTTAAAAAGACACTGTCTCAACT 540

Query 541 GTGGTGTTAGCACCAGCCAGCTCTCTGTACATTTGCTAGCTTGTAGTTTCTAAGACTGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 GTGGTGTTAGCACCAGCCAGCTCTCTGTACATTTGCTAGCTTGTAGTTTCTAAGACTGA 600

Query 601 GTAAACTTCTTATTTTTTAGAAAGTGGAGGTCTGGTTTGTAACCTTCCTTGTACTIONAATTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 GTAAACTTCTTATTTTTTAGAAAGTGGAGGTCTGGTTTGTAACCTTCCTTGTACTIONAATTG 660

Query 661 GGTAAGAGT 669
          ||||||||
Sbjct 661 GGTAAGAGT 669
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Sequence 1216 matched with Sequence 430

Query= Sequence ID - 1216 nt: 484
Length=484

SEQ ID NO: 430 nt: 484

ALIGNMENTS

Identities = 484/484 (100%), Gaps = 0/484 (0%)

Query	1	CAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGCGATAGAAATTGAAACCTGGCG	60
Sbjct	1	CAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGCGATAGAAATTGAAACCTGGCG	60
Query	61	CAATAGATATAGTACCGCAAGGGAAAGATGAAAAATTATAACCAAGCATAATATAGCAAG	120
Sbjct	61	CAATAGATATAGTACCGCAAGGGAAAGATGAAAAATTATAACCAAGCATAATATAGCAAG	120
Query	121	GACTAACCCCTATACCTTCTGCATAATGAATTAAGTAACTAGAAATAACTTTGCAAGGAGAGCC	180
Sbjct	121	GACTAACCCCTATACCTTCTGCATAATGAATTAAGTAACTAGAAATAACTTTGCAAGGAGAGCC	180
Query	181	AAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCCGT	240
Sbjct	181	AAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCCGT	240
Query	241	CTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGT	300
Sbjct	241	CTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGT	300
Query	301	GATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAACCCCTC	360
Sbjct	301	GATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAACCCCTC	360
Query	361	TAAATCCCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGA	420
Sbjct	361	TAAATCCCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGA	420
Query	421	AAAAACCTTGTTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACC	480
Sbjct	421	AAAAACCTTGTTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACC	480

PATENT SEQUENCE ALIGNMENT

Query	481	AATT	484
Sbjct	481	AATT	484

Sequence 1217 matched with Sequence 431

Query= Sequence ID 1217
Length=576

SEQ ID NO: 431

ALIGNMENTS

Identities = 576/576 (100%), Gaps = 0/576 (0%)

Query	1	GACAGGCGGGGGCCAGCGGCCGGGTGAAGGCCGGGTGGCTCTGTGAATCAAAGGAGAGT	60
Sbjct	1	GACAGGCGGGGGCCAGCGGCCGGGTGAAGGCCGGGTGGCTCTGTGAATCAAAGGAGAGT	60
Query	61	CCCAGAAAACCTGTGACTGTTGAAGAAAATTCATCTGTGAATTTTATATTCAAGGAGTC	120
Sbjct	61	CCCAGAAAACCTGTGACTGTTGAAGAAAATTCATCTGTGAATTTTATATTCAAGGAGTC	120
Query	121	AGTATTTATATTCATCTTTTAAACTGGGAAGATTTATATTTTACTTTAAACTTCTTGAT	180
Sbjct	121	AGTATTTATATTCATCTTTTAAACTGGGAAGATTTATATTTTACTTTAAACTTCTTGAT	180
Query	181	AATAATTTACAATGAATGGACACAGTGATGAAGAAAGTGTTAGAAACAGTAGTGGAGAAT	240
Sbjct	181	AATAATTTACAATGAATGGACACAGTGATGAAGAAAGTGTTAGAAACAGTAGTGGAGAAT	240
Query	241	CAAGGTAAGTAAGCACTTTGTTATCAATTGTTTACTATGAAGAGAGTTGAAAACCTTGACT	300
Sbjct	241	CAAGGTAAGTAAGCACTTTGTTATCAATTGTTTACTATGAAGAGAGTTGAAAACCTTGACT	300
Query	301	TTTTTCTTTATTGTTATTGTTGTTATTTAGTTTTCTCATAGGTAGCAGAGTTTTCAGGT	360
Sbjct	301	TTTTTCTTTATTGTTATTGTTGTTATTTAGTTTTCTCATAGGTAGCAGAGTTTTCAGGT	360
Query	361	TTTCCTCTTAGCTATCCAAATACTaaaaaaTTCTGATATACGAACCTTTTTTCATAATA	420
Sbjct	361	TTTCCTCTTAGCTATCCAAATACTAAAAAATTCTGATATACGAACCTTTTTTCATAATA	420
Query	421	CAGGTTTTAATTATATTTTTTCATTCAGATACACAGTAGATCTTAAATATAGAAAGTTTTT	480
Sbjct	421	CAGGTTTTAATTATATTTTTTCATTCAGATACACAGTAGATCTTAAATATAGAAAGTTTTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GTTTACTTAAATCTATTTGGAAGTTTATATTTGAGCTAATAATTAAGCTGGAGCATGTAT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTTTACTTAAATCTATTTGGAAGTTTATATTTGAGCTAATAATTAAGCTGGAGCATGTAT  540

Query  541  AATAGATTTAAATTGTTTTGACTGTTAGTGAAATTT  576
          |||||||||||||||||||||||||||||||
Sbjct  541  AATAGATTTAAATTGTTTTGACTGTTAGTGAAATTT  576
```

Sequence 1218 matched with Sequence 432

Query= Sequence ID 1218

Length=669

SEQ ID NO: 432

ALIGNMENTS

Identities = 669/669 (100%), Gaps = 0/669 (0%)

Query	1	CTCACTTGGTGGGTGAGCCTCCAATGACTACACCCAAGGAGGATTTAACACAGGGATTTT	60
Sbjct	1	CTCACTTGGTGGGTGAGCCTCCAATGACTACACCCAAGGAGGATTTAACACAGGGATTTT	60
Query	61	ATGACTTGCAACAAGTCAGGAGGACATGGGGTTGGGGTAGTTTCAGCAGTGCCTGTCTGAA	120
Sbjct	61	ATGACTTGCAACAAGTCAGGAGGACATGGGGTTGGGGTAGTTTCAGCAGTGCCTGTCTGAA	120
Query	121	CAAAGGTGAAAATTGGGCTTTTATTGGGCTGATCAAGGGGGAGTAAAGGCAGCCAGGAGC	180
Sbjct	121	CAAAGGTGAAAATTGGGCTTTTATTGGGCTGATCAAGGGGGAGTAAAGGCAGCCAGGAGC	180
Query	181	AGTCGCCTGTCATGCTTCTACCTATATTGCATGTATAGAAAAGGGAAAAATAAACTCCTTC	240
Sbjct	181	AGTCGCCTGTCATGCTTCTACCTATATTGCATGTATAGAAAAGGGAAAAATAAACTCCTTC	240
Query	241	CTGGGCAGGGTTTTAGTATGCTAAGGAGGGGAGTTATTCAACTTCAATCCAACTCAAGCA	300
Sbjct	241	CTGGGCAGGGTTTTAGTATGCTAAGGAGGGGAGTTATTCAACTTCAATCCAACTCAAGCA	300
Query	301	TCAGCATTGCTGCGTCCATCCCAGTTTTGTTTTGCTGGGGCTGAACTTCTTCCTATAACT	360
Sbjct	301	TCAGCATTGCTGCGTCCATCCCAGTTTTGTTTTGCTGGGGCTGAACTTCTTCCTATAACT	360
Query	361	TTTTGAAACAACAAGAACTCAAGGTGTGACAGTTACAAGTGGGCCCTTTTTCACAGTGTG	420
Sbjct	361	TTTTGAAACAACAAGAACTCAAGGTGTGACAGTTACAAGTGGGCCCTTTTTCACAGTGTG	420
Query	421	TACCTAAACACGTGAGGACCCTGGATTACAGAATGACAGACTCGAAGTGACTCAAGTTCC	480
Sbjct	421	TACCTAAACACGTGAGGACCCTGGATTACAGAATGACAGACTCGAAGTGACTCAAGTTCC	480

PATENT SEQUENCE ALIGNMENT

Query	481	GGTTGTTTCATCTTTAGATGGTAAAGATGGCTGTACGTACTATCCTTGCTTATTTCCAATC	540
Sbjct	481	GGTTGTTTCATCTTTAGATGGTAAAGATGGCTGTACGTACTATCCTTGCTTATTTCCAATC	540
Query	541	TATTGTTTAAACTCTTGTATATGTAATACCGCAGAGGCTAGAGATACAACCTTTGACCAA	600
Sbjct	541	TATTGTTTAAACTCTTGTATATGTAATACCGCAGAGGCTAGAGATACAACCTTTGACCAA	600
Query	601	ATGAGTGAATTCAAGTAATCCATTACTAATGTGATCTGGAAACAAACATGGTGTGGAATG	660
Sbjct	601	ATGAGTGAATTCAAGTAATCCATTACTAATGTGATCTGGAAACAAACATGGTGTGGAATG	660
Query	661	TGCATATGT	669
Sbjct	661	TGCATATGT	669

Sequence 1219 matched with Sequence 433

Query= Sequence ID - 1219 nt: 559
Length=559

SEQ ID NO: 433 nt: 559

ALIGNMENTS

Identities = 559/559 (100%), Gaps = 0/559 (0%)

Query	1	CTTGGCAGCTCCGTTATGTGCCCAGCTCTTTGCAAGGGCATACTGGGAAATGAGTGGAGA	60
Sbjct	1	CTTGGCAGCTCCGTTATGTGCCCAGCTCTTTGCAAGGGCATACTGGGAAATGAGTGGAGA	60
Query	61	TAAAGGACCCAATCATAAGCATTTTACAGTATGGATACCCCATTTTAAAAAGGTAAACTG	120
Sbjct	61	TAAAGGACCCAATCATAAGCATTTTACAGTATGGATACCCCATTTTAAAAAGGTAAACTG	120
Query	121	AGGCACAATGCAAttttttttttttttAAGGAGTTTATTTGAGCAAACAGTGATTCATG	180
Sbjct	121	AGGCACAATGCAATTTTTTTTTTTTTTTAAGGAGTTTATTTGAGCAAACAGTGATTCATG	180
Query	181	AATCAGGCAGCACCAAACCAGAAGGAGGCTTTGCTGAANAAGGATGAGGGACAAGCATTT	240
Sbjct	181	AATCAGGCAGCACCAAACCAGAAGGAGGCTTTGCTGAANAAGGATGAGGGACAAGCATTT	240
Query	241	ATAAAGTGAATGTAGATGTAATACAAAGAAAATATTTGAACCGGGTGCGGTGGCTTACAC	300
Sbjct	241	ATAAAGTGAATGTAGATGTAATACAAAGAAAATATTTGAACCGGGTGCGGTGGCTTACAC	300
Query	301	TTGTAATCCCAACACTTTGGGAGGCCAAGGCGGGCAGATCACAAGATCAAGAGATCGAGA	360
Sbjct	301	TTGTAATCCCAACACTTTGGGAGGCCAAGGCGGGCAGATCACAAGATCAAGAGATCGAGA	360
Query	361	CCATCCTGGTCAACATGGTGAAACCCCATCTNTACTAAAAAATACAAAAATTANCTGGGC	420
Sbjct	361	CCATCCTGGTCAACATGGTGAAACCCCATCTNTACTAAAAAATACAAAAATTANCTGGGC	420
Query	421	GTGGTGGTGCGTGCCTGTAGTCCCAGCTACTTGGGCGGCTGAGGCAGGANAATTGCTTGA	480
Sbjct	421	GTGGTGGTGCGTGCCTGTAGTCCCAGCTACTTGGGCGGCTGAGGCAGGANAATTGCTTGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ACCCGGGAGGTGGAGGTTGCAGTAAGCCGAGATTGCACCATTGCACTACTCCAGCCTGGT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ACCCGGGAGGTGGAGGTTGCAGTAAGCCGAGATTGCACCATTGCACTACTCCAGCCTGGT  540

Query  541  GACAGAGAGAGACTCCATC  559
          |||||||||||||||
Sbjct  541  GACAGAGAGAGACTCCATC  559
```


Sequence 1220 matched with Sequence 434

Length=1354

Identities = 1343/1343 (100%), Gaps = 0/1343 (0%)

Query	6	GTGCGATANNATGNNTGTCTTTTTTTTAAAGTNTTTCNNATNGNAGNGAANCCCCCNAN	65
Sbjct	6	GTGCGATANNATGNNTGTCTTTTTTTTAAAGTNTTTCNNATNGNAGNGAANCCCCCNAN	65
Query	66	NTNNCATAANGAGAGATNACTACNGTACANATAGNGNCANACNGATAGTAGTANCAANAT	125
Sbjct	66	NTNNCATAANGAGAGATNACTACNGTACANATAGNGNCANACNGATAGTAGTANCAANAT	125
Query	126	TGTNTTAGCTANATNANTCAATAGATATCNAGATanaanaananCNNGGATATACAGCGA	185
Sbjct	126	TGTNTTAGCTANATNANTCAATAGATATCNAGATANAANAANANCNNGGATATACAGCGA	185
Query	186	TGTNTNANNGGnnnnnnnnanGGAACGAACATCNACNTTAANNATAAGCTNGNGGAGAGAG	245
Sbjct	186	TGTNTNANNGGNNNNNNNANGGAACGAACATCNACNTTAANNATAAGCTNGNGGAGAGAG	245
Query	246	ACANGTANGTTATANANNAGAATNGNAGTAGGNGTGATCATAATAGnnnnnnannTANTAT	305
Sbjct	246	ACANGTANGTTATANANNAGAATNGNAGTAGGNGTGATCATAATAGNNNNNANNTANTAT	305
Query	306	ATANGATNTTANTGNNCTNTNNTNNGTTTATCNNNAATNTCTATNCTNGAGAGNAGCNNN	365
Sbjct	306	ATANGATNTTANTGNNCTNTNNTNNGTTTATCNNNAATNTCTATNCTNGAGAGNAGCNNN	365
Query	366	ATNNNNAGGCGANGANATTGGGNNNTNCTCNTNATAGANANCTGGTGTcnnaanaantacn	425
Sbjct	366	ATNNNNAGGCGANGANATTGGGNNNTNCTCNTNATAGANANCTGGTGTcnnanaantacn	425
Query	426	tcacatctattnanctctcacnanatggnannatanagnagnnnntnnanaggantangca	485
Sbjct	426	TCATCTATTNANCTCTCACNANATGGNANNATANAGNAGNGNNNTNNANAGGANTANGCA	485
Query	486	tagngnntnnctnaaacaannnnataaganntctcgnaananGGGCCTNTNNTNTAGC	545
Sbjct	486	TAGNGNNTNNCTNAAACAAAANNNATAAGANNTCTCGNNAANANGGGCCTNTNNTNTAGC	545
Query	546	GAGGNNTTANTTTNTATANTTTNCTCTtnnaatanntangatanatganctngnngt	605

PATENT SEQUENCE ALIGNMENT

Sbjct	546	 GAGGNNTTANTTTNTATANTTTTCNCTCTTNNAAATANNTANGATANATGANCTNGNNGT	605
Query	606	gatanatannnnntacngtnaanntntantcntataatagatanaaatataggatntTNC 	665
Sbjct	606	GATANATANNNNNTACNGTNAANNTNTANTCNTATAATAGATANAAATATAGGATNTTNC	665
Query	666	TCTGGCNGGTNGAANANTTNNNTNCNNTTTNAATAATGNTGTAGNGACNGNGNTNTnana 	725
Sbjct	666	TCTGGCNGGTNGAANANTTNNNTNCNNTTTNAATAATGNTGTAGNGACNGNGNTNTNANA	725
Query	726	nnnnnTTAGAAAGGTACTCTATATACTNNTATGNTNCGGCNNATAATANAACAGATGTTT 	785
Sbjct	726	NNNNNTTAGAAAGGTACTCTATATACTNNTATGNTNCGGCNNATAATANAACAGATGTTT	785
Query	786	GTATNAATATnaaanaaGGTCNNTTTTCGNCAGAGAANNNTGNCTGGTNATAGAATTAGC 	845
Sbjct	786	GTATNAATATNAAANAAGGTTCNNTTTTCGNCAGAGAANNNTGNCTGGTNATAGAATTAGC	845
Query	846	ATAANTTANNTANTATGATNNANTNNTNCTACNANTNTTAGCNNTTNGCAGNAGTCATTN 	905
Sbjct	846	ATAANTTANNTANTATGATNNANTNNTNCTACNANTNTTAGCNNTTNGCAGNAGTCATTN	905
Query	906	NGNATNTATNNNGNNTANTAGTNANTTGGGNCTNNTNCagantatatntngngaanatga 	965
Sbjct	906	NGNATNTATNNNGNNTANTAGTNANTTGGGNCTNNTNCAGANTATATTNTGNGAANATGA	965
Query	966	anntacgnantcctnngnantatnatnntgantanganancnananntntntannant 	1025
Sbjct	966	ANNTACGNANTCCTNNGNANTATNATNNTGANTANGANAANCNANANTNTTNTANNANT	1025
Query	1026	gnctatanattgccnngatanattntnnnaatgaanCGATAGCCCGCNCTAAGGanntnn 	1085
Sbjct	1026	GNCTATANATTGCCNNGATANATTNTNNNAATGAANCGATAGCCCGCNCTAAGGANNTNN	1085
Query	1086	gtnanntaaanntctcagataanntacntntntttattaancnannatcacantatanC 	1145
Sbjct	1086	GTNANNTAAANNTCTCAGATAANNTACNTNTTNTTTATTAANCNANNATCACANTATANC	1145
Query	1146	NGNGACANNNGCGANANTATATGTATGNNANTATNACNGNTCCNNNCCGNGAANNTANTC 	1205
Sbjct	1146	NGNGACANNNGCGANANTATATGTATGNNANTATNACNGNTCCNNNCCGNGAANNTANTC	1205

PATENT SEQUENCE ALIGNMENT

Query	1206	NTANNAGGCATTCNGNNGAGCTNTTCTNCTAGACNATTTnnantgaaannatgcngnnaa	1265
Sbjct	1206	NTANNAGGCATTCNGNNGAGCTNTTCTNCTAGACNATTTNNANTGAAANNATGCNGNNA	1265
Query	1266	aaaCGACNNNCTTNAANTTNTGTCTACANTCCGCNNTNTTTNTACAGATNGCAGNTAAGN	1325
Sbjct	1266	AAACGACNNNCTTNAANTTNTGTCTACANTCCGCNNTNTTTNTACAGATNGCAGNTAAGN	1325
Query	1326	NNANTNANNGCTCTCANCTNGCT	1348
Sbjct	1326	NNANTNANNGCTCTCANCTNGCT	1348

Sequence 1221 matched with Sequence 435

Query= Sequence ID - 1221 nt: 741
Length=741

SEQ ID NO: 435 nt: 741

ALIGNMENTS

Identities = 741/741 (100%), Gaps = 0/741 (0%)

Query	1	AAGCAGAANTNTCTCTAAAAACATTATCTCCTTAAATCTTGAGGTGCATATNAGAGCCA	60
Sbjct	1	AAGCAGAANTNTCTCTAAAAACATTATCTCCTTAAATCTTGAGGTGCATATNAGAGCCA	60
Query	61	CAGGCAATCTCTGACATATAAAATTGCAGTACAGGCCTTTCAAATTTGGCATTTCCTGG	120
Sbjct	61	CAGGCAATCTCTGACATATAAAATTGCAGTACAGGCCTTTCAAATTTGGCATTTCCTGG	120
Query	121	TACAATACAACAACCAAGATATATAATAACTGTACAGTGCCTAGACATTCCAGTAAGAAC	180
Sbjct	121	TACAATACAACAACCAAGATATATAATAACTGTACAGTGCCTAGACATTCCAGTAAGAAC	180
Query	181	CATTATTTTCTTTAATGTAGAATGATTAATACATATTCTACAAGGGGCAGTAAGGTTAGT	240
Sbjct	181	CATTATTTTCTTTAATGTAGAATGATTAATACATATTCTACAAGGGGCAGTAAGGTTAGT	240
Query	241	AATTCTATAGGGTATGTCCCGACATAATTTTCAAATTGTACAATAACACAAACAACCTTG	300
Sbjct	241	AATTCTATAGGGTATGTCCCGACATAATTTTCAAATTGTACAATAACACAAACAACCTTG	300
Query	301	TTAAGGCCATGTTTTATTTGCTGATTAATGGACAAAAGGCAATGTAATTTATTTTCAAGT	360
Sbjct	301	TTAAGGCCATGTTTTATTTGCTGATTAATGGACAAAAGGCAATGTAATTTATTTTCAAGT	360
Query	361	ATTTTCTTGAAAGTCTGTGCTCATAAAAATCATGAAAAGTTGGAAAGACTGTTAAATCAC	420
Sbjct	361	ATTTTCTTGAAAGTCTGTGCTCATAAAAATCATGAAAAGTTGGAAAGACTGTTAAATCAC	420
Query	421	TGAAACTTCAAATATATCTTACACAATCTTGTTTGTACAAAAATACAAGTTAAATATAAA	480
Sbjct	421	TGAAACTTCAAATATATCTTACACAATCTTGTTTGTACAAAAATACAAGTTAAATATAAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CATAAAGCAATCATGGTAATTTTATGCAAATCTGTTTTATGTGATCATCAGTTATATATA	540
Sbjct	481	CATAAAGCAATCATGGTAATTTTATGCAAATCTGTTTTATGTGATCATCAGTTATATATA	540
Query	541	AAAGTTTCTCAGTTCTGTTATTTGTGAAAAGATCAATACCAGATTGAATGACTACCTATT	600
Sbjct	541	AAAGTTTCTCAGTTCTGTTATTTGTGAAAAGATCAATACCAGATTGAATGACTACCTATT	600
Query	601	GGCAAAGGGCCCTAAAAAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTC	660
Sbjct	601	GGCAAAGGGCCCTAAAAAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTC	660
Query	661	CTAATTTGAGATCACCTAAACACTGGAAAAAGaaaaaaaTGAAAGGGCAGTATGTCCATA	720
Sbjct	661	CTAATTTGAGATCACCTAAACACTGGAAAAAGAAAAAAATGAAAGGGCAGTATGTCCATA	720
Query	721	AACCAACAAATAATTTGGCTG	741
Sbjct	721	AACCAACAAATAATTTGGCTG	741

nt: 485

nt: 485

Identities = 485/485 (100%), Gaps = 0/485 (0%)

Query	1	CGAAATTTTCCTTGTGACACAGAGGAAGGGCAAAGGTCTGAGCCCAGAGTTGACGGAGGGA	60
Sbjct	1	CGAAATTTTCCTTGTGACACAGAGGAAGGGCAAAGGTCTGAGCCCAGAGTTGACGGAGGGA	60
Query	61	GTATTTTCAGGGTTCACTTCAGGGGCTCCCAAAGCGACAAGATCGTTAGGGAGAGAGGCCC	120
Sbjct	61	GTATTTTCAGGGTTCACTTCAGGGGCTCCCAAAGCGACAAGATCGTTAGGGAGAGAGGCCC	120
Query	121	AGGGTGGGGACTGGGAATTTAAGGAGAGCTGGGAACGGATCCCTTAGGTTTCAGGAAGCTT	180
Sbjct	121	AGGGTGGGGACTGGGAATTTAAGGAGAGCTGGGAACGGATCCCTTAGGTTTCAGGAAGCTT	180
Query	181	CTGTGCAAGCTGCGAGGATGGCTTGGGCCGAAGGGTTGCTCTGCCCGCCGCGCTAGCTGT	240
Sbjct	181	CTGTGCAAGCTGCGAGGATGGCTTGGGCCGAAGGGTTGCTCTGCCCGCCGCGCTAGCTGT	240
Query	241	GAGCTGAGCAAAGCCCTGGGCTCACAGCACCCCAAAAGCCTGTGGCTTCAGTCCTGCGTC	300
Sbjct	241	GAGCTGAGCAAAGCCCTGGGCTCACAGCACCCCAAAAGCCTGTGGCTTCAGTCCTGCGTC	300
Query	301	TGCACCACACAATCAAAAGGATCGTTTTGTTTTGTTTTTAAAGAAAGGTGAGATTGGCTT	360
Sbjct	301	TGCACCACACAATCAAAAGGATCGTTTTGTTTTGTTTTTAAAGAAAGGTGAGATTGGCTT	360
Query	361	GGTTCTTCATGAGCACATTTGATATAGCTCTTTTTCTGTTTTTCCTTGCTCATTTGTTTT	420
Sbjct	361	GGTTCTTCATGAGCACATTTGATATAGCTCTTTTTCTGTTTTTCCTTGCTCATTTGTTTT	420
Query	421	TGGGGAAGAAATCTGTACTGTATTGGGATTGTAAAGAACATCTCTGCACTCAGACAGTTT	480
Sbjct	421	TGGGGAAGAAATCTGTACTGTATTGGGATTGTAAAGAACATCTCTGCACTCAGACAGTTT	480

PATENT SEQUENCE ALIGNMENT

Query	481	ACAGA	485
Sbjct	481	ACAGA	485

Sequence 1226 matched with Sequence 437

Query= Sequence ID 1226
Length=637

SEQ ID NO: 437

ALIGNMENTS

Identities = 637/637 (100%), Gaps = 0/637 (0%)

Query	1	GGTTTTTATACTTGCCATGAAACTGTTCTTTGGGATATTATTTTGTTCAGGTTCCCCACT	60
Sbjct	1	GGTTTTTATACTTGCCATGAAACTGTTCTTTGGGATATTATTTTGTTCAGGTTCCCCACT	60
Query	61	TGGACAGCAGAGGGGGTGACTCTGCCCATCCCTGCCACTGGTAGCCAGGCGGGCAATGTC	120
Sbjct	61	TGGACAGCAGAGGGGGTGACTCTGCCCATCCCTGCCACTGGTAGCCAGGCGGGCAATGTC	120
Query	121	TGCTAGCAGTCTGCTTCTGTCTGAACTCAGCCAGCAGAGGCAAACCTCCCGTTCCCCGAG	180
Sbjct	121	TGCTAGCAGTCTGCTTCTGTCTGAACTCAGCCAGCAGAGGCAAACCTCCCGTTCCCCGAG	180
Query	181	AAACACTCTGAAGGCAGGGTGGGTGACTCCACCCACCACCGCTCTCCTAGCCATGCAGG	240
Sbjct	181	AAACACTCTGAAGGCAGGGTGGGTGACTCCACCCACCACCGCTCTCCTAGCCATGCAGG	240
Query	241	CCATGTCTGCTAGAGCTTCCAGCGCAGTGGTCCTAATTCTGTCTGAATCCGGCTGAGGGG	300
Sbjct	241	CCATGTCTGCTAGAGCTTCCAGCGCAGTGGTCCTAATTCTGTCTGAATCCGGCTGAGGGG	300
Query	301	TGCAGCCTCCTGTTACTGCCCAGGGAAACACCCAGATGGCAGGGTGGGTGACTCCAACCA	360
Sbjct	301	TGCAGCCTCCTGTTACTGCCCAGGGAAACACCCAGATGGCAGGGTGGGTGACTCCAACCA	360
Query	361	CCTCTGCCTGTGGTAGCCAGATGGGCCACACCTGCTAGAGCTTCCAGCCCAGCAGTCCCG	420
Sbjct	361	CCTCTGCCTGTGGTAGCCAGATGGGCCACACCTGCTAGAGCTTCCAGCCCAGCAGTCCCG	420
Query	421	CTACTCTGTGGGTGGGTGCCATCCCCTGTTCTCTGGGAAGCACCCAGACAGCTGATTAC	480
Sbjct	421	CTACTCTGTGGGTGGGTGCCATCCCCTGTTCTCTGGGAAGCACCCAGACAGCTGATTAC	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 GTGACCCACCCACTTCTGCAGATCCTAGCTGAGCAGGACTTGCTGGTTTGGACAATGCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 GTGACCCACCCACTTCTGCAGATCCTAGCTGAGCAGGACTTGCTGGTTTGGACAATGCC 540

Query 541 CAAGCAGGGAAGAGCCCTCATTCTCTTATCACTGACAGAGGTGAGATGTCCGANTTTGTA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 CAAGCAGGGAAGAGCCCTCATTCTCTTATCACTGACAGAGGTGAGATGTCCGANTTTGTA 600

Query 601 NGCTGGTGGAGGAGTGAGGTGGAGGAGGTATGCCTCT 637
          ||||||||||||||||||||||||||||||||
Sbjct 601 NGCTGGTGGAGGAGTGAGGTGGAGGAGGTATGCCTCT 637
```

Sequence 1228 matched with Sequence 438

Query= Sequence ID 1228
Length=420

SEQ ID NO: 438

ALIGNMENTS

Identities = 420/420 (100%), Gaps = 0/420 (0%)

Query	1	GTTATTTCAGGTATCCATCAAAATTTTATAAGAGGGCCGGAACATCGGCTCACACCTGTA	60
Sbjct	1	GTTATTTCAGGTATCCATCAAAATTTTATAAGAGGGCCGGAACATCGGCTCACACCTGTA	60
Query	61	ATCCCAGCACTTTGGGAGGCTGAGGCAGGTGGTTCACCTTGAGGTCAGGAGTTCGAGACCA	120
Sbjct	61	ATCCCAGCACTTTGGGAGGCTGAGGCAGGTGGTTCACCTTGAGGTCAGGAGTTCGAGACCA	120
Query	121	GCCTGGCCAACATGGCAAAACCCCGTCACTATTAAAAATACAAAACATTAGCTGGGTGTA	180
Sbjct	121	GCCTGGCCAACATGGCAAAACCCCGTCACTATTAAAAATACAAAACATTAGCTGGGTGTA	180
Query	181	GTGGCAGGTGCCTGTAATCCCAGCTATTCGGGAGGCCTAGGAAGGAAAAATGGCTTGAACC	240
Sbjct	181	GTGGCAGGTGCCTGTAATCCCAGCTATTCGGGAGGCCTAGGAAGGAAAAATGGCTTGAACC	240
Query	241	TGGGGGTGGAGGTTGGAGTGAGGCAAGATCACACCACTGCACTCCAGCCTGGGCGACAGA	300
Sbjct	241	TGGGGGTGGAGGTTGGAGTGAGGCAAGATCACACCACTGCACTCCAGCCTGGGCGACAGA	300
Query	301	GCGAGACTCCATCTCAAAAGAAGaaaaaaaaaacaacaaaaaaaaCCTTTATCAGATTATC	360
Sbjct	301	GCGAGACTCCATCTCAAAAGAAGAAAAAAAAAACAACAAAAAACCTTTATCAGATTATC	360
Query	361	AGAGGTTATCACTACAGAGGGAGGTAAAAATTGGAGGGAAAAGGGTACAAATTTATTTAC	420
Sbjct	361	AGAGGTTATCACTACAGAGGGAGGTAAAAATTGGAGGGAAAAGGGTACAAATTTATTTAC	420

Sequence 1230 matched with Sequence 439

Query= Sequence ID - 1230
Length=741

nt: 741

SEQ ID NO: 439

nt: 741

ALIGNMENTS

Identities = 741/741 (100%), Gaps = 0/741 (0%)

Query	1	AAGCAGAANTNTCTCTAAAAACATTATCTCCTTAAATCTTGAGGTGCATATNAGAGCCA	60
Sbjct	1	AAGCAGAANTNTCTCTAAAAACATTATCTCCTTAAATCTTGAGGTGCATATNAGAGCCA	60
Query	61	CAGGCAATCTCTGACATATAAAATTGCAGTACAGGCCTTTCAAATTTGGCATTTCCTGG	120
Sbjct	61	CAGGCAATCTCTGACATATAAAATTGCAGTACAGGCCTTTCAAATTTGGCATTTCCTGG	120
Query	121	TACAATACAACAACCAAGATATATAATAACTGTACAGTGCCTAGACATTCCAGTAAGAAC	180
Sbjct	121	TACAATACAACAACCAAGATATATAATAACTGTACAGTGCCTAGACATTCCAGTAAGAAC	180
Query	181	CATTATTTTCTTTAATGTAGAATGATTAATACATATTCTACAAGGGGCAGTAAGGTTAGT	240
Sbjct	181	CATTATTTTCTTTAATGTAGAATGATTAATACATATTCTACAAGGGGCAGTAAGGTTAGT	240
Query	241	AATTCTATAGGGTATGTCCCGACATAATTTTCAAATTGTACAATAACACAAACAACCTTG	300
Sbjct	241	AATTCTATAGGGTATGTCCCGACATAATTTTCAAATTGTACAATAACACAAACAACCTTG	300
Query	301	TTAAGGCCATGTTTTATTTGCTGATTAATGGACAAAAGGCAATGTAATTTATTTTCAAGT	360
Sbjct	301	TTAAGGCCATGTTTTATTTGCTGATTAATGGACAAAAGGCAATGTAATTTATTTTCAAGT	360
Query	361	ATTTTCTTGAAAGTCTGTGCTCATAAAAAATCATGAAAAGTTGGAAAGACTGTTAAATCAC	420
Sbjct	361	ATTTTCTTGAAAGTCTGTGCTCATAAAAAATCATGAAAAGTTGGAAAGACTGTTAAATCAC	420
Query	421	TGAAACTTCAAATATATCTTACACAATCTTGTTTGTACAAAAATACAAGTTAAATATAAA	480
Sbjct	421	TGAAACTTCAAATATATCTTACACAATCTTGTTTGTACAAAAATACAAGTTAAATATAAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CATAAAGCAATCATGGTAATTTTATGCAAATCTGTTTTATGTGATCATCAGTTATATATA	540
Sbjct	481	CATAAAGCAATCATGGTAATTTTATGCAAATCTGTTTTATGTGATCATCAGTTATATATA	540
Query	541	AAAGTTTCTCAGTTCTGTTATTTGTGAAAAGATCAATACCAGATTGAATGACTACCTATT	600
Sbjct	541	AAAGTTTCTCAGTTCTGTTATTTGTGAAAAGATCAATACCAGATTGAATGACTACCTATT	600
Query	601	GGCAAAGGGCCCTAAAAAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTC	660
Sbjct	601	GGCAAAGGGCCCTAAAAAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTC	660
Query	661	CTAATTTGAGATCACCTAAACACTGGAAAAAGaaaaaaaTGAAAGGGCAGTATGTCCATA	720
Sbjct	661	CTAATTTGAGATCACCTAAACACTGGAAAAAGAAAAAAATGAAAGGGCAGTATGTCCATA	720
Query	721	AACCAACAAATAATTTGGCTG	741
Sbjct	721	AACCAACAAATAATTTGGCTG	741

Sequence 1231 matched with Sequence 440

Query= Sequence ID - 1231 nt: 203
Length=203

SEQ ID NO: 440 nt: 203

ALIGNMENTS

Identities = 203/203 (100%), Gaps = 0/203 (0%)

Query	1	TTGAGGAAGGGTCTACTGTCTTTTTAAATGGCACAATTTTAAGAGGTTTGAGAGGTACAG	60
Sbjct	1	TTGAGGAAGGGTCTACTGTCTTTTTAAATGGCACAATTTTAAGAGGTTTGAGAGGTACAG	60
Query	61	TCCCTTAACCTGCCACGGGAGAGGGGCCCCAACTTTCTTCCCCCACA	120
Sbjct	61	TCCCTTAACCTGCCACGGGAGAGGGGCCCCAACTTTCTTCCCCCACA	120
Query	121	TCTGTGTGGAGGGGAGCAGGGATATCTAAGCTGTGGTGTGAAAGGGTAGGAGAGATGCT	180
Sbjct	121	TCTGTGTGGAGGGGAGCAGGGATATCTAAGCTGTGGTGTGAAAGGGTAGGAGAGATGCT	180
Query	181	GGAGGTGGGGGTGCTGTGTTCTA	203
Sbjct	181	GGAGGTGGGGGTGCTGTGTTCTA	203

Sequence 1239 matched with Sequence 441

Query= Sequence ID 1239

Length=874

SEQ ID NO: 441

ALIGNMENTS

Identities = 874/874 (100%), Gaps = 0/874 (0%)

Query	1	TTTCCTCGGGAAGCGCGCCATTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACAttt	60
Sbjct	1	TTTCCTCGGGAAGCGCGCCATTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACATTT	60
Query	61	ttttttttttttttttttttAGAATGATTAACAATTTATTGAGTTTTATTATCTACAAAAA	120
Sbjct	61	TTTTTTTTTTTTTTTTTTAGAATGATTAACAATTTATTGAGTTTTATTATCTACAAAAA	120
Query	121	TATAGCAATACAGNGAACTTCACCAAATCCTAAATATTAGTACCTGAACTGGCTACAAC	180
Sbjct	121	TATAGCAATACAGNGAACTTCACCAAATCCTAAATATTAGTACCTGAACTGGCTACAAC	180
Query	181	ACCGNGTGCACACCCAGTTCCTGCAGAATCTCTTGAGATATGGGAGAGTCAGCCAGTGA	240
Sbjct	181	ACCGNGTGCACACCCAGTTCCTGCAGAATCTCTTGAGATATGGGAGAGTCAGCCAGTGA	240
Query	241	AAAGATCCATTTCTTGGAATCCTTGTCAACAAGACCAGTTCAGAAATCCAGGATATATA	300
Sbjct	241	AAAGATCCATTTCTTGGAATCCTTGTCAACAAGACCAGTTCAGAAATCCAGGATATATA	300
Query	301	GAAGCCTACTGTAATTTaaaaacagtaacaaaaacccaacaaaacccaaatcaacaaaG	360
Sbjct	301	GAAGCCTACTGTAATTTAAAAACAGTAACAAAAACCCAACAAAACCCAAATCAACAAAG	360
Query	361	ACCAAGATAAAGGNGTGATAAACATTAATTGTAATGGTTTTCTTTACATGCAATACATG	420
Sbjct	361	ACCAAGATAAAGGNGTGATAAACATTAATTGTAATGGTTTTCTTTACATGCAATACATG	420
Query	421	CATTTTAAAATCACTAAGAAACACGAAATTTTGTAGAGCAAAGTTTGNGTTTCACGTAAG	480
Sbjct	421	CATTTTAAAATCACTAAGAAACACGAAATTTTGTAGAGCAAAGTTTGNGTTTCACGTAAG	480

PATENT SEQUENCE ALIGNMENT

Sequence 1255 matched with Sequence 442

Query= Sequence ID 1255
Length=928

SEQ ID NO: 442

ALIGNMENTS

Identities = 68/68 (100%), Gaps = 0/68 (0%)

Query	497	TAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTTAGGTGTTTTCACTTGC	556
Sbjct	565	TAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTTAGGTGTTTTCACTTGC	624
Query	557	ATTTCCTT	564
Sbjct	625	ATTTCCTT	632

Sequence 1256 matched with Sequence 443

Query= Sequence ID 1256
Length=954

SEQ ID NO: 443

ALIGNMENTS

Identities = 925/925 (100%), Gaps = 0/925 (0%)

Query	1	TTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACGGAGTTTTACCTTATTACACTTTA	60
Sbjct	1	TTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACGGAGTTTTACCTTATTACACTTTA	60
Query	61	ATCTCTGGATTACCCCATCTCATTTCTCTTTTAGGAAAAGTGTGTGTATGTGGTGGCTT	120
Sbjct	61	ATCTCTGGATTACCCCATCTCATTTCTCTTTTAGGAAAAGTGTGTGTATGTGGTGGCTT	120
Query	121	TGATGGTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAAGTAGAAATGAATGGAA	180
Sbjct	121	TGATGGTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAAGTAGAAATGAATGGAA	180
Query	181	GATGATGGGAAATATGACTTCACCAAGGAGCAATGCTGGGATTGCAACTGTAGGGAACAC	240
Sbjct	181	GATGATGGGAAATATGACTTCACCAAGGAGCAATGCTGGGATTGCAACTGTAGGGAACAC	240
Query	241	CATTTATGCAGTGGGAGGATTCGATGGCAATGAATTTCTGAATACGGTGGAAGTCTATAA	300
Sbjct	241	CATTTATGCAGTGGGAGGATTCGATGGCAATGAATTTCTGAATACGGTGGAAGTCTATAA	300
Query	301	CCTTGAGTCAAATGAATGGAGCCCCTATACAAAGATTTTCCAGTTTAAACAAATTTAAGA	360
Sbjct	301	CCTTGAGTCAAATGAATGGAGCCCCTATACAAAGATTTTCCAGTTTAAACAAATTTAAGA	360
Query	361	CCCTCTCAAACAAACAGGCTTAGTGATGTAATTATGGTTAGCAGAGGTACACTTGTGAAT	420
Sbjct	361	CCCTCTCAAACAAACAGGCTTAGTGATGTAATTATGGTTAGCAGAGGTACACTTGTGAAT	420
Query	421	AAAGAGGGTGGGTGGGTATAGATGTTGCTAACAGCAACACAAAGCTTTTGCATATTGCAT	480
Sbjct	421	AAAGAGGGTGGGTGGGTATAGATGTTGCTAACAGCAACACAAAGCTTTTGCATATTGCAT	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 ACTATTAAACATGCTGTACATACTTTTGGGTTTATTTGGAAAGGAATGCAAAGATGAAG 540
          |||
Sbjct 481 ACTATTAAACATGCTGTACATACTTTTGGGTTTATTTGGAAAGGAATGCAAAGATGAAG 540

Query 541 GTCTGTTTTGTGTACTTTTAAGACTTTGGTTATTTTACTTTTTGGAAAAGAATAAACCAA 600
          |||
Sbjct 541 GTCTGTTTTGTGTACTTTTAAGACTTTGGTTATTTTACTTTTTGGAAAAGAATAAACCAA 600

Query 601 GAATTGATTGGGCACATCATTTCAAGAAGTCCCCTCTCCTCCACATTGTTTTGCCAATT 660
          |||
Sbjct 601 GAATTGATTGGGCACATCATTTCAAGAAGTCCCCTCTCCTCCACATTGTTTTGCCAATT 660

Query 661 TGCACATTAAATGACTCTTCCCTCAAATGTGTACTATGGGGTAAAAGGGGTAGGGNTTAA 720
          |||
Sbjct 661 TGCACATTAAATGACTCTTCCCTCAAATGTGTACTATGGGGTAAAAGGGGTAGGGNTTAA 720

Query 721 ANATGTAAACAGTTGGGTTTTTTAAGGGNCCTTTTTTCATAACTGGAACACTCTNTACAAG 780
          |||
Sbjct 721 ANATGTAAACAGTTGGGTTTTTTAAGGGNCCTTTTTTCATAACTGGAACACTCTNTACAAG 780

Query 781 GNTNCTTNTTAAATAAATAAAGTACTTTTTTGTNTTAAANGNANCTTCNTGCTTCCA 840
          |||
Sbjct 781 GNTNCTTNTTAAATAAATAAAGTACTTTTTTGTNTTAAANGNANCTTCNTGCTTCCA 840

Query 841 TaaaaaaaaaTTTAANTNGNCANCTNTGCTGCTGCGNCCANTTNGCTNGNCCNTGGCA 900
          |||
Sbjct 841 TAAAAAAAAAAATTTAANTNGNCANCTNTGCTGCTGCGNCCANTTNGCTNGNCCNTGGCA 900

Query 901 TTCCCTAGGGANGNTNAATANTGGC 925
          |||
Sbjct 901 TTCCCTAGGGANGNTNAATANTGGC 925
```

Sequence 1331 matched with Sequence 444

Query= Sequence ID 1331
Length=787

SEQ ID NO: 444

ALIGNMENTS

Identities = 787/787 (100%), Gaps = 0/787 (0%)

Query	1	GGGCGATGCATGCTTTATTAAGGCTCTTGTTTCACCTGGCAGTGTACTGTATCAACGTAT	60
Sbjct	1	GGGCGATGCATGCTTTATTAAGGCTCTTGTTTCACCTGGCAGTGTACTGTATCAACGTAT	60
Query	61	AATACAGaaaaaaaTCTCTTTAAGGTCCTCCTTCACAAAGACATAGAGTGAAACTCCCT	120
Sbjct	61	AATACAGAAAAAAATCTCTTTAAGGTCCTCCTTCACAAAGACATAGAGTGAAACTCCCT	120
Query	121	TTACATGTCAGTATTTGTTCAACACTTTAGGCAACTTGACTGTCAGTGTTAAATGGAAA	180
Sbjct	121	TTACATGTCAGTATTTGTTCAACACTTTAGGCAACTTGACTGTCAGTGTTAAATGGAAA	180
Query	181	ACAGGAAAAATGGAAAAATCTGACCAATTCTGCCACCTTGAGACTTTCATATAGACCTTGC	240
Sbjct	181	ACAGGAAAAATGGAAAAATCTGACCAATTCTGCCACCTTGAGACTTTCATATAGACCTTGC	240
Query	241	ACAACAATTGTATAGATCACACACCGGCTGTATTTAATATGTAACATTTTCACACATATT	300
Sbjct	241	ACAACAATTGTATAGATCACACACCGGCTGTATTTAATATGTAACATTTTCACACATATT	300
Query	301	AAAGATACAGAAGTATTAaaaaacccccAATGTTAATGTATTTGCTTAAAAGGCACAAGT	360
Sbjct	301	AAAGATACAGAAGTATTAaaaaacccccAATGTTAATGTATTTGCTTAAAAGGCACAAGT	360
Query	361	TTCACATATCTGTCTAGCTATCTGTTGGTAATACAGAAAGTATACTACTTTTTTAAAAAA	420
Sbjct	361	TTCACATATCTGTCTAGCTATCTGTTGGTAATACAGAAAGTATACTACTTTTTTAAAAAA	420
Query	421	GTGGGCAGAATTCTtgtgtatgtatatatttgtgtgtacagtatgtgtatgtgtgtatatat	480
Sbjct	421	GTGGGCAGAATTCTTGTGTATGTATATTGTGTGTACAGTATGTGTATGTGTGTATATAT	480

PATENT SEQUENCE ALIGNMENT

```
Query 481  atatattatatatatagataaatatataaatatTTTTTTAAGGAGAACTAGAATGTTTA 540
          |||
Sbjct 481  ATATATTATATATATAGATAATATATAAAATATTTTTTTAAGGAGAACTAGAATGTTTA 540

Query 541  GCTAGAAAATTCCACAGCCTGTGAAGAAATATTTCAAATGGCCATAAAGGAGGTAAAAA 600
          |||
Sbjct 541  GCTAGAAAATTCCACAGCCTGTGAAGAAATATTTCAAATGGCCATAAAGGAGGTAAAAA 600

Query 601  TGAAAACCATAACCTAACTTTTATAGAGGCTTTATCTTTAATTTAACGATGTGCGGAGGA 660
          |||
Sbjct 601  TGAAAACCATAACCTAACTTTTATAGAGGCTTTATCTTTAATTTAACGATGTGCGGAGGA 660

Query 661  CTTTCTTGCTTGAATCTGTTCCGGGCTGTCTGCTCTGTCCATCAAATGGGCAGGTCTGGG 720
          |||
Sbjct 661  CTTTCTTGCTTGAATCTGTTCCGGGCTGTCTGCTCTGTCCATCAAATGGGCAGGTCTGGG 720

Query 721  AATGAGGCACCTTCGGCCGTTTCAAGTGGCCTGAACAGAATGCTGGAACCCAGGCTGGA 780
          |||
Sbjct 721  AATGAGGCACCTTCGGCCGTTTCAAGTGGCCTGAACAGAATGCTGGAACCCAGGCTGGA 780

Query 781  CTCGGAC 787
          |||
Sbjct 781  CTCGGAC 787
```

SEQ ID NO: 445

Identities = 171/191 (89%), Gaps = 12/191 (6%)

Page 745

Sequence 1335 matched with Sequence 446

Query= Sequence ID 1335
Length=688

SEQ ID NO: 446

ALIGNMENTS

Identities = 688/688 (100%), Gaps = 0/688 (0%)

Query	1	CAAGACTCCATCTCaaaaaaaaaaaaaaaaTCTACAGTGCTGAGTATATAAAATTATTAAC	60
Sbjct	1	CAAGACTCCATCTCAAAAAAAAAAAAAAAAAATCTACAGTGCTGAGTATATAAAATTATTAAC	60
Query	61	ACATTTTCAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAACAGGTAAT	120
Sbjct	61	ACATTTTCAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAACAGGTAAT	120
Query	121	TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT	180
Sbjct	121	TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT	180
Query	181	GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT	240
Sbjct	181	GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT	240
Query	241	TTGTTCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT	300
Sbjct	241	TTGTTCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT	300
Query	301	GCCAAATATGGGTAAATAAGGGAAAAATTTTGTTTAATATTTAGTCCTTCTGAGATGGCTT	360
Sbjct	301	GCCAAATATGGGTAAATAAGGGAAAAATTTTGTTTAATATTTAGTCCTTCTGAGATGGCTT	360
Query	361	GAATATTTGAATTTTGTGTTGTACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA	420
Sbjct	361	GAATATTTGAATTTTGTGTTGTACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA	420
Query	421	GAGGAAAGATGGATTTTCAGTCTGTATTTTAAACATCATTTATTTTAAATCTGGTGCTGA	480
Sbjct	421	GAGGAAAGATGGATTTTCAGTCTGTATTTTAAACATCATTTATTTTAAATCTGGTGCTGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AAAATAAGaaaaaaTTAAACTGCATTCTGCTGTTCTTCTTTAGAAGCATTCTGCGTAA  540
          |||
Sbjct  481  AAAATAAGAAAAAAATTAAGTGCATTCTGCTGTTCTTCTTTAGAAGCATTCTGCGTAA  540

Query  541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA  600
          |||
Sbjct  541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA  600

Query  601  GTGtttttttgtttttttCCTAGAAATGTTTGTCTTCCCCACCTGTTGATCCAGGTTA  660
          |||
Sbjct  601  GTGTTTTTTTGTTTTTTTCCTAGAAATGTTTGTCTTCCCCACCTGTTGATCCAGGTTA  660

Query  661  AGGAATACTTTTTTACACTTTATTCAAA  688
          |||
Sbjct  661  AGGAATACTTTTTTACACTTTATTCAAA  688
```

Sequence 1336 matched with Sequence 447

Query= Sequence ID 1336
Length=724

SEQ ID NO: 447

ALIGNMENTS

Identities = 724/724 (100%), Gaps = 0/724 (0%)

Query	1	CTTTTCCTCCCGCTGTCCCCACGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGTG	60
Sbjct	1	CTTTTCCTCCCGCTGTCCCCACGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGTG	60
Query	61	AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCTG	120
Sbjct	61	AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCTG	120
Query	121	GGAAGTGTTTTTGAGAAGTCTCGGTCCGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA	180
Sbjct	121	GGAAGTGTTTTTGAGAAGTCTCGGTCCGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA	180
Query	181	ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCAGATGAGGCAGCTGTGACTGTGTC	240
Sbjct	181	ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCAGATGAGGCAGCTGTGACTGTGTC	240
Query	241	AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA	300
Sbjct	241	AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA	300
Query	301	AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACTA	360
Sbjct	301	AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACTA	360
Query	361	TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCTACAACAGTGTCTGG	420
Sbjct	361	TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCTACAACAGTGTCTGG	420
Query	421	GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG	480
Sbjct	421	GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 CTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 CTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAA 540

Query 541 GAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACCTCTGACAACCAC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 GAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACCTCTGACAACCAC 600

Query 601 AATCATGAGGATGATGTGTTGGGGTTTCCCAGCAATCAGGACTTGTATTGGTCAGAGGAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 AATCATGAGGATGATGTGTTGGGGTTTCCCAGCAATCAGGACTTGTATTGGTCAGAGGAC 660

Query 661 GATCAAGAGCTCATAATCCCATGCCTTGCGCTGGTGAGAGCATCCAAAGCCTGCCTGAAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 661 GATCAAGAGCTCATAATCCCATGCCTTGCGCTGGTGAGAGCATCCAAAGCCTGCCTGAAG 720

Query 721 AAAA 724
          ||||
Sbjct 721 AAAA 724
```

Sequence 1337 matched with Sequence 448

Query= Sequence ID 1337
Length=622

SEQ ID NO: 448

ALIGNMENTS

Identities = 622/622 (100%), Gaps = 0/622 (0%)

Query	1	CAAGAACTCTGGGACATTTGCAAAGGGTATGGCATATGTGTAATGGGAATACCAGAGGAG	60
Sbjct	1	CAAGAACTCTGGGACATTTGCAAAGGGTATGGCATATGTGTAATGGGAATACCAGAGGAG	60
Query	61	AGGAAAGACAGGAAGTCaaaaaaGAATTTTCCAAATTAATGATAGGTTCCAAACCACA	120
Sbjct	61	AGGAAAGACAGGAAGTCAAAAAAGAATTTTCCAAATTAATGATAGGTTCCAAACCACA	120
Query	121	GATGCAGGAAGCTTAAACACCAACAGGATAAATAAAACAAAATCTACGCTTAAGCATATC	180
Sbjct	121	GATGCAGGAAGCTTAAACACCAACAGGATAAATAAAACAAAATCTACGCTTAAGCATATC	180
Query	181	ATACTTAACCTGCAGAAAATTACAGACAAAAGAAAAACACCAGAGGGGAAGCTGGCAGAA	240
Sbjct	181	ATACTTAACCTGCAGAAAATTACAGACAAAAGAAAAACACCAGAGGGGAAGCTGGCAGAA	240
Query	241	ACATACCACCTATAGCGGAAGAAGAATAAGAATTACATCAGACTTCCCTTCAGAAATCTT	300
Sbjct	241	ACATACCACCTATAGCGGAAGAAGAATAAGAATTACATCAGACTTCCCTTCAGAAATCTT	300
Query	301	GCAAACAAAAAGATGTAGCACAAATATTTAAAGTATTAAAGGAGGCCGGGCCCGGTGGCTC	360
Sbjct	301	GCAAACAAAAAGATGTAGCACAAATATTTAAAGTATTAAAGGAGGCCGGGCCCGGTGGCTC	360
Query	361	GGGCCTGTAATCCTAACACTTTGGGAGGCTGAGGCAGGAGGACCATGAGGTCAGGAGATC	420
Sbjct	361	GGGCCTGTAATCCTAACACTTTGGGAGGCTGAGGCAGGAGGACCATGAGGTCAGGAGATC	420
Query	421	GAGACCATCCTGGTGATGGTGATACCCCATCTCTACTAAAAATACAAAAAATTAACCGGG	480
Sbjct	421	GAGACCATCCTGGTGATGGTGATACCCCATCTCTACTAAAAATACAAAAAATTAACCGGG	480

Query	481	CATGGTGACACGCACCTGTAATCCCAGCTACTTGGGAGGCTGAAGCAGGAGAATCGTTTG	540
Sbjct	481	CATGGTGACACGCACCTGTAATCCCAGCTACTTGGGAGGCTGAAGCAGGAGAATCGTTTG	540
Query	541	AGCCCAGGAGGTGGAGGTTGCAGTGAGCCGAGATCACATCACTGCACGCCTGGGCAACAG	600
Sbjct	541	AGCCCAGGAGGTGGAGGTTGCAGTGAGCCGAGATCACATCACTGCACGCCTGGGCAACAG	600
Query	601	AGCGAGACTCCATCTCAAAAAA	622
Sbjct	601	AGCGAGACTCCATCTCAAAAAA	622

Sequence 1338 matched with Sequence 449

Query= Sequence ID 1338
Length=834

SEQ ID NO: 449

ALIGNMENTS

Identities = 834/834 (100%), Gaps = 0/834 (0%)

Query	1	CGACCCGTTTTAGTCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCTGCCTCGGCC	60
Sbjct	1	CGACCCGTTTTAGTCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCTGCCTCGGCC	60
Query	61	TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGTAAATCAGGTTTTTTA	120
Sbjct	61	TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGTAAATCAGGTTTTTTA	120
Query	121	AATGTTTGCCAAACCTTATCACTGACTTTTATAACAAAATTATTTACTATAATCATTAGG	180
Sbjct	121	AATGTTTGCCAAACCTTATCACTGACTTTTATAACAAAATTATTTACTATAATCATTAGG	180
Query	181	GAATATTTAAGTTCTGCTAATACTTAAAAATTGCAGAGTGCTAAAACCAGCAGTGAGTTTA	240
Sbjct	181	GAATATTTAAGTTCTGCTAATACTTAAAAATTGCAGAGTGCTAAAACCAGCAGTGAGTTTA	240
Query	241	GAATCAAGCTAAGCTTTATTGTTGCTACTATTTGAGGCATATTAGTTGACTGGTGTTTCAT	300
Sbjct	241	GAATCAAGCTAAGCTTTATTGTTGCTACTATTTGAGGCATATTAGTTGACTGGTGTTTCAT	300
Query	301	ATGCAAGGCAGTCTACTGGGTGCAACAAGGGTTAGAAGGATATTTTAAAAAACTGACCC	360
Sbjct	301	ATGCAAGGCAGTCTACTGGGTGCAACAAGGGTTAGAAGGATATTTTAAAAAACTGACCC	360
Query	361	TATTCTCAGGATGAAAATAATACACTAGTAATAGTCTGCTCTGTTGGTTAACTCCTCGTA	420
Sbjct	361	TATTCTCAGGATGAAAATAATACACTAGTAATAGTCTGCTCTGTTGGTTAACTCCTCGTA	420
Query	421	AGGAGGTACAATTAAAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAAGAATCATATTCCT	480
Sbjct	421	AGGAGGTACAATTAAAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAAGAATCATATTCCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCACTAGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTGAAGGA	540
Sbjct	481	TCACTAGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTGAAGGA	540
Query	541	TTGGTAAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATTTATTG	600
Sbjct	541	TTGGTAAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATTTATTG	600
Query	601	CATGCTTATCTTGTATCAAGCATTGTGATGAAAGCACAGAATGAAAGAGGAGGGAGAAT	660
Sbjct	601	CATGCTTATCTTGTATCAAGCATTGTGATGAAAGCACAGAATGAAAGAGGAGGGAGAAT	660
Query	661	GTTTAGAGAATAAGGGCTGAAACACAGATTTTGTAGGGAGCGTAGGGGAGACTGANAAGA	720
Sbjct	661	GTTTAGAGAATAAGGGCTGAAACACAGATTTTGTAGGGAGCGTAGGGGAGACTGANAAGA	720
Query	721	CAGGTTCAGGTTAGTAAGGGCGCTCATATTTTGACCCTGAATGTAACTATGTGCACATC	780
Sbjct	721	CAGGTTCAGGTTAGTAAGGGCGCTCATATTTTGACCCTGAATGTAACTATGTGCACATC	780
Query	781	ATGCTAGCTATTCTAAATCAGGCATTTTCAAATGGAAGCAGGCACTGACATTTT	834
Sbjct	781	ATGCTAGCTATTCTAAATCAGGCATTTTCAAATGGAAGCAGGCACTGACATTTT	834

Sequence 1344 matched with Sequence 450

Query= Sequence ID 1344
Length=624

SEQ ID NO: 450

ALIGNMENTS

Identities = 624/624 (100%), Gaps = 0/624 (0%)

Query	1	CGTGAAGGGTCTTTATGTATTAGTATTAGAGTGATCTTTTGATTATTTTCCTCACTATAA	60
Sbjct	1	CGTGAAGGGTCTTTATGTATTAGTATTAGAGTGATCTTTTGATTATTTTCCTCACTATAA	60
Query	61	GGAAATTATTTTCCTCAGGATGAGCTGCCATAACATTCCACTGTCTGATGGCAATTTTAAA	120
Sbjct	61	GGAAATTATTTTCCTCAGGATGAGCTGCCATAACATTCCACTGTCTGATGGCAATTTTAAA	120
Query	121	GCCTGAAATTGAAGCCCATGGCTAGGCTATGAGAACCCTAGTTCGTATAGTAAAGTTGAT	180
Sbjct	121	GCCTGAAATTGAAGCCCATGGCTAGGCTATGAGAACCCTAGTTCGTATAGTAAAGTTGAT	180
Query	181	ATCTTCTGGATGTATACTAATTTTAGGCTTTATTTTAAAACTGCTGGAAACTGAAACTTA	240
Sbjct	181	ATCTTCTGGATGTATACTAATTTTAGGCTTTATTTTAAAACTGCTGGAAACTGAAACTTA	240
Query	241	GACAAAAGTATTTTCAGGACATCATTTACAATGTTTAGCCCTAAAGAGTCAAGCTGTGGG	300
Sbjct	241	GACAAAAGTATTTTCAGGACATCATTTACAATGTTTAGCCCTAAAGAGTCAAGCTGTGGG	300
Query	301	ATTCTGAGTCTTTCATATGTTACAGCAGAACTTAAAAGCAAGAGGAAATTGGCTGGGCA	360
Sbjct	301	ATTCTGAGTCTTTCATATGTTACAGCAGAACTTAAAAGCAAGAGGAAATTGGCTGGGCA	360
Query	361	CAGTGGCTCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGTGGATCATGAGGTCAAGA	420
Sbjct	361	CAGTGGCTCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGTGGATCATGAGGTCAAGA	420
Query	421	GATTGAGACCATCCTAGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTA	480
Sbjct	421	GATTGAGACCATCCTAGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCTGGGCGTGGTGGCACACGCCTGTAATCCCAGCTAGTCAGGAGGCTGAGGCAGGAGAAT	540
Sbjct	481	GCTGGGCGTGGTGGCACACGCCTGTAATCCCAGCTAGTCAGGAGGCTGAGGCAGGAGAAT	540
Query	541	ATCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCAAGATTACATCACTGCACTCCAGCC	600
Sbjct	541	ATCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCAAGATTACATCACTGCACTCCAGCC	600
Query	601	TGGTGACAGAGCGAGACTCCGACT	624
Sbjct	601	TGGTGACAGAGCGAGACTCCGACT	624

PATENT SEQUENCE ALIGNMENT

Query	481	CTATTAAGTGACTGATGTCAACATTAGTTACATGGCAAACATAAGAGGCATTATACATTT	540
Sbjct	481	CTATTAAGTGACTGATGTCAACATTAGTTACATGGCAAACATAAGAGGCATTATACATTT	540
Query	541	TTAAACACACTAACATATAACTGTAGATAATGTAAGGTTTATTTATATGCATATTTTCAT	600
Sbjct	541	TTAAACACACTAACATATAACTGTAGATAATGTAAGGTTTATTTATATGCATATTTTCAT	600
Query	601	AGtataatgtaaatgtttaaatataaaaaagggtttttaaacacttttaatttttatcttt	660
Sbjct	601	AGTATATTTAAATGTTTAAATATAAAAAAGGTTTTTAAACACTTTTAATTTTTATCTTT	660
Query	661	gatttttttttATTGATATCTCTTTCCAGGCTACTAATAAAATTGCCAGAACTAACTATC	720
Sbjct	661	GATTTTTTTTATTGATATCTCTTTCCAGGCTACTAATAAAATTGCCAGAACTAACTATC	720
Query	721	AGGTAAAGGTTAAGGCATCAATTGACAAGTAAGTTTTCTAATTTTCGTTTTGAATTACAAT	780
Sbjct	721	AGGTAAAGGTTAAGGCATCAATTGACAAGTAAGTTTTCTAATTTTCGTTTTGAATTACAAT	780
Query	781	TCCAAATGTAAGACTTTTAAAAATGAATGGCCTTTATTTTATAGAATAATTTTGACCTTT	840
Sbjct	781	TCCAAATGTAAGACTTTTAAAAATGAATGGCCTTTATTTTATAGAATAATTTTGACCTTT	840
Query	841	TAAATTTACTTATCTAACATTATATAATGAATGTACTTCAAATATTTGACTTTGAAGTCA	900
Sbjct	841	TAAATTTACTTATCTAACATTATATAATGAATGTACTTCAAATATTTGACTTTGAAGTCA	900
Query	901	ACATTAACAAATTCATGGATCCTAATTAATTTTACTATAAACTGGAATCATTATTAC	960
Sbjct	901	ACATTAACAAATTCATGGATCCTAATTAATTTTACTATAAACTGGAATCATTATTAC	960
Query	961	TTCCTT 966	
Sbjct	961	TTCCTT 966	

Sequence 1351 matched with Sequence 452

Query= Sequence ID 1351
Length=725

SEQ ID NO: 452

ALIGNMENTS

Identities = 725/725 (100%), Gaps = 0/725 (0%)

Query	1	tttttttttttttAAAAGAGATGGGTTCTCACTATGTTGCCATAATGTTTATGAGATTA	60
Sbjct	1	TTTTTTTTTTTTTAAAAGAGATGGGTTCTCACTATGTTGCCATAATGTTTATGAGATTA	60
Query	61	AGTTCATCTTTTTTATCTGAGTAGTATTTTATTGTATGAATATACCACCATTTATTTATC	120
Sbjct	61	AGTTCATCTTTTTTATCTGAGTAGTATTTTATTGTATGAATATACCACCATTTATTTATC	120
Query	121	TGTTGGTTATTTCCAGTTTTGGGCTATAATCCAAAATGCTTTTTTCAAACAATAGGCTAT	180
Sbjct	121	TGTTGGTTATTTCCAGTTTTGGGCTATAATCCAAAATGCTTTTTTCAAACAATAGGCTAT	180
Query	181	ATATCATTAATGTCCGTTTATCAGCAGtataaaatatcttaccataaatattaataaaag	240
Sbjct	181	ATATCATTAATGTCCGTTTATCAGCAGTATAAAATATCTTACCATAAATATTAATAAAAG	240
Query	241	aagcattcatatataaaatatagatatTTCAAACCCTACAGAGGGCCTTTTAATGATTAA	300
Sbjct	241	AAGCATTATATATAAAATATAGATATTCAAACCCTACAGAGGGCCTTTTAATGATTAA	300
Query	301	ATATTTTGTCTTACAAAAAGGTCCAGGTAATTACACCCATGAGGTAAACCTGCCTTAGT	360
Sbjct	301	ATATTTTGTCTTACAAAAAGGTCCAGGTAATTACACCCATGAGGTAAACCTGCCTTAGT	360
Query	361	GCAGGACTTAAAATAAGGCTTCTCCTGCCATCTCTCTCCATTTGTAGAATGTGAAATTCT	420
Sbjct	361	GCAGGACTTAAAATAAGGCTTCTCCTGCCATCTCTCTCCATTTGTAGAATGTGAAATTCT	420
Query	421	TTAAAATGCATCCTATATTAGGAATACTATAGCTGTGCACTGGTGTTTGTCTCTTCTTT	480
Sbjct	421	TTAAAATGCATCCTATATTAGGAATACTATAGCTGTGCACTGGTGTTTGTCTCTTCTTT	480

PATENT SEQUENCE ALIGNMENT

Query	481	AAACTCGGGACCGTATATATCTGCTCAAATTGCCCAAGTATACATATGCTGCACTCCATC	540
Sbjct	481	AAACTCGGGACCGTATATATCTGCTCAAATTGCCCAAGTATACATATGCTGCACTCCATC	540
Query	541	AAGTGTCAAGGCCACATTCTATCAGCACAGCGTGACTGCCTATCAGTGACAATATAAGTGA	600
Sbjct	541	AAGTGTCAAGGCCACATTCTATCAGCACAGCGTGACTGCCTATCAGTGACAATATAAGTGA	600
Query	601	GCTCTATTTGGATCCCTCTTACCCTACCTTTTATATTTATGACAGCATTATCATAAAACT	660
Sbjct	601	GCTCTATTTGGATCCCTCTTACCCTACCTTTTATATTTATGACAGCATTATCATAAAACT	660
Query	661	CCAATATTCTTCAATAACTTACATGTTTGTGTAGGATAAAATTATTACCCTCAATGAAC	720
Sbjct	661	CCAATATTCTTCAATAACTTACATGTTTGTGTAGGATAAAATTATTACCCTCAATGAAC	720
Query	721	TACAT	725
Sbjct	721	TACAT	725

Sequence 1352 matched with Sequence 453

Query= Sequence ID 1352
Length=715

SEQ ID NO: 453

ALIGNMENTS

Identities = 715/715 (100%), Gaps = 0/715 (0%)

Query	1	ACCAGCTTCTTCACAGGTTCCACGAGTCATGTCAACACAGCGTGTGCTAACACATCAAC	60
Sbjct	1	ACCAGCTTCTTCACAGGTTCCACGAGTCATGTCAACACAGCGTGTGCTAACACATCAAC	60
Query	61	ACAGACAATGGGTCCACGTCCTGCAGCTGCAGCCGCTGCAGCTACTCCTGCTGTCCGCAC	120
Sbjct	61	ACAGACAATGGGTCCACGTCCTGCAGCTGCAGCCGCTGCAGCTACTCCTGCTGTCCGCAC	120
Query	121	CGTTCCACAGTATAAATATGCTGCAGGAGTTCGCAATCCTCAGCAACATCTTAATGCACA	180
Sbjct	121	CGTTCCACAGTATAAATATGCTGCAGGAGTTCGCAATCCTCAGCAACATCTTAATGCACA	180
Query	181	GCCACAAGTTACAATGCAACAGCCTGCTGTTTCATGTACAAGGTCAGGAACCTTTGACTGC	240
Sbjct	181	GCCACAAGTTACAATGCAACAGCCTGCTGTTTCATGTACAAGGTCAGGAACCTTTGACTGC	240
Query	241	TTCCATGTTGGCATCTGCCCCTCCTCAAGAGCAAAAGCAAATGTTGGGTGAACGGCTGTT	300
Sbjct	241	TTCCATGTTGGCATCTGCCCCTCCTCAAGAGCAAAAGCAAATGTTGGGTGAACGGCTGTT	300
Query	301	TCCTCTTATTCAAGCCATGCACCCTACTCTTGCTGGTAAAATCACTGGCATGTTGTTGGA	360
Sbjct	301	TCCTCTTATTCAAGCCATGCACCCTACTCTTGCTGGTAAAATCACTGGCATGTTGTTGGA	360
Query	361	GATTGATAATTCAGAACTTCTTCATATGCTCGAGTCTCCAGAGTCACTCCGTTCTAAGGT	420
Sbjct	361	GATTGATAATTCAGAACTTCTTCATATGCTCGAGTCTCCAGAGTCACTCCGTTCTAAGGT	420
Query	421	TGATGAAGCTGTAGCTGTACTACAAGCCCACCAAGCTAAAGAGGCTGCCAGAAAGCAGT	480
Sbjct	421	TGATGAAGCTGTAGCTGTACTACAAGCCCACCAAGCTAAAGAGGCTGCCAGAAAGCAGT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TAACAGTGCCACCGGTGTTCCAACGTGTTTAAAATTGATCAGGGACCATGAAAAGAACTT	540
Sbjct	481	TAACAGTGCCACCGGTGTTCCAACGTGTTTAAAATTGATCAGGGACCATGAAAAGAACTT	540
Query	541	GTGCTTCACCGAAGaaaaatatctaaacatcgaaaaacttaaataattatggaaaaaaaaac	600
Sbjct	541	GTGCTTCACCGAAGAAAAATATCTAAACATCGAAAAACTTAAATATTATGAAAAAAAAAC	600
Query	601	attgcaaaatataaaataaataaaaaaaggaaaggaaaCTTTGAACCTTATGTACCGAGC	660
Sbjct	601	ATTGCAAAATATAAAATAAATAAAAAAAGGAAAGGAACTTTGAACCTTATGTACCGAGC	660
Query	661	AAATGCCAGGTCTAGCAAACATAATGCTAGTCCTAGATTACTTATTGATTTAAAA	715
Sbjct	661	AAATGCCAGGTCTAGCAAACATAATGCTAGTCCTAGATTACTTATTGATTTAAAA	715

Sequence 1353 matched with Sequence 454

Query= Sequence ID 1353
Length=573

SEQ ID NO: 454

ALIGNMENTS

Identities = 573/573 (100%), Gaps = 0/573 (0%)

Query	1	ACATTCTGAAAAAGGCAAAAGGGAGGAAGAACTGATTAGTGGTTAGCCCAGGGTTAGAGT	60
Sbjct	1	ACATTCTGAAAAAGGCAAAAGGGAGGAAGAACTGATTAGTGGTTAGCCCAGGGTTAGAGT	60
Query	61	TGGGGAGAGGATATAATGAGGGAACCTTTTGTGGATTCTGTACCATGATTATGATTACACA	120
Sbjct	61	TGGGGAGAGGATATAATGAGGGAACCTTTTGTGGATTCTGTACCATGATTATGATTACACA	120
Query	121	AACCTATGCATACATTGAAACACATAGAACTATACGTTGAAAAAAGTGAATCTGCCTGTA	180
Sbjct	121	AACCTATGCATACATTGAAACACATAGAACTATACGTTGAAAAAAGTGAATCTGCCTGTA	180
Query	181	TGTaaattttaaagaaaaatatttttttaaaaaaaCAGATGCTTCTTAACACATTATCAT	240
Sbjct	181	TGTAAATTTAAAAGAAAAATATTTTTTTAAAAAAACAGATGCTTCTTAACACATTATCAT	240
Query	241	CTATGTCAGTTTAACAGTTAGTAGACTTAGGCCAGGTGTCATGGCTCACTCCTGTAATCC	300
Sbjct	241	CTATGTCAGTTTAACAGTTAGTAGACTTAGGCCAGGTGTCATGGCTCACTCCTGTAATCC	300
Query	301	CAGTGCTTTGGGAGTCTGAGGTGGGACGATCTCTTGAGACTAGGAGGGAGTTTGAGACAA	360
Sbjct	301	CAGTGCTTTGGGAGTCTGAGGTGGGACGATCTCTTGAGACTAGGAGGGAGTTTGAGACAA	360
Query	361	ACCTAGGCAATGTAATGAGACTCTTTCTCTACAAAAAATTTTAAAGTTATCTGGACATGG	420
Sbjct	361	ACCTAGGCAATGTAATGAGACTCTTTCTCTACAAAAAATTTTAAAGTTATCTGGACATGG	420
Query	421	TGGTGCCTGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGTGGGAGGATTCCTTGAGCCC	480
Sbjct	421	TGGTGCCTGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGTGGGAGGATTCCTTGAGCCC	480

PATENT SEQUENCE ALIGNMENT

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Query  481  AGAAGTTCAAGGCTACAGTGTGCTATGATAGAGCCACTGCACTCCAGCCTGGGCAACCAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGAAGTTCAAGGCTACAGTGTGCTATGATAGAGCCACTGCACTCCAGCCTGGGCAACCAG  540

Query  541  GTGAGACCTTGTCTCTAAAATGAATAAAATAAAT  573
          ||||||||||||||||||||||||||||
Sbjct  541  GTGAGACCTTGTCTCTAAAATGAATAAAATAAAT  573
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Sequence 1355 matched with Sequence 455

Query= Sequence ID 1355

Length=498

SEQ ID NO: 455

ALIGNMENTS

Identities = 498/498 (100%), Gaps = 0/498 (0%)

Query	1	TGGTCTTTCACCCAGCCAGGGAGAAGGTTCTTCGCTCAGTATGAAGAAAAGCAACCCAAA	60
Sbjct	1	TGGTCTTTCACCCAGCCAGGGAGAAGGTTCTTCGCTCAGTATGAAGAAAAGCAACCCAAA	60
Query	61	ACTCTCAATCTGATTTGTTTTTGTATGTCGATGCCCTGTAGTTTGAAAGTGAAGTAAA	120
Sbjct	61	ACTCTCAATCTGATTTGTTTTTGTATGTCGATGCCCTGTAGTTTGAAAGTGAAGTAAA	120
Query	121	GATTTAGAAATTCACCTAAGTCCAAAGGAAAACACGTGGTTTTTAAAGCCATTAGGTaaaa	180
Sbjct	121	GATTTAGAAATTCACCTAAGTCCAAAGGAAAACACGTGGTTTTTAAAGCCATTAGGTAAAA	180
Query	181	aaaGTTCTCAATAAAGGCATTACAATTTTTTAGGTTTAGAAAGATGGACTTTTCTGATAA	240
Sbjct	181	AAAGTTCTCAATAAAGGCATTACAATTTTTTAGGTTTAGAAAGATGGACTTTTCTGATAA	240
Query	241	ATCTTGGCAGACATCTaaaaaaaaaCCATATTTTTTACAAGAAAATGCAAGTTACTttt	300
Sbjct	241	ATCTTGGCAGACATCTAAAAAAAAAACCATATTTTTTACAAGAAAATGCAAGTTACTTTT	300
Query	301	tttGGAAATAATACTCACTGATTATGGATAAAATGGAATATTTTCAGATACTATATTGGC	360
Sbjct	301	TTTGGAAATAATACTCACTGATTATGGATAAAATGGAATATTTTCAGATACTATATTGGC	360
Query	361	TGTTTCAAAATAGTACTATTCTTTAACTTGTAATTTTGCTAAGTTATTTGTCTTTGTT	420
Sbjct	361	TGTTTCAAAATAGTACTATTCTTTAACTTGTAATTTTGCTAAGTTATTTGTCTTTGTT	420
Query	421	GTATCTATAAATATGTAAAAAATATTTAAATAGATGTACCTGTTTTGCTTTCACACTTAA	480
Sbjct	421	GTATCTATAAATATGTAAAAAATATTTAAATAGATGTACCTGTTTTGCTTTCACACTTAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TAAAAAAAtttttttttGT	498
Sbjct	481	TAAAAAATTTTTTTTGT	498

Sequence 1359 matched with Sequence 456

Query= Sequence ID 1359
Length=732

SEQ ID NO: 456

ALIGNMENTS

Identities = 732/732 (100%), Gaps = 0/732 (0%)

Query	1	CGGGATCCCTAGTATAACACATTCAGTGTTC	60
Sbjct	1	CGGGATCCCTAGTATAACACATTCAGTGTTC	60
Query	61	TGATGTGGCTTTGAAGAACTTTGCCAAATACTTTCTTCACCAATCTCATGAGGAGAGGGA	120
Sbjct	61	TGATGTGGCTTTGAAGAACTTTGCCAAATACTTTCTTCACCAATCTCATGAGGAGAGGGA	120
Query	121	ACATGCTGAGAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGA	180
Sbjct	121	ACATGCTGAGAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGA	180
Query	181	TATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATT	240
Sbjct	181	TATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATT	240
Query	241	ACATTTGGAAAAAATGTGAATCAGTCACTACTGGAAGTGCACAAACTGGCCACTGACAAA	300
Sbjct	241	ACATTTGGAAAAAATGTGAATCAGTCACTACTGGAAGTGCACAAACTGGCCACTGACAAA	300
Query	301	AATGACCCCCATGTGAGTATTGGAACCCCAGGAAATAAATGGAGGAAATCATTTGCCTTA	360
Sbjct	301	AATGACCCCCATGTGAGTATTGGAACCCCAGGAAATAAATGGAGGAAATCATTTGCCTTA	360
Query	361	GGGATTGGGAAAGCTGCCCACTAACTGTCTTCCCCATTGTTTTGCAGTTGTGTGACTTCA	420
Sbjct	361	GGGATTGGGAAAGCTGCCCACTAACTGTCTTCCCCATTGTTTTGCAGTTGTGTGACTTCA	420
Query	421	TTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGAATTGGGTGACCACGTGA	480
Sbjct	421	TTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGAATTGGGTGACCACGTGA	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 CCAACTTGCGCAAGATGGGAGCGCCCGAATCTGGCTTGGCGGAATATCTCTTTGACAAGC 540
          |||
Sbjct 481 CCAACTTGCGCAAGATGGGAGCGCCCGAATCTGGCTTGGCGGAATATCTCTTTGACAAGC 540

Query 541 ACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTAATTTCCCATAGCCGTG 600
          |||
Sbjct 541 ACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTAATTTCCCATAGCCGTG 600

Query 601 GGGTGA CTTCCTGGTCACCAAGGCAGTGCATGCATGTTGGGGTTTCCTTTACCTTTTCT 660
          |||
Sbjct 601 GGGTGA CTTCCTGGTCACCAAGGCAGTGCATGCATGTTGGGGTTTCCTTTACCTTTTCT 660

Query 661 ATAAGTTGTACCAAAACATCCACTTAAGTTCTTTGATTTGTACCATTCCTTCAAATAAAG 720
          |||
Sbjct 661 ATAAGTTGTACCAAAACATCCACTTAAGTTCTTTGATTTGTACCATTCCTTCAAATAAAG 720

Query 721 AAATTTGGTACC 732
          |||
Sbjct 721 AAATTTGGTACC 732
```

Sequence 1360 matched with Sequence 457

Query= Sequence ID 1360

Length=465

SEQ ID NO: 457

ALIGNMENTS

Identities = 465/465 (100%), Gaps = 0/465 (0%)

Query	1	TGCGCAGACCAGACTTCGCTCGTACTCGTGCGCCTCGCTTCGCTTTTCCTCCGCAACCAT	60
Sbjct	1	TGCGCAGACCAGACTTCGCTCGTACTCGTGCGCCTCGCTTCGCTTTTCCTCCGCAACCAT	60
Query	61	GTCTGACAAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAAACTGAAGAAGAC	120
Sbjct	61	GTCTGACAAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAAACTGAAGAAGAC	120
Query	121	AGAGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAACGATTGAACAGGAGAAGCAAGC	180
Sbjct	121	AGAGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAACGATTGAACAGGAGAAGCAAGC	180
Query	181	AGGCGAATCGTAATGAGGCGTGCGCCGCCAATATGCACTGTACATTCCACAAGCATTGCC	240
Sbjct	181	AGGCGAATCGTAATGAGGCGTGCGCCGCCAATATGCACTGTACATTCCACAAGCATTGCC	240
Query	241	TTCTTATTTTACTTCTTTTAGCTGTTTAACTTTGTAAGATGCAAAGAGGTTGGATCAAGT	300
Sbjct	241	TTCTTATTTTACTTCTTTTAGCTGTTTAACTTTGTAAGATGCAAAGAGGTTGGATCAAGT	300
Query	301	TTAAATGACTGTGCTGCCCCTTTCACATCAAAGAACTACTGACAACGAAGGCCGCGCCTG	360
Sbjct	301	TTAAATGACTGTGCTGCCCCTTTCACATCAAAGAACTACTGACAACGAAGGCCGCGCCTG	360
Query	361	CCTTTCCCATCTGTCTATCTATCTGGCTGGCAGGGAAGGAAAGAACTTGCATGTTGGTGA	420
Sbjct	361	CCTTTCCCATCTGTCTATCTATCTGGCTGGCAGGGAAGGAAAGAACTTGCATGTTGGTGA	420
Query	421	AGGAAGAAGTGGGGTGGAAGAAGTGGGGTGGGACGACAGTGAAAT	465
Sbjct	421	AGGAAGAAGTGGGGTGGAAGAAGTGGGGTGGGACGACAGTGAAAT	465

Sequence 1361 matched with Sequence 458

Query= Sequence ID 1361

Length=788

SEQ ID NO: 458

ALIGNMENTS

Identities = 788/788 (100%), Gaps = 0/788 (0%)

Query	1	TATAAATACACTCCGGGATGATTTACCCCCGGAGGTCAGCTAGTAAAATACATGAGTAGA	60
Sbjct	1	TATAAATACACTCCGGGATGATTTACCCCCGGAGGTCAGCTAGTAAAATACATGAGTAGA	60
Query	61	ATTCCTTAAAGTATGTGATAATTGCTCATCACTATCCAAGTGTGACATAAATCATAAAAA	120
Sbjct	61	ATTCCTTAAAGTATGTGATAATTGCTCATCACTATCCAAGTGTGACATAAATCATAAAAA	120
Query	121	GAATTGACAAAATCAGGGTCGCAAAGAGAATTGaaaaaaTCTGTCACAACCAAAATTTA	180
Sbjct	121	GAATTGACAAAATCAGGGTCGCAAAGAGAATTGAAAAAATCTGTCACAACCAAAATTTA	180
Query	181	AATTGACCTCTGTCCTAGAGTATGAGAGCCCACTGAACAGAAAAACCAGATAAATCTTT	240
Sbjct	181	AATTGACCTCTGTCCTAGAGTATGAGAGCCCACTGAACAGAAAAACCAGATAAATCTTT	240
Query	241	TATAAAATATTCATTTGCAGCCCCATTAACGTTGCTTGTCACCCCACCTCCCCATGTCCT	300
Sbjct	241	TATAAAATATTCATTTGCAGCCCCATTAACGTTGCTTGTCACCCCACCTCCCCATGTCCT	300
Query	301	TGGACAAACTGAATGTATAGTAACATCATCCCAGGCCAGGCGCGGTGGCTCATGCCTGTA	360
Sbjct	301	TGGACAAACTGAATGTATAGTAACATCATCCCAGGCCAGGCGCGGTGGCTCATGCCTGTA	360
Query	361	ATCCCAGCACTTTGTGAGGCTAAGGCAGGCAGATCAGGAGGTCAGGAGTTCAGGACCAGC	420
Sbjct	361	ATCCCAGCACTTTGTGAGGCTAAGGCAGGCAGATCAGGAGGTCAGGAGTTCAGGACCAGC	420
Query	421	CTGGCCAAAAAGGTGAAACTCCGTCTCTACTAACAATACAAAAATTAGCTGGGTGCGGTA	480
Sbjct	421	CTGGCCAAAAAGGTGAAACTCCGTCTCTACTAACAATACAAAAATTAGCTGGGTGCGGTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	GTAGGCGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTCAAACCCGG	540
Sbjct	481	GTAGGCGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTCAAACCCGG	540
Query	541	AAGGTGGAGGTTGCAGTGAGCTGAGATCGTGCCACTGCACTCCAGCCTGGGTGACAGAGC	600
Sbjct	541	AAGGTGGAGGTTGCAGTGAGCTGAGATCGTGCCACTGCACTCCAGCCTGGGTGACAGAGC	600
Query	601	AAGACTCTGTCTCGGGAGGGGGGTGGCGGAGATAAAGAAATAACATCATCTTATACTGT	660
Sbjct	601	AAGACTCTGTCTCGGGAGGGGGGTGGCGGAGATAAAGAAATAACATCATCTTATACTGT	660
Query	661	CAAGCTCAAGGTGTCTGCAGCCTTATCTTCAGGGGAAGTTGTGTCTTCTCAGGGAAGAT	720
Sbjct	661	CAAGCTCAAGGTGTCTGCAGCCTTATCTTCAGGGGAAGTTGTGTCTTCTCAGGGAAGAT	720
Query	721	ACAGATTTCAATTTAGAGCAAGACAGAGAGAAGTTACATTACAGAGAGGAAAATGCAGTAG	780
Sbjct	721	ACAGATTTCAATTTAGAGCAAGACAGAGAGAAGTTACATTACAGAGAGGAAAATGCAGTAG	780
Query	781	TCTAACTG	788
Sbjct	781	TCTAACTG	788

Sequence 1364 matched with Sequence 459

Query= Sequence ID 1364
Length=423

SEQ ID NO: 459

ALIGNMENTS

Identities = 423/423 (100%), Gaps = 0/423 (0%)

Query	1	GCGGCCGCGCTCTTTTCAATTTTAAAAAGAAGTTTGTTCATTTCAGTAATTTCTGC	60
Sbjct	1	GCGGCCGCGCTCTTTTCAATTTTAAAAAGAAGTTTGTTCATTTCAGTAATTTCTGC	60
Query	61	TTTGATCTTCCTTATGTCCTCCTATTGAGTTGATCAGCTTTCTTTATTCTTGCCTTTTCT	120
Sbjct	61	TTTGATCTTCCTTATGTCCTCCTATTGAGTTGATCAGCTTTCTTTATTCTTGCCTTTTCT	120
Query	121	CCTCTGTGTGCCCTTTCTATTAACGTATTTACCCTTAGGCTGGGCACAATGGCTGATGCC	180
Sbjct	121	CCTCTGTGTGCCCTTTCTATTAACGTATTTACCCTTAGGCTGGGCACAATGGCTGATGCC	180
Query	181	TGTAATCCCTGCACTTTGGGAGGCCGAGGCAGGTGGATCACCTAAGGTCAGGAGTTCAAG	240
Sbjct	181	TGTAATCCCTGCACTTTGGGAGGCCGAGGCAGGTGGATCACCTAAGGTCAGGAGTTCAAG	240
Query	241	ACCAGCCTGGCCAACATGGTGAAACCTGGTCTCTACTAAAAACACAAAAATTAGCCAGGC	300
Sbjct	241	ACCAGCCTGGCCAACATGGTGAAACCTGGTCTCTACTAAAAACACAAAAATTAGCCAGGC	300
Query	301	ATGGTGGTGTGCACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGA	360
Sbjct	301	ATGGTGGTGTGCACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGA	360
Query	361	ACCTGGGAGGCGGAGATTGTGCCAAAGCACTCCAGCCTGGGCAACAAAATGAGACTTTGT	420
Sbjct	361	ACCTGGGAGGCGGAGATTGTGCCAAAGCACTCCAGCCTGGGCAACAAAATGAGACTTTGT	420
Query	421	GTC	423
Sbjct	421	GTC	423

Sequence 1365 matched with Sequence 460

Query= Sequence ID 1365
Length=231

SEQ ID NO: 460

ALIGNMENTS

Identities = 231/231 (100%), Gaps = 0/231 (0%)

Query	1	CACCAGGCTGTCTTCAGATACTTCATACAGAAATGAGCCTCCCTGTGGGGTCCTCTTCCC	60
Sbjct	1	CACCAGGCTGTCTTCAGATACTTCATACAGAAATGAGCCTCCCTGTGGGGTCCTCTTCCC	60
Query	61	TCCTTCAGCCTGTCCATCAACACAGCATTGCGGGATCCTTACCATGGCATCCAGCCCTGG	120
Sbjct	61	TCCTTCAGCCTGTCCATCAACACAGCATTGCGGGATCCTTACCATGGCATCCAGCCCTGG	120
Query	121	AGATGCTTCAGGAAAGTTGCAGGTCCATGCTGCAGGACAGGCTCAGATCAGCAGAGACGC	180
Sbjct	121	AGATGCTTCAGGAAAGTTGCAGGTCCATGCTGCAGGACAGGCTCAGATCAGCAGAGACGC	180
Query	181	ATCTCACATCGGGCTGTGAAATTCAAGTTGAGCTGCAATTGGCAATGAGAA	231
Sbjct	181	ATCTCACATCGGGCTGTGAAATTCAAGTTGAGCTGCAATTGGCAATGAGAA	231

Sequence 1366 matched with Sequence 461

Query= Sequence ID 1366
Length=687

SEQ ID NO: 461

ALIGNMENTS

Identities = 687/687 (100%), Gaps = 0/687 (0%)

Query	1	GTTATTCACTGAGACCGTGCCCCGGTTATGAGGTTGTACCAGAAAGCAAGTATTCACTAT	60
Sbjct	1	GTTATTCACTGAGACCGTGCCCCGGTTATGAGGTTGTACCAGAAAGCAAGTATTCACTAT	60
Query	61	GCACACTATTACCGCTCACCTAGCATTGAAGCCAGCCTGTAGCCTGAAAGCCTTTGCT	120
Sbjct	61	GCACACTATTACCGCTCACCTAGCATTGAAGCCAGCCTGTAGCCTGAAAGCCTTTGCT	120
Query	121	TTGAGGGCAGGTCTTTCCCCAAAATGCAGACACGAAGGTGCAAAGTGAAGCTGCCAGTCT	180
Sbjct	121	TTGAGGGCAGGTCTTTCCCCAAAATGCAGACACGAAGGTGCAAAGTGAAGCTGCCAGTCT	180
Query	181	TGCAAAAGATGTAACCTGTACGAAGGCCACGAGTGGCAGGGAGAGCTGTCCACATTTG	240
Sbjct	181	TGCAAAAGATGTAACCTGTACGAAGGCCACGAGTGGCAGGGAGAGCTGTCCACATTTG	240
Query	241	CGGAAGTGGCTATGTGAGGACGGGGGAGGCGGGTCCCTTAGAGATGAGACAATCATAAGG	300
Sbjct	241	CGGAAGTGGCTATGTGAGGACGGGGGAGGCGGGTCCCTTAGAGATGAGACAATCATAAGG	300
Query	301	GGAGATATCAGAGAAAATCGTAAGGGGAGCAGATGGTTGTCAAGAGAATAGGCTGACCAT	360
Sbjct	301	GGAGATATCAGAGAAAATCGTAAGGGGAGCAGATGGTTGTCAAGAGAATAGGCTGACCAT	360
Query	361	CGAAGGACTGGCAGAAGCTTTCAGAAAACCACTGGACGGCTGGGCACAGTGGCTTAGGCC	420
Sbjct	361	CGAAGGACTGGCAGAAGCTTTCAGAAAACCACTGGACGGCTGGGCACAGTGGCTTAGGCC	420
Query	421	TGTAATCCCAGCACTTTGGGAGGCTGACGCAGGTGAATCACTTGAGGTCAGGAGTTCCAG	480
Sbjct	421	TGTAATCCCAGCACTTTGGGAGGCTGACGCAGGTGAATCACTTGAGGTCAGGAGTTCCAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	ACCAGCCTGGCCAACATGGTGAAACCCCATCTCTACAGAAAATATAAAAATTAGCCAGGC	540
Sbjct	481	ACCAGCCTGGCCAACATGGTGAAACCCCATCTCTACAGAAAATATAAAAATTAGCCAGGC	540
Query	541	GTGGTGGCACAAGCCTAGAAATCCCAGCTACTTGGGAGGCTGAGGCAGGCGAATGGCTTGA	600
Sbjct	541	GTGGTGGCACAAGCCTAGAAATCCCAGCTACTTGGGAGGCTGAGGCAGGCGAATGGCTTGA	600
Query	601	ACCCAGGAGTCAGAGGCTGCAGTGAGTCGAGATTGTTCCACTGCACTCCAGCCTGGGTGA	660
Sbjct	601	ACCCAGGAGTCAGAGGCTGCAGTGAGTCGAGATTGTTCCACTGCACTCCAGCCTGGGTGA	660
Query	661	CAGTGCAAGACTCCTTCCaaaaaaaaa	687
Sbjct	661	CAGTGCAAGACTCCTTCCAAAAAAAAA	687

Sequence 1367 matched with Sequence 462

Query= Sequence ID 1367
Length=874

SEQ ID NO: 462

ALIGNMENTS

Identities = 874/874 (100%), Gaps = 0/874 (0%)

Query	1	TTCGTGAGTGATGGCGTCCCGGGTTGCTTGCCGGTGCTGGCCGCCGCCGGGAGAGCCCGG	60
Sbjct	1	TTCGTGAGTGATGGCGTCCCGGGTTGCTTGCCGGTGCTGGCCGCCGCCGGGAGAGCCCGG	60
Query	61	GGCAGAGCAGAGGTGCTCATCAGCACTGTAGGCCCGGAAGATTGTGTGGTCCCGTTCCTG	120
Sbjct	61	GGCAGAGCAGAGGTGCTCATCAGCACTGTAGGCCCGGAAGATTGTGTGGTCCCGTTCCTG	120
Query	121	ACCCGGCCTAAGGTCCCTGTCTTGACGCTGGATAGCGGCAACTACCTCTTCTCCACTAGT	180
Sbjct	121	ACCCGGCCTAAGGTCCCTGTCTTGACGCTGGATAGCGGCAACTACCTCTTCTCCACTAGT	180
Query	181	GCAATCTGCCGATAtttttttttGTTATCTGGCTGGGAGCAAGATGACCTCACTAACCAG	240
Sbjct	181	GCAATCTGCCGATATTTTTTTTTGTTATCTGGCTGGGAGCAAGATGACCTCACTAACCAG	240
Query	241	TGGCTGGAATGGGAAGCGACAGAGCTGCAGCCAGCTTTGTCTGCTGCCCTGTACTATTTA	300
Sbjct	241	TGGCTGGAATGGGAAGCGACAGAGCTGCAGCCAGCTTTGTCTGCTGCCCTGTACTATTTA	300
Query	301	GTGGTCCAAGGCAAGAAGGGGGAAGATGTTCTTGGTTCAGTGCGGAGAGCCCTGACTCAC	360
Sbjct	301	GTGGTCCAAGGCAAGAAGGGGGAAGATGTTCTTGGTTCAGTGCGGAGAGCCCTGACTCAC	360
Query	361	ATTGACCACAGCTTGAGTCGTCAGAACTGTCCTTTCCTGGCTGGGGAGACAGAATCTCTA	420
Sbjct	361	ATTGACCACAGCTTGAGTCGTCAGAACTGTCCTTTCCTGGCTGGGGAGACAGAATCTCTA	420
Query	421	GCCGACATTGTTTTGTGGGGAGCCCTATACCCATTACTGCAAGATCCCGCCTACCTCCCT	480
Sbjct	421	GCCGACATTGTTTTGTGGGGAGCCCTATACCCATTACTGCAAGATCCCGCCTACCTCCCT	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 GAGGAGCTGAGTGCCCTGCACAGCTGGTTCCAGACACTGAGTACCCAGGAACCATGTCAG 540
          |||
Sbjct 481 GAGGAGCTGAGTGCCCTGCACAGCTGGTTCCAGACACTGAGTACCCAGGAACCATGTCAG 540

Query 541 CGAGCTGCAGAGACTGTACTGAAACAGCAAGGTGTCCTGGCTCTCCGGCCTTACCTCCAA 600
          |||
Sbjct 541 CGAGCTGCAGAGACTGTACTGAAACAGCAAGGTGTCCTGGCTCTCCGGCCTTACCTCCAA 600

Query 601 AAGCAGCCCCAGCCCAGCCCCGCTGAGGGAAGGGCTGTCACCAATGAGCCTGAGGAGGAG 660
          |||
Sbjct 601 AAGCAGCCCCAGCCCAGCCCCGCTGAGGGAAGGGCTGTCACCAATGAGCCTGAGGAGGAG 660

Query 661 GAGCTGGCTACCCTATCTGAGGAGGAGATTGCTATGGCTGTTACTGCTTGGGAGAANGGC 720
          |||
Sbjct 661 GAGCTGGCTACCCTATCTGAGGAGGAGATTGCTATGGCTGTTACTGCTTGGGAGAANGGC 720

Query 721 CTAGAAAGTTTGGCCCCGCTGCGGCCCCAGCANAATCCAGTGTTGCCTGTGGCTGGAGA 780
          |||
Sbjct 721 CTAGAAAGTTTGGCCCCGCTGCGGCCCCAGCANAATCCAGTGTTGCCTGTGGCTGGAGA 780

Query 781 AAGGAATGTGCTCATCACCAGTGCCCTCCNTTACGTCAACAATGTCCCCACCTTGGGAA 840
          |||
Sbjct 781 AAGGAATGTGCTCATCACCAGTGCCCTCCNTTACGTCAACAATGTCCCCACCTTGGGAA 840

Query 841 CATCATTGGTTGTGTGCTCAGTGCCCGATGTCTT 874
          |||
Sbjct 841 CATCATTGGTTGTGTGCTCAGTGCCCGATGTCTT 874
```

Sequence 1368 matched with Sequence 463

Query= Sequence ID 1368

Length=585

SEQ ID NO: 463

ALIGNMENTS

Identities = 585/585 (100%), Gaps = 0/585 (0%)

Query	1	CAGTGAGCCAAGATCACACCACTGCACTCCAGCCTGGACAACAGAACGAGACTCCATATC	60
Sbjct	1	CAGTGAGCCAAGATCACACCACTGCACTCCAGCCTGGACAACAGAACGAGACTCCATATC	60
Query	61	aaaaaaattaaattaaaatataataaatTTCTTGCCGGGCGCAGTGGCTCACACCTGTAA	120
Sbjct	61	AAAAAAATTAAATTAAATATAATAAATTTCTTGCCGGGCGCAGTGGCTCACACCTGTAA	120
Query	121	TCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAAGTCAGGAGATTGAGACCATCC	180
Sbjct	121	TCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAAGTCAGGAGATTGAGACCATCC	180
Query	181	TGGCTAATACAGTGAAACCCCGTCTCTACTATAAATACAAAAAATTAGCTGGGCATGGTG	240
Sbjct	181	TGGCTAATACAGTGAAACCCCGTCTCTACTATAAATACAAAAAATTAGCTGGGCATGGTG	240
Query	241	GCGGGCGTCTGTAGTCCCAGCTACTCAGGAGTCTGAGGCAGGAGAATGGTGTGAACCCGG	300
Sbjct	241	GCGGGCGTCTGTAGTCCCAGCTACTCAGGAGTCTGAGGCAGGAGAATGGTGTGAACCCGG	300
Query	301	GAGGCGGAGCTTGCAGTGAGCCGAGATCGTGCCACTGCAATCCAGCCTGGGCAGCAGAAC	360
Sbjct	301	GAGGCGGAGCTTGCAGTGAGCCGAGATCGTGCCACTGCAATCCAGCCTGGGCAGCAGAAC	360
Query	361	GAGACTCCATCTCaaataaataaataaataaaatGAATTTTCAGCTAGAAGAGCCTTATTC	420
Sbjct	361	GAGACTCCATCTCAAATAAATAAATAAATAAAATGAATTTTCAGCTAGAAGAGCCTTATTC	420
Query	421	CATTTTCCTTTTATTAAACATCTGGCATAAGTTGGTAAGTATGTGAAGTTTATCATATA	480
Sbjct	421	CATTTTCCTTTTATTAAACATCTGGCATAAGTTGGTAAGTATGTGAAGTTTATCATATA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TTCTTATGCGAATTATTATTTTCGCCtttttttttATAATTCTGTCTGGGATTTGAATAG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTCTTATGCGAATTATTATTTTCGCCTTTTTTTTTATAATTCTGTCTGGGATTTGAATAG  540

Query  541  TAGAGTTTGAATTCAGGAAGGACACCTGTGATAGGACAATAAAAT  585
          |||||||||||||||||||||||||||||||||||||||
Sbjct  541  TAGAGTTTGAATTCAGGAAGGACACCTGTGATAGGACAATAAAAT  585
```


Sequence 1369 matched with Sequence 464

Query= Sequence ID 1369
Length=305

SEQ ID NO: 464

ALIGNMENTS

Identities = 305/305 (100%), Gaps = 0/305 (0%)

Query	1	CTGATTGCAAAAACATTACAACCTCAGTACTGCGGCTTTCATTCAAATAGGTTATATGTAT	60
Sbjct	1	CTGATTGCAAAAACATTACAACCTCAGTACTGCGGCTTTCATTCAAATAGGTTATATGTAT	60
Query	61	AAACTGAGGTTCAACAATATTGTATTTGAGATGGGAAAGTTAAAGAAATGCAATAATGTA	120
Sbjct	61	AAACTGAGGTTCAACAATATTGTATTTGAGATGGGAAAGTTAAAGAAATGCAATAATGTA	120
Query	121	AATAATACTTAAGAAAATAAGATCTCAGGAAACTGTGTATACTCTGTACTTTTATGCAAC	180
Sbjct	121	AATAATACTTAAGAAAATAAGATCTCAGGAAACTGTGTATACTCTGTACTTTTATGCAAC	180
Query	181	TTTATCAGATCATTTTCAGTATATGCATCAAGGATATAGTGTATATGACATGAACTTTGAG	240
Sbjct	181	TTTATCAGATCATTTTCAGTATATGCATCAAGGATATAGTGTATATGACATGAACTTTGAG	240
Query	241	TGCAAAAACCTGTACTATGTACCTTTTGTTTATTTTGCTGTCAACATCTAAATAAAGGttt	300
Sbjct	241	TGCAAAAACCTGTACTATGTACCTTTTGTTTATTTTGCTGTCAACATCTAAATAAAGGTTT	300
Query	301	ttttG 305	
Sbjct	301	TTTTG 305	

Sequence 1370 matched with Sequence 465

Query= Sequence ID 1370

Length=422

SEQ ID NO: 465

ALIGNMENTS

Identities = 422/422 (100%), Gaps = 0/422 (0%)

Query	1	CGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAA	60
Sbjct	1	CGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAA	60
Query	61	TGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTT	120
Sbjct	61	TGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTT	120
Query	121	GAAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATG	180
Sbjct	121	GAAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATG	180
Query	181	ACGCAGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAA	240
Sbjct	181	ACGCAGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAA	240
Query	241	ATGGAAAGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTTGAAG	300
Sbjct	241	ATGGAAAGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTTGAAG	300
Query	301	TGGAAAACCTGGAAGACAGAAGTACGGGAAGGCgaagaaaagaatagataagataggga	360
Sbjct	301	TGGAAAACCTGGAAGACAGAAGTACGGGAAGGCGAAGAAAAGAATAGATAAGATAGGGAAA	360
Query	361	ttagaagataaaaaacatacttttagaagaaaaaagataaaTTTAAACCTGAAAAGTAGGA	420
Sbjct	361	TTAGAAGATAAAAAACATACTTTTAGAAGAAAAAAGATAAATTTAAACCTGAAAAGTAGGA	420
Query	421	AG 422	
Sbjct	421	AG 422	

Sequence 1371 matched with Sequence 466

Query= Sequence ID 1371
Length=833

SEQ ID NO: 466

ALIGNMENTS

Identities = 833/833 (100%), Gaps = 0/833 (0%)

Query	1	GTCCAGNAGAAAAGTTCAGTGACTTGTCCAGAGCTGCAGGTCTTAAGAGGCTGAAATCTCG	60
Sbjct	1	GTCCAGNAGAAAAGTTCAGTGACTTGTCCAGAGCTGCAGGTCTTAAGAGGCTGAAATCTCG	60
Query	61	CCTCTGCCTCGAGGCTGCGGTTCCACTGACCCATACTACTTGCCTTCAGGAAAGAGAAAT	120
Sbjct	61	CCTCTGCCTCGAGGCTGCGGTTCCACTGACCCATACTACTTGCCTTCAGGAAAGAGAAAT	120
Query	121	GGTGTAGGAAGGCTGTGGATGAAGACGCTTACATTCATGAAGGATTTGGATAGGCGAACA	180
Sbjct	121	GGTGTAGGAAGGCTGTGGATGAAGACGCTTACATTCATGAAGGATTTGGATAGGCGAACA	180
Query	181	TGAGCTTTTCCACCAAATTTTCAAGATTTTAAGAAATGCCTTAAATTATTTCTTAAAAATC	240
Sbjct	181	TGAGCTTTTCCACCAAATTTTCAAGATTTTAAGAAATGCCTTAAATTATTTCTTAAAAATC	240
Query	241	AATTTGGGGCAGACGAGAAGTTCTGATAATAGTTTTTAGGGAACATGATAAAATTCTGAC	300
Sbjct	241	AATTTGGGGCAGACGAGAAGTTCTGATAATAGTTTTTAGGGAACATGATAAAATTCTGAC	300
Query	301	CTTAGAAGTGGTATACCAGTTTGAGAAGAAGAACAAGCTATAAACGGTGTAGATAACATT	360
Sbjct	301	CTTAGAAGTGGTATACCAGTTTGAGAAGAAGAACAAGCTATAAACGGTGTAGATAACATT	360
Query	361	CACGGCTATTTAAGAAAGAGTTACTAAGGGAAACCAGAATGACTTAAGAGTGTTACTCTT	420
Sbjct	361	CACGGCTATTTAAGAAAGAGTTACTAAGGGAAACCAGAATGACTTAAGAGTGTTACTCTT	420
Query	421	CTTTTTCTGAGAGAACAATAGCATCATCTCAGAAAGCCTTTCATGCCATTAATAGGTAAG	480
Sbjct	421	CTTTTTCTGAGAGAACAATAGCATCATCTCAGAAAGCCTTTCATGCCATTAATAGGTAAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	AATCTGGGCTTCTTGGACCATGGGTTAGACTTTCTTACAAAACCATAATATGCATTTTCCT	540
Sbjct	481	AATCTGGGCTTCTTGGACCATGGGTTAGACTTTCTTACAAAACCATAATATGCATTTTCCT	540
Query	541	AGCAAAATTTATGCTATTACATTTCTTATCTCAACAAAGACTGGTAAATTCAGTACTTA	600
Sbjct	541	AGCAAAATTTATGCTATTACATTTCTTATCTCAACAAAGACTGGTAAATTCAGTACTTA	600
Query	601	TTCCTCAATTTTCCTACCCTTAAAATGGGGATATTCTGCCTCTCCAAGGAATGCTGGGAA	660
Sbjct	601	TTCCTCAATTTTCCTACCCTTAAAATGGGGATATTCTGCCTCTCCAAGGAATGCTGGGAA	660
Query	661	CAAGCAAGTCCTCATGTTAGGGGTCTTTGAGTTTTTCATGGAAGTTTAGGTTATTTATATG	720
Sbjct	661	CAAGCAAGTCCTCATGTTAGGGGTCTTTGAGTTTTTCATGGAAGTTTAGGTTATTTATATG	720
Query	721	ATGACATAGTTGTCAACTTACTTTTCAGGATGGACTTTTCTTTTGTGAGTTTGTGACCTAA	780
Sbjct	721	ATGACATAGTTGTCAACTTACTTTTCAGGATGGACTTTTCTTTTGTGAGTTTGTGACCTAA	780
Query	781	ATACAATAGTTGTTATGCATGTCCAGTTTATGGAAGTACCACTGCAATANCAG	833
Sbjct	781	ATACAATAGTTGTTATGCATGTCCAGTTTATGGAAGTACCACTGCAATANCAG	833

Sequence 1372 matched with Sequence 467

Query= Sequence ID 1372

Length=594

SEQ ID NO: 467

ALIGNMENTS

Identities = 594/594 (100%), Gaps = 0/594 (0%)

Query	1	CAGTGCAGCCAAGTATCACACCACTGCACTCCAGTCCTGGACAACAGAAACGANTACTCC	60
Sbjct	1	CAGTGCAGCCAAGTATCACACCACTGCACTCCAGTCCTGGACAACAGAAACGANTACTCC	60
Query	61	ATATCaaaaaaaTTAAATTAAANGATAATAAATTTCTTGCCGGGCGCAGTGGCTCACACC	120
Sbjct	61	ATATCAAAAAAATTAAATTAAANGATAATAAATTTCTTGCCGGGCGCAGTGGCTCACACC	120
Query	121	TGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAAGTCAGGAGATTGAGAC	180
Sbjct	121	TGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAAGTCAGGAGATTGAGAC	180
Query	181	CATCCTGGCTAATACAGTGAAATCCCCGTCTCTACTATAAATACAAAAAATTAGCTGGGC	240
Sbjct	181	CATCCTGGCTAATACAGTGAAATCCCCGTCTCTACTATAAATACAAAAAATTAGCTGGGC	240
Query	241	ATGGTGGCGGGCGTCTGTAGTCCCAGCTACTCAGGAGTCTGAGGCAGGAGAATGGTGTGA	300
Sbjct	241	ATGGTGGCGGGCGTCTGTAGTCCCAGCTACTCAGGAGTCTGAGGCAGGAGAATGGTGTGA	300
Query	301	ACCCGGGAGGCGGAGCTTGCACTGAGCCGAGATCGTGCCACTGCAATCCAGCCTGGGCAG	360
Sbjct	301	ACCCGGGAGGCGGAGCTTGCACTGAGCCGAGATCGTGCCACTGCAATCCAGCCTGGGCAG	360
Query	361	CAGAACGAGACTCCATCTCaaataaataaataaataaaatGAATTTTCAGCTAGAAGAGCC	420
Sbjct	361	CAGAACGAGACTCCATCTCAAATAAATAAATAAATAAATGAATTTTCAGCTAGAAGAGCC	420
Query	421	TTATTCCATTTTCCTTTTTATTAAACATCTGGCATAAGTTGGTAAGTATGTGAAGTTTAT	480
Sbjct	421	TTATTCCATTTTCCTTTTTATTAAACATCTGGCATAAGTTGGTAAGTATGTGAAGTTTAT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CATATATTCTTATGCGAATTATTATTTTCGCcttttttttATAATTCTGTCTGGGATTT  540
          |||
Sbjct  481  CATATATTCTTATGCGAATTATTATTTTCGCCTTTTTTTTATAATTCTGTCTGGGATTT  540

Query  541  GAATAGTAGAGTTTGAATTCAGGAAGGACACCTGTGATAGGACAATAAAATCTA  594
          |||
Sbjct  541  GAATAGTAGAGTTTGAATTCAGGAAGGACACCTGTGATAGGACAATAAAATCTA  594
```

Sequence 1374 matched with Sequence 468

Query= Sequence ID 1374
Length=112

SEQ ID NO: 468

ALIGNMENTS

Identities = 112/112 (100%), Gaps = 0/112 (0%)

Query	1	GAAAGCACATATGATATACATGTGTGTCATATGTATTATTTGTTTGCCATCTGAGTCTT	60
Sbjct	1	GAAAGCACATATGATATACATGTGTGTCATATGTATTATTTGTTTGCCATCTGAGTCTT	60
Query	61	CAAAATTTGTTACAGAATACCTGCATATTAATATTTCAAGGTATGGATTAAT	112
Sbjct	61	CAAAATTTGTTACAGAATACCTGCATATTAATATTTCAAGGTATGGATTAAT	112

Sequence 1378 matched with Sequence 469

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 1378
Length=40

SEQ ID NO: 469	79.8	1e-21
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ALIGNMENTS

Identities = 40/40 (100%), Gaps = 0/40 (0%)

Query	1	CTGAGTATTA	AAAAAAAAAAAAAAAAAAAAAAAAAAAA	40
Sbjct	1	CTGAGTATTA	AAAAAAAAAAAAAAAAAAAAAAAAAAAA	40

Sequence 1380 matched with Sequence 470

Query= Sequence ID 1380
Length=933

SEQ ID NO: 470

ALIGNMENTS

Identities = 933/933 (100%), Gaps = 0/933 (0%)

Query	1	CCAAACCCAACTGGTCCAGTAGGATACTCACCTTACAGGGGGCGTCTCAAGAGTCTCACA	60
Sbjct	1	CCAAACCCAACTGGTCCAGTAGGATACTCACCTTACAGGGGGCGTCTCAAGAGTCTCACA	60
Query	61	GTTCCCTTGGGTCTTAAGAGACTCACTGTTGGACCAGGCGTGGTGACTCACGCCTGTAAA	120
Sbjct	61	GTTCCCTTGGGTCTTAAGAGACTCACTGTTGGACCAGGCGTGGTGACTCACGCCTGTAAA	120
Query	121	ACCAGCACTTTGGGAGGCCGAGGCGGGCGGATCAGTTGAGGTCAAGAGTTCAAGACCAGC	180
Sbjct	121	ACCAGCACTTTGGGAGGCCGAGGCGGGCGGATCAGTTGAGGTCAAGAGTTCAAGACCAGC	180
Query	181	CTGACCAAGGTGCTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTG	240
Sbjct	181	CTGACCAAGGTGCTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTG	240
Query	241	GTGTGCGCCTGTAATCCCAGCTACTCCAGAGGCTGAGGCAGGAGAATCTCTTGAACCCAG	300
Sbjct	241	GTGTGCGCCTGTAATCCCAGCTACTCCAGAGGCTGAGGCAGGAGAATCTCTTGAACCCAG	300
Query	301	GAGGTGGAGGTTGCAGTGAGTCGAGATCATGCCACTGCACTCCAGCCTGGGTGACAGAGC	360
Sbjct	301	GAGGTGGAGGTTGCAGTGAGTCGAGATCATGCCACTGCACTCCAGCCTGGGTGACAGAGC	360
Query	361	GAGACTCCGTCTTAGAAAAAAAAAAAAAAAAAAAAAAAAAAGAACCTCACAGTTCAGCAGGGTTC	420
Sbjct	361	GAGACTCCGTCTTAGAAAAAAAAAAAAAAAAAAAAAAAAAAGAACCTCACAGTTCAGCAGGGTTC	420
Query	421	TAGCATGAGACAATGAGGACAAGGGTAGGTGAGCAGGTGGAAGAGTGAGAACAGGTCAA	480
Sbjct	421	TAGCATGAGACAATGAGGACAAGGGTAGGTGAGCAGGTGGAAGAGTGAGAACAGGTCAA	480

PATENT SEQUENCE ALIGNMENT

Sequence 1382 matched with Sequence 471

Query= Sequence ID 1382
Length=896

SEQ ID NO: 471

ALIGNMENTS

Identities = 896/896 (100%), Gaps = 0/896 (0%)

Query	1	CTTACTACCTCCAACATGAAACAAGCAGCCCCGCACTTCTCGAAGGTCTGAGTTACTTGG	60
Sbjct	1	CTTACTACCTCCAACATGAAACAAGCAGCCCCGCACTTCTCGAAGGTCTGAGTTACTTGG	60
Query	61	AATCGTTTTACCACATGATGGACAGAAGGAATATTTTCAGATATCTCTGAAAACCTCAAGC	120
Sbjct	61	AATCGTTTTACCACATGATGGACAGAAGGAATATTTTCAGATATCTCTGAAAACCTCAAGC	120
Query	121	GTTACCTTCTTCAGTATTTTAAGCCAGTGATTGACAGGCAAAGCTGGAGTGACAAGGGCT	180
Sbjct	121	GTTACCTTCTTCAGTATTTTAAGCCAGTGATTGACAGGCAAAGCTGGAGTGACAAGGGCT	180
Query	181	CAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCCTGTGACCTGAACCATG	240
Sbjct	181	CAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCCTGTGACCTGAACCATG	240
Query	241	CTCCTTGCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGATGGAATCCAGTGGAAAAT	300
Sbjct	241	CTCCTTGCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGATGGAATCCAGTGGAAAAT	300
Query	301	TAAATATACCAACAGATGTTTTAAAGATTGTGTATTCTGTGGGTGCTCAGACAACAGCAG	360
Sbjct	301	TAAATATACCAACAGATGTTTTAAAGATTGTGTATTCTGTGGGTGCTCAGACAACAGCAG	360
Query	361	GATGGAATTACCTTTTAGAGCAATATGAACTGTCAATGTCAAGTGCTGAACAAAACAAAA	420
Sbjct	361	GATGGAATTACCTTTTAGAGCAATATGAACTGTCAATGTCAAGTGCTGAACAAAACAAAA	420
Query	421	TTCTGTATGCTTTGTCAACGAGCAAGCATCAGGAAAAGTTACTGAAGTTAATTGAACTAG	480
Sbjct	421	TTCTGTATGCTTTGTCAACGAGCAAGCATCAGGAAAAGTTACTGAAGTTAATTGAACTAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	GAATGGAAGGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTCCTTCATGCGATTGCCA	540
Sbjct	481	GAATGGAAGGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTCCTTCATGCGATTGCCA	540
Query	541	GACGTCCAAAGGGGCAGCAACTAGCATGGGATTTTGTAAAGAGAAAATTGGACCCATCTTC	600
Sbjct	541	GACGTCCAAAGGGGCAGCAACTAGCATGGGATTTTGTAAAGAGAAAATTGGACCCATCTTC	600
Query	601	TGAAAAAATTTGACTTGGGCTCATATGACATAAGGATGATCATCTCTGGCACAACAGCTC	660
Sbjct	601	TGAAAAAATTTGACTTGGGCTCATATGACATAAGGATGATCATCTCTGGCACAACAGCTC	660
Query	661	ACTTTTCTTCCAAGGATAAGTTGCAAGAGGTGAAACTATTTTTTGAATCTCTTGAGGCTC	720
Sbjct	661	ACTTTTCTTCCAAGGATAAGTTGCAAGAGGTGAAACTATTTTTTGAATCTCTTGAGGCTC	720
Query	721	AAGGATCACATCTGGATATTTTTCAAACGTCTTGAAACGATAACCAAAAATATAAAAT	780
Sbjct	721	AAGGATCACATCTGGATATTTTTCAAACGTCTTGAAACGATAACCAAAAATATAAAAT	780
Query	781	GGCTGGAGAAGAATCTTCCGACTCTGAGGACTTGGCTAATGGTTAATACTTAAATGGTCA	840
Sbjct	781	GGCTGGAGAAGAATCTTCCGACTCTGAGGACTTGGCTAATGGTTAATACTTAAATGGTCA	840
Query	841	ATAGAAAAAGTAGGCTGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGA	896
Sbjct	841	ATAGAAAAAGTAGGCTGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGA	896

Sequence 1389 matched with Sequence 473

Query= Sequence ID 1389

Length=896

SEQ ID NO: 473

ALIGNMENTS

Identities = 895/895 (100%), Gaps = 0/895 (0%)

Query	1	ttttttttttttttttgggagtcagttttcttttcttttcttttcttttttttttttgnntt	60
Sbjct	1	TTTTTTTTTTTTTTTGGGAGTCAGTTTCTTTCTTTCTTTCTTTCTTTTTTTTTTTTGNNTT	60
Query	61	ttCGGAAACGGAGTCTCGCTTTCTCGCCCACTCTGGAGTGGNGCAGTGGGGNGGTCTCAG	120
Sbjct	61	TTCGGAAACGGAGTCTCGCTTTCTCGCCCACTCTGGAGTGGNGCAGTGGGGNGGTCTCAG	120
Query	121	CTACCCACAGCCTCCACCTCCTGGGCCCAAGCGATCCTNTCACCTCAGCCTCCTGCGTAG	180
Sbjct	121	CTACCCACAGCCTCCACCTCCTGGGCCCAAGCGATCCTNTCACCTCAGCCTCCTGCGTAG	180
Query	181	CTGGGACTACAGGCGTGCACCACCATTCCCAGGTAATTTTTGTATTTTTGTANANACAG	240
Sbjct	181	CTGGGACTACAGGCGTGCACCACCATTCCCAGGTAATTTTTGTATTTTTGTANANACAG	240
Query	241	GGTTTCACTGTTGTTGCCCAGGCTGGTCTCGAACTCCTGCTTCAGTCTGCCANAATGCTG	300
Sbjct	241	GGTTTCACTGTTGTTGCCCAGGCTGGTCTCGAACTCCTGCTTCAGTCTGCCANAATGCTG	300
Query	301	GATTCTAGGCGTGAGCCACCGNGCCTGGCCCCAAAAGTTACTTTTCTTACAGAAGCAAAGC	360
Sbjct	301	GATTCTAGGCGTGAGCCACCGNGCCTGGCCCCAAAAGTTACTTTTCTTACAGAAGCAAAGC	360
Query	361	TTTAATGCATTTTACTGAATGCTTATAGCTTTGTAGATACTGAAAAGAGTATGAGCGTCA	420
Sbjct	361	TTTAATGCATTTTACTGAATGCTTATAGCTTTGTAGATACTGAAAAGAGTATGAGCGTCA	420
Query	421	CATACAGACACATNTAACAGCACTGCCTCCAACCAGCCCCTACCCACTGGTCAGGNGAGT	480
Sbjct	421	CATACAGACACATNTAACAGCACTGCCTCCAACCAGCCCCTACCCACTGGTCAGGNGAGT	480

PATENT SEQUENCE ALIGNMENT

Query	481	AANAATCAAAAATTCTTTTCTGNGAGTGGAACGGAAATTTTCATCTCTCCTCCTCAGGCAAG	540
Sbjct	481	AANAATCAAAAATTCTTTTCTGNGAGTGGAACGGAAATTTTCATCTCTCCTCCTCAGGCAAG	540
Query	541	TAGTTAANAGGCTGGNGGGAGTCATGGCCCCATTTTGTTCAAAATACAAGCTCCACAGGA	600
Sbjct	541	TAGTTAANAGGCTGGNGGGAGTCATGGCCCCATTTTGTTCAAAATACAAGCTCCACAGGA	600
Query	601	ACAAAAGGCTGAACTGCTCACCTCCCAACTGATGAACCTCGTCTTTGTTCCATGTCAAAG	660
Sbjct	601	ACAAAAGGCTGAACTGCTCACCTCCCAACTGATGAACCTCGTCTTTGTTCCATGTCAAAG	660
Query	661	GGGCCTTTGTGTTACTGCAGCAGAAACTCCAGCTATCAAACCATCAGGCACCAAAAGTAA	720
Sbjct	661	GGGCCTTTGTGTTACTGCAGCAGAAACTCCAGCTATCAAACCATCAGGCACCAAAAGTAA	720
Query	721	AACTCCTTTCTCTAAAAAGACCTCTCTTTACCTGAGCCTTTCAATGCATCTTTGCCCCCA	780
Sbjct	721	AACTCCTTTCTCTAAAAAGACCTCTCTTTACCTGAGCCTTTCAATGCATCTTTGCCCCCA	780
Query	781	NATAATCCTGGATGAGATAATCCCCAGAGGAANACCAGCGCTTGCCTAGTGAAATTATAC	840
Sbjct	781	NATAATCCTGGATGAGATAATCCCCAGAGGAANACCAGCGCTTGCCTAGTGAAATTATAC	840
Query	841	TATGAGACAAGGGTAAAAGACCTCAAANACCGGGTTGGCAGGTAAGGGAGTAGGG	895
Sbjct	841	TATGAGACAAGGGTAAAAGACCTCAAANACCGGGTTGGCAGGTAAGGGAGTAGGG	895

Sequence 1390 matched with Sequence 474

Query= Sequence ID 1390
Length=350

SEQ ID NO: 474

ALIGNMENTS

Identities = 347/347 (100%), Gaps = 0/347 (0%)

Query	4	GTGGCACCCGTTTCCGGCACCTTCAGACTCTGAAGAGCCACCTGCGAATCCACACAGGAG	63
Sbjct	4	GTGGCACCCGTTTCCGGCACCTTCAGACTCTGAAGAGCCACCTGCGAATCCACACAGGAG	63
Query	64	AGAAACCTTACCATGTACGTAAGCCTCTTGAGGCCGCTCTCTGACCTGCggggatgtgga	123
Sbjct	64	AGAAACCTTACCATGTACGTAAGCCTCTTGAGGCCGCTCTCTGACCTGCGGGGATGTGGA	123
Query	124	gggcaggggaaggaggtggagcgcaggggaaggaggtggagcagggaggcagtgggaACTGTT	183
Sbjct	124	GGGCAGGGAAGGAGGTGGAGCGCAGGGAAGGAGGTGGAGCAGGGAGGCAGTGGAAGTGTGTT	183
Query	184	TGCTCCCATCTCAAGCACACAGTGGGGCAACCACTACGCTAATGGTTGGAAGACCTAGAT	243
Sbjct	184	TGCTCCCATCTCAAGCACACAGTGGGGCAACCACTACGCTAATGGTTGGAAGACCTAGAT	243
Query	244	CTGGGCCCCAATGGCCAGACACCCTGCTTGACCTTGGCCCAAGCATTAGGGGACTCATCTT	303
Sbjct	244	CTGGGCCCCAATGGCCAGACACCCTGCTTGACCTTGGCCCAAGCATTAGGGGACTCATCTT	303
Query	304	TAAAATGAGGGTATGGGACTAGATGATCTGGGCCTTAGGAGAGGAGT	350
Sbjct	304	TAAAATGAGGGTATGGGACTAGATGATCTGGGCCTTAGGAGAGGAGT	350

Sequence 1391 matched with Sequence 475

Query= Sequence ID 1391

Length=835

SEQ ID NO: 475

ALIGNMENTS

Identities = 835/835 (100%), Gaps = 0/835 (0%)

Query	1	CGGCTNCTACCCTGCGGAGATCACACTGACCTGGCAGTGGGATGGGGAGGACCAA	60
Sbjct	1	CGGCTNCTACCCTGCGGAGATCACACTGACCTGGCAGTGGGATGGGGAGGACCAA	60
Query	61	GGACACCGAGCTTGTGGAGACCAGGCCAGCAGGAGATGGAACCTTCCAGAAGTGGGCAGC	120
Sbjct	61	GGACACCGAGCTTGTGGAGACCAGGCCAGCAGGAGATGGAACCTTCCAGAAGTGGGCAGC	120
Query	121	TGTGGTGGTGCCTTCTGGAGAAGAGCAGAGATACACGTGCCATGTTTCAGCACGAGGGGCT	180
Sbjct	121	TGTGGTGGTGCCTTCTGGAGAAGAGCAGAGATACACGTGCCATGTTTCAGCACGAGGGGCT	180
Query	181	GCCGGAGCCCCTCACCTGAGATGGAAGCCGTCTTCCCAGCCCACCATCCCCATCGTGGG	240
Sbjct	181	GCCGGAGCCCCTCACCTGAGATGGAAGCCGTCTTCCCAGCCCACCATCCCCATCGTGGG	240
Query	241	CATCGTTGCTGGCCTGGCTGTCCTAGCTGTCCTAGGAGCTATGGTGGCTGT	300
Sbjct	241	CATCGTTGCTGGCCTGGCTGTCCTAGCTGTCCTAGGAGCTATGGTGGCTGT	300
Query	301	TGTGATGTGTAGGAGGAAGAGCTCAGGTGGAAAAGGAGGGAGCTGCTCTCAGGCTGCGTC	360
Sbjct	301	TGTGATGTGTAGGAGGAAGAGCTCAGGTGGAAAAGGAGGGAGCTGCTCTCAGGCTGCGTC	360
Query	361	CAGCAACAGTGCCCAGGGCTCTGATGAGTCTCTCATCGCTTGTAAGCCTGAGACAGCTG	420
Sbjct	361	CAGCAACAGTGCCCAGGGCTCTGATGAGTCTCTCATCGCTTGTAAGCCTGAGACAGCTG	420
Query	421	CCTGTGTGGGACTGAGATGCAGGATTTCTTCACACCTCTCCTTTGTGACTTCAAGAGCCT	480
Sbjct	421	CCTGTGTGGGACTGAGATGCAGGATTTCTTCACACCTCTCCTTTGTGACTTCAAGAGCCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	CTGGCATCTCTTTCTGCAAAGGCATCTGAATGTGTCTGCGTTCCTGTTAGCATAATGTGA	540
Sbjct	481	CTGGCATCTCTTTCTGCAAAGGCATCTGAATGTGTCTGCGTTCCTGTTAGCATAATGTGA	540
Query	541	GGAGGTGGAGAGACAGCCACCCCCGTGTCCACCGTGACCCCTGTCCCCACACTGACCTG	600
Sbjct	541	GGAGGTGGAGAGACAGCCACCCCCGTGTCCACCGTGACCCCTGTCCCCACACTGACCTG	600
Query	601	TGTTCCCTCCCCGATCATCTTTCTGTTCAGAGAAGTGGGCTGGATGTCTCCATCTCTG	660
Sbjct	601	TGTTCCCTCCCCGATCATCTTTCTGTTCAGAGAAGTGGGCTGGATGTCTCCATCTCTG	660
Query	661	TCTCAACTTCATGGTGCCTGAGCTGCAACTTCTTACTTCCCTAATGAAGTTAAGAACCT	720
Sbjct	661	TCTCAACTTCATGGTGCCTGAGCTGCAACTTCTTACTTCCCTAATGAAGTTAAGAACCT	720
Query	721	GAATATAAATTTGTTTTCTCAAATATTTGCTATGAAGGGTTGATGGATTAATTAAATAAG	780
Sbjct	721	GAATATAAATTTGTTTTCTCAAATATTTGCTATGAAGGGTTGATGGATTAATTAAATAAG	780
Query	781	TCAATTCCTGGAAGTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCANAATCCG	835
Sbjct	781	TCAATTCCTGGAAGTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCANAATCCG	835

Sequence 1392 matched with Sequence 476

Query= Sequence ID 1392
Length=437

SEQ ID NO: 476

ALIGNMENTS

Identities = 437/437 (100%), Gaps = 0/437 (0%)

Query	1	TGAAACAAAATGAATTTNTATGGGTAAGAGAGGGTAATATTTTAGAGTTGTGTTACAAAA	60
Sbjct	1	TGAAACAAAATGAATTTNTATGGGTAAGAGAGGGTAATATTTTAGAGTTGTGTTACAAAA	60
Query	61	CTACAAATTTTATTAAATTAATAAATCAGAATACTAAATCCATGTGtttttttCTTTCT	120
Sbjct	61	CTACAAATTTTATTAAATTAATAAATCAGAATACTAAATCCATGTGTTTTTTCTTTCT	120
Query	121	TAAAAAATATCTTTTGGCTGGGCACGGTAGCTCATGGCTGTAATCCCAGCACTTTGGGAG	180
Sbjct	121	TAAAAAATATCTTTTGGCTGGGCACGGTAGCTCATGGCTGTAATCCCAGCACTTTGGGAG	180
Query	181	GCTGAGGTGGGTGGATCGCCTGATGTCAGGAGTTCAAGACCAGCCTGGTCAACATGTTGA	240
Sbjct	181	GCTGAGGTGGGTGGATCGCCTGATGTCAGGAGTTCAAGACCAGCCTGGTCAACATGTTGA	240
Query	241	AACCCCATCTCTACTAAAAATATAAAAAATTAGCCGGTGTGGTGGTGGGCGCCTGTAATCC	300
Sbjct	241	AACCCCATCTCTACTAAAAATATAAAAAATTAGCCGGTGTGGTGGTGGGCGCCTGTAATCC	300
Query	301	CAGCTACTCAGGAGGCTAAGGCAGGAGAATTGCGTGAACCCAGGAGTTCAGTGATGTAGC	360
Sbjct	301	CAGCTACTCAGGAGGCTAAGGCAGGAGAATTGCGTGAACCCAGGAGTTCAGTGATGTAGC	360
Query	361	GGGGAGCTGAGATTGTGCCACTACACTCCAGCCTGGATGACAGAGTGAGACTCCATCTCa	420
Sbjct	361	GGGGAGCTGAGATTGTGCCACTACACTCCAGCCTGGATGACAGAGTGAGACTCCATCTCA	420
Query	421	aaaaaaaaaaaaaaaaaaaa 437	
Sbjct	421	AAAAAAAAAAAAAAAAAAAA 437	

Sequence 1394 matched with Sequence 477

Query= Sequence ID 1394
Length=369

SEQ ID NO: 477

ALIGNMENTS

Identities = 369/369 (100%), Gaps = 0/369 (0%)

Query	1	GCATAATGTGAGGAGGTGGAGAGACAGCCCACCCCGTGTCCACCGTGACCCCTGTTCCC	60
Sbjct	1	GCATAATGTGAGGAGGTGGAGAGACAGCCCACCCCGTGTCCACCGTGACCCCTGTTCCC	60
Query	61	ATGCTGACTTGTGTTTCCTCCCCAGTCATCTTTCCTGTTCCAGAGAGGTGGGGCTGGATG	120
Sbjct	61	ATGCTGACTTGTGTTTCCTCCCCAGTCATCTTTCCTGTTCCAGAGAGGTGGGGCTGGATG	120
Query	121	TCTCCATCTCTGTCTCAACTTTATGTGCACTGAGCTGCAACTTCTTACTTCCCTACTGAA	180
Sbjct	121	TCTCCATCTCTGTCTCAACTTTATGTGCACTGAGCTGCAACTTCTTACTTCCCTACTGAA	180
Query	181	AATAAGAATCTGAATATAAATTTGTTTTCTCAAATATTTGCTATGAGAGGTTGATGGATT	240
Sbjct	181	AATAAGAATCTGAATATAAATTTGTTTTCTCAAATATTTGCTATGAGAGGTTGATGGATT	240
Query	241	AATTAAATAAGTCAATTCCTGGAATTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCAG	300
Sbjct	241	AATTAAATAAGTCAATTCCTGGAATTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCAG	300
Query	301	aaa	360
Sbjct	301	AAA	360
Query	361	aaaaaaaa 369	
Sbjct	361	AAAAAAAAA 369	

Sequence 1395 matched with Sequence 478

Query= Sequence ID 1395

Length=642

SEQ ID NO: 478

ALIGNMENTS

Identities = 642/642 (100%), Gaps = 0/642 (0%)

Query	1	CTTACCATGTCAGTGCACAGAAATGCTGTCTTGGGATGTAGGAAAAATAAATCCACAAAA	60
Sbjct	1	CTTACCATGTCAGTGCACAGAAATGCTGTCTTGGGATGTAGGAAAAATAAATCCACAAAA	60
Query	61	GCTACCAAGTTTGAAGGGGACCATGAGTCTTCAGGCTGGAGCTTCCAAACCAGATGAAAA	120
Sbjct	61	GCTACCAAGTTTGAAGGGGACCATGAGTCTTCAGGCTGGAGCTTCCAAACCAGATGAAAA	120
Query	121	CCCCACAATTAACCTGCAGTTTAAGATCCAGCAGCTGGCCATTTCTGGACTCAAGGTGAA	180
Sbjct	121	CCCCACAATTAACCTGCAGTTTAAGATCCAGCAGCTGGCCATTTCTGGACTCAAGGTGAA	180
Query	181	TCGTCTGGATATGTATGGAGAAAAGTACAAACCCTTTAAGGGCATAAAAATACATGACCAA	240
Sbjct	181	TCGTCTGGATATGTATGGAGAAAAGTACAAACCCTTTAAGGGCATAAAAATACATGACCAA	240
Query	241	AGCTGGGAAGTTCCAAGTTCGAACCTGAAGGGAGCATTTGCTGAGGGAATAGTCTTGCAC	300
Sbjct	241	AGCTGGGAAGTTCCAAGTTCGAACCTGAAGGGAGCATTTGCTGAGGGAATAGTCTTGCAC	300
Query	301	ATTTTTTCATTTCTTACTTGTCTAAAAGTaaaaaaaaTATCAGCCTGTCTCCTAGGTCA	360
Sbjct	301	ATTTTTTCATTTCTTACTTGTCTAAAAGTAAAAAAAAATATCAGCCTGTCTCCTAGGTCA	360
Query	361	GTCCCCTCCTGGACCCACCCGCTCCCTTTTTTCCTTAGCCTTCAGTGCCATGGAAC TAAT	420
Sbjct	361	GTCCCCTCCTGGACCCACCCGCTCCCTTTTTTCCTTAGCCTTCAGTGCCATGGAAC TAAT	420
Query	421	CAAGGGAGGAAAAGGTCACCAGGGAGAACTGGACAGAACTGAAACACAGCAACACCAGTT	480
Sbjct	421	CAAGGGAGGAAAAGGTCACCAGGGAGAACTGGACAGAACTGAAACACAGCAACACCAGTT	480

Query	481	CTCAAGGACAAGGTGTGTGATGGGGGTAGGAAGCTTGGTGCTTATGTAACCATTTTAAAC	540
Sbjct	481	CTCAAGGACAAGGTGTGTGATGGGGGTAGGAAGCTTGGTGCTTATGTAACCATTTTAAAC	540
Query	541	GTGGTTTCTATAGGAAAGACCAACATTTGTTTAGCTTGCTTGGCTTTAATTATCTAAAGC	600
Sbjct	541	GTGGTTTCTATAGGAAAGACCAACATTTGTTTAGCTTGCTTGGCTTTAATTATCTAAAGC	600
Query	601	CAATGAAAGACTTCTTTGTTGATTTTTTAAGATAGAAAGATT	642
Sbjct	601	CAATGAAAGACTTCTTTGTTGATTTTTTAAGATAGAAAGATT	642

Sequence 1396 matched with Sequence 479

Query= Sequence ID 1396

Length=912

SEQ ID NO: 479

ALIGNMENTS

Identities = 909/909 (100%), Gaps = 0/909 (0%)

Query	1	CAAACACTATGTTATTTTATGAANAAGACTTGAACATCTATGGATTTTGGTATTTGCAAG	60
Sbjct	1	CAAACACTATGTTATTTTATGAANAAGACTTGAACATCTATGGATTTTGGTATTTGCAAG	60
Query	61	GGGTGAATGGGGTATTTGCAAGCAGTGAATGAGGAGGCCTGGAACCAATCTTCTGCTGAT	120
Sbjct	61	GGGTGAATGGGGTATTTGCAAGCAGTGAATGAGGAGGCCTGGAACCAATCTTCTGCTGAT	120
Query	121	ATTGAGGCACAACCTGAAAAAGGTATATTACTTAAATCTCTTATTGTATTGTAACTGTAT	180
Sbjct	121	ATTGAGGCACAACCTGAAAAAGGTATATTACTTAAATCTCTTATTGTATTGTAACTGTAT	180
Query	181	AAGTAATGAAATTAAAAGGCAGAAATTGTCAGACTGAATAAAATGAAAAGACCAACAAT	240
Sbjct	181	AAGTAATGAAATTAAAAGGCAGAAATTGTCAGACTGAATAAAATGAAAAGACCAACAAT	240
Query	241	ATGCTGCTTACAAGAAACACAATTCAAATATAAGGACACAATTAGTTTAAAGGAAAAGAA	300
Sbjct	241	ATGCTGCTTACAAGAAACACAATTCAAATATAAGGACACAATTAGTTTAAAGGAAAAGAA	300
Query	301	CTGGAAAAGATATACCATGATAACACAAGTCAGAAGAAAGCTGCTGTGGATATATTAATA	360
Sbjct	301	CTGGAAAAGATATACCATGATAACACAAGTCAGAAGAAAGCTGCTGTGGATATATTAATA	360
Query	361	TGAGATGTAGATTTTCAGAGCAGTGAATATTGCCAGGCATAAAGAAAGTTATTACATAATA	420
Sbjct	361	TGAGATGTAGATTTTCAGAGCAGTGAATATTGCCAGGCATAAAGAAAGTTATTACATAATA	420
Query	421	ATTAAGGTATCAGTTCATCAAGAAGATGTAATAACCCTAAGTATTTATACAACCTAATATC	480
Sbjct	421	ATTAAGGTATCAGTTCATCAAGAAGATGTAATAACCCTAAGTATTTATACAACCTAATATC	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGAGCTTCAAAATACATGAAGCAAAAACCAAGTGAATTGATAGGAGAAACACACAATTAC	540
Sbjct	481	AGAGCTTCAAAATACATGAAGCAAAAACCAAGTGAATTGATAGGAGAAACACACAATTAC	540
Query	541	ACAATTATAGTCAGAATTTTCAACATATCTTTCTCAATGGAGAAAACAACTAGACAGGAA	600
Sbjct	541	ACAATTATAGTCAGAATTTTCAACATATCTTTCTCAATGGAGAAAACAACTAGACAGGAA	600
Query	601	ATCATTAAGGATATAGATGATTTAAATTATATGATCAACTACCTGGACGTAATTGGCATT	660
Sbjct	601	ATCATTAAGGATATAGATGATTTAAATTATATGATCAACTACCTGGACGTAATTGGCATT	660
Query	661	TATGGAACACTGCACCACCAACAGCAGAGTACATATTATTTTCAAGTACACAGAAAACAG	720
Sbjct	661	TATGGAACACTGCACCACCAACAGCAGAGTACATATTATTTTCAAGTACACAGAAAACAG	720
Query	721	TTACCAATATAGACCATTTTCTGGGTCATAAAACACATCTCAATAAATGTAAACAATTA	780
Sbjct	721	TTACCAATATAGACCATTTTCTGGGTCATAAAACACATCTCAATAAATGTAAACAATTA	780
Query	781	ATGTTATATAAAGTATGTGCTCTGACCNCAAAGGAATTAGAGATCAATAAAAGAACATCT	840
Sbjct	781	ATGTTATATAAAGTATGTGCTCTGACCNCAAAGGAATTAGAGATCAATAAAAGAACATCT	840
Query	841	TTGAAAAATCTCACNTATTTAAAAACTAATAACTCACTTCTAAATAACTCCTGTNTCAAG	900
Sbjct	841	TTGAAAAATCTCACNTATTTAAAAACTAATAACTCACTTCTAAATAACTCCTGTNTCAAG	900
Query	901	AGAATNAAA 909	
Sbjct	901	AGAATNAAA 909	

Sequence 1397 matched with Sequence 480

Query= Sequence ID 1397
Length=873

SEQ ID NO: 480

ALIGNMENTS

Identities = 873/873 (100%), Gaps = 0/873 (0%)

Query	1	CCCAGCCTCACTGCGCCCCGTCAGGCCAGGCAGCTGCCCTCAGGGTCTGCCAAGGTGGGG	60
Sbjct	1	CCCAGCCTCACTGCGCCCCGTCAGGCCAGGCAGCTGCCCTCAGGGTCTGCCAAGGTGGGG	60
Query	61	GTCAAGGGCCATGGGGGCAGGTAGCTCTGCCTGCAAAGCCCACAAGCATGTCAGATCACC	120
Sbjct	61	GTCAAGGGCCATGGGGGCAGGTAGCTCTGCCTGCAAAGCCCACAAGCATGTCAGATCACC	120
Query	121	TGGGCTGCAGACAGACAAACACCTGAGCTGTTCTGAATACCTTCAGGTTCTGGCCTCGC	180
Sbjct	121	TGGGCTGCAGACAGACAAACACCTGAGCTGTTCTGAATACCTTCAGGTTCTGGCCTCGC	180
Query	181	TGAGCAAGTGCAGAAATTTTTACCTTCAAGGATCAGGgtttttctgtttgtttgtttttt	240
Sbjct	181	TGAGCAAGTGCAGAAATTTTTACCTTCAAGGATCAGGTTTTTCTGTTTGTGTTTTTTT	240
Query	241	AACACACACATATGTGAACAAAGAGTATGCGTTTGTACTGGCAGAAGAAGCGTCTGGTAA	300
Sbjct	241	AACACACACATATGTGAACAAAGAGTATGCGTTTGTACTGGCAGAAGAAGCGTCTGGTAA	300
Query	301	GACAACCAGCAAGTTAACAATGGTCACCTCCAGAAATGGGCTGGGTAAACCAAAGAAttt	360
Sbjct	301	GACAACCAGCAAGTTAACAATGGTCACCTCCAGAAATGGGCTGGGTAAACCAAAGAATTT	360
Query	361	ttttgtttttgttttttttGAGTCAGGGTCTAGCTCTGTCACCCAGGCTGGAACGCACTG	420
Sbjct	361	TTTTGTTTTTGTGTTTTTTTGTGAGTCAGGGTCTAGCTCTGTCACCCAGGCTGGAACGCACTG	420
Query	421	GTGTGATCACGGCTCACTGCAGCCTTGACCTCCCTGGCTCAAGCAATCCTCCCAGCTCAG	480
Sbjct	421	GTGTGATCACGGCTCACTGCAGCCTTGACCTCCCTGGCTCAAGCAATCCTCCCAGCTCAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCTCCTGAGTCGTTGGGACTACAGGCACGTGCCACCACGCCTGACACATTTTTTAAATTT	540
Sbjct	481	CCTCCTGAGTCGTTGGGACTACAGGCACGTGCCACCACGCCTGACACATTTTTTAAATTT	540
Query	541	TTGTAGAGACAGTGTTCACCATGTTGCCCAGGCAGGTCTCAAACCTCCTGGGCTCAAGTG	600
Sbjct	541	TTGTAGAGACAGTGTTCACCATGTTGCCCAGGCAGGTCTCAAACCTCCTGGGCTCAAGTG	600
Query	601	GTCCTCCAGCTTCAGCCTCCCAAAGTGCTAGGATTATAGGTGTGAGCCACAGTGCCCAGC	660
Sbjct	601	GTCCTCCAGCTTCAGCCTCCCAAAGTGCTAGGATTATAGGTGTGAGCCACAGTGCCCAGC	660
Query	661	CCCGTAGTGGAGAATTTCTGTTGAATGAACCAAAAGCAACTGCCAACCTCTCCATGCACC	720
Sbjct	661	CCCGTAGTGGAGAATTTCTGTTGAATGAACCAAAAGCAACTGCCAACCTCTCCATGCACC	720
Query	721	ATGTGTTTCAGAGGAGAAAGCACAGTGAAGAATGCAGTGTGTTCTGAGGTCCTGTCACCC	780
Sbjct	721	ATGTGTTTCAGAGGAGAAAGCACAGTGAAGAATGCAGTGTGTTCTGAGGTCCTGTCACCC	780
Query	781	CTGAGGCTGTGTGTGTCCTTTGCCAAATTAAAGAGTCTTACTGAATGCGGTGCATCCAGG	840
Sbjct	781	CTGAGGCTGTGTGTGTCCTTTGCCAAATTAAAGAGTCTTACTGAATGCGGTGCATCCAGG	840
Query	841	AGACAGGCCNAGGTTTGGACTGGTaaaaaaaaa	873
Sbjct	841	AGACAGGCCNAGGTTTGGACTGGTAAAAAAAAA	873

Sequence 1399 matched with Sequence 481

Query= Sequence ID 1399
Length=778

SEQ ID NO: 481

ALIGNMENTS

Identities = 778/778 (100%), Gaps = 0/778 (0%)

Query	1	CAGACACCTGGNAGAACGGAAGGAGACGCTGCAGCGCGCGGACCCCCAAAGACACATG	60
Sbjct	1	CAGACACCTGGNAGAACGGAAGGAGACGCTGCAGCGCGCGGACCCCCAAAGACACATG	60
Query	61	TGACCCACCACCCCATCTNTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCT	120
Sbjct	61	TGACCCACCACCCCATCTNTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCT	120
Query	121	ACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGCGAGGACCAAACCTCAGGACACCG	180
Sbjct	121	ACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGCGAGGACCAAACCTCAGGACACCG	180
Query	181	AGCTTGTGGAGACCAGACCAGCAGGAGACAGAACCTTCCAGAAGTGGGCAGCTGTGGTGG	240
Sbjct	181	AGCTTGTGGAGACCAGACCAGCAGGAGACAGAACCTTCCAGAAGTGGGCAGCTGTGGTGG	240
Query	241	TGCCTTCTGGAGAAGAGCAGAGATACACATGCCATGTACAGCATGAGGGGCTGCCGAAGC	300
Sbjct	241	TGCCTTCTGGAGAAGAGCAGAGATACACATGCCATGTACAGCATGAGGGGCTGCCGAAGC	300
Query	301	CCCTCACCTGAGATGGGAGCCATCTTCCAGTCCACCGTCCCCATCGTGGGCATTGTTG	360
Sbjct	301	CCCTCACCTGAGATGGGAGCCATCTTCCAGTCCACCGTCCCCATCGTGGGCATTGTTG	360
Query	361	CTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTGGTCGCTGCTGTGATGTGTA	420
Sbjct	361	CTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTGGTCGCTGCTGTGATGTGTA	420
Query	421	GGAGGAAGAGTTCAGGTGGAAAAGGAGGGAGCTACTCTCAGGCTGCGTCCAGCGACAGTG	480
Sbjct	421	GGAGGAAGAGTTCAGGTGGAAAAGGAGGGAGCTACTCTCAGGCTGCGTCCAGCGACAGTG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCCAGGGCTCTGATGTGTCTCTCACAGCTTGAAAAGCCTGAGACAGCTGTNTTGTGAGGG	540
Sbjct	481	CCCAGGGCTCTGATGTGTCTCTCACAGCTTGAAAAGCCTGAGACAGCTGTNTTGTGAGGG	540
Query	541	ACTGAGATGCAGGATTTCTTCACGCCTCCCCTTTGTGACTTCAAGAGCCTCTGGCATCTC	600
Sbjct	541	ACTGAGATGCAGGATTTCTTCACGCCTCCCCTTTGTGACTTCAAGAGCCTCTGGCATCTC	600
Query	601	TTTCTGCAAAGGCACCTGAATGTGTCTGCGTCCTTGTTAGCATAATGTGAGGAGGTGGAG	660
Sbjct	601	TTTCTGCAAAGGCACCTGAATGTGTCTGCGTCCTTGTTAGCATAATGTGAGGAGGTGGAG	660
Query	661	AGACAGCCCACCCTTGTGTCAACTGTGACCCCCTGTTCCCATGCTGACCTGTGTTTCCTC	720
Sbjct	661	AGACAGCCCACCCTTGTGTCAACTGTGACCCCCTGTTCCCATGCTGACCTGTGTTTCCTC	720
Query	721	CCCAGTCATCTTTTTTGTTCNCAATAGGTGGGGCCTGGATGTCTCCATCTCTGTNTCA	778
Sbjct	721	CCCAGTCATCTTTTTTGTTCNCAATAGGTGGGGCCTGGATGTCTCCATCTCTGTNTCA	778

Sequence 1440 matched with Sequence 482

Query= Sequence ID 1440
Length=666

SEQ ID NO: 482

ALIGNMENTS

Identities = 666/666 (100%), Gaps = 0/666 (0%)

Query	1	TTATAAGGTACTTTTAAGGTATTTTAGTTGTCTTAGTCTATATTTCTGTACTCACCTTTC	60
Sbjct	1	TTATAAGGTACTTTTAAGGTATTTTAGTTGTCTTAGTCTATATTTCTGTACTCACCTTTC	60
Query	61	TTTATCCACTCATCAGTTGATGGGCATGTAGGTTGGTTCCATATCTTTGCAATTCTGAAT	120
Sbjct	61	TTTATCCACTCATCAGTTGATGGGCATGTAGGTTGGTTCCATATCTTTGCAATTCTGAAT	120
Query	121	TGTGCTGTGATCAGGTGTCTTTTTAGTATAATGATTTACTCTCCTTTGGGTAGATACCCA	180
Sbjct	121	TGTGCTGTGATCAGGTGTCTTTTTAGTATAATGATTTACTCTCCTTTGGGTAGATACCCA	180
Query	181	GTAGTGGGATTGCTGGATCGAATGGTTTTTATAATTTTCTATTTTACCACAGTTTCTCTC	240
Sbjct	181	GTAGTGGGATTGCTGGATCGAATGGTTTTTATAATTTTCTATTTTACCACAGTTTCTCTC	240
Query	241	TGCATTTTTCCTCTTTGACCACTAACCATGTGAAATTCTCATATTGACCTTTATAATGAT	300
Sbjct	241	TGCATTTTTCCTCTTTGACCACTAACCATGTGAAATTCTCATATTGACCTTTATAATGAT	300
Query	301	CATGAACTCTTAGTATCATTGGGAAGGCCACATTTGCCACTTATGATTGTAAACCTTATC	360
Sbjct	301	CATGAACTCTTAGTATCATTGGGAAGGCCACATTTGCCACTTATGATTGTAAACCTTATC	360
Query	361	CTCCATTTTTCCTGTTATTGTTGGTGCAAAAAGCACCTATTATAACCAGGACTTTAAAAAT	420
Sbjct	361	CTCCATTTTTCCTGTTATTGTTGGTGCAAAAAGCACCTATTATAACCAGGACTTTAAAAAT	420
Query	421	CAGTCTGATAAGTCTTTGATAAGTCTAATAATAATAACTGATAAGTCCATTGAATTTGCT	480
Sbjct	421	CAGTCTGATAAGTCTTTGATAAGTCTAATAATAATAACTGATAAGTCCATTGAATTTGCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCTGATTACTTTTTCTTTAGTAGCTAAACATGTATGTACTCCTATGATTACAATGAACAC	540
Sbjct	481	TCTGATTACTTTTTCTTTAGTAGCTAAACATGTATGTACTCCTATGATTACAATGAACAC	540
Query	541	TCCTCTCCATTTAAATTAATTATTTACATTGATGAAATAGCAAAATGTTAATGACTAAAT	600
Sbjct	541	TCCTCTCCATTTAAATTAATTATTTACATTGATGAAATAGCAAAATGTTAATGACTAAAT	600
Query	601	ACTGTCTTGGTTTTTTCGTTCCAGGTCAGTCAATATTAACCTTCTTATAATTTTCtttttt	660
Sbjct	601	ACTGTCTTGGTTTTTTCGTTCCAGGTCAGTCAATATTAACCTTCTTATAATTTTCTTTTTT	660
Query	661	ttCTTT	666
Sbjct	661	TTCTTT	666

Sequence 1447 matched with Sequence 483

Query= Sequence ID 1447
Length=630

SEQ ID NO: 483

ALIGNMENTS

Identities = 630/630 (100%), Gaps = 0/630 (0%)

Query	1	GCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAAGTAGAAATAACTTTGCAAGGA	60
Sbjct	1	GCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAAGTAGAAATAACTTTGCAAGGA	60
Query	61	GAGCCAAAGCTAAGACCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACA	120
Sbjct	61	GAGCCAAAGCTAAGACCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACA	120
Query	121	CCCGTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGC	180
Sbjct	121	CCCGTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGC	180
Query	181	CTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAA	240
Sbjct	181	CTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAA	240
Query	241	CCCTCTAAATCCCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACAC	300
Sbjct	241	CCCTCTAAATCCCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACAC	300
Query	301	TAGGAAAAAACCTTGTTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAG	360
Sbjct	301	TAGGAAAAAACCTTGTTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAG	360
Query	361	CCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAATCCCAAACATATA	420
Sbjct	361	CCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAATCCCAAACATATA	420
Query	421	ACTGAACTCCTCACACCCAATTGGACCAATCTATCACCTATAGAAGAACTAATGTTAGT	480
Sbjct	421	ACTGAACTCCTCACACCCAATTGGACCAATCTATCACCTATAGAAGAACTAATGTTAGT	480

Query	481	ATAAGTAACATGAAAACATTCTCTCCGCATAAGCCTGCGTCAGATTAAAACACTGAACT	540
Sbjct	481	ATAAGTAACATGAAAACATTCTCTCCGCATAAGCCTGCGTCAGATTAAAACACTGAACT	540
Query	541	GACAATTAACAGCCCAATATCTACAATCAACCAACAAGTCATTATTACCCTCACTGTCAA	600
Sbjct	541	GACAATTAACAGCCCAATATCTACAATCAACCAACAAGTCATTATTACCCTCACTGTCAA	600
Query	601	CCCAACACAGGCATGCTCATAAGGAAAGGT	630
Sbjct	601	CCCAACACAGGCATGCTCATAAGGAAAGGT	630

Sequence 1448 matched with Sequence 484

Query= Sequence ID 1448
Length=612

SEQ ID NO: 484

ALIGNMENTS

Identities = 612/612 (100%), Gaps = 0/612 (0%)

Query	1	GGCCACCGGGTGCAAGGTCAGGGCTGGGGTGGAGGCTGGGAAGCCCAGGGCTTGGCCCAC	60
Sbjct	1	GGCCACCGGGTGCAAGGTCAGGGCTGGGGTGGAGGCTGGGAAGCCCAGGGCTTGGCCCAC	60
Query	61	TGTGGCCGCCTTGTGTGGTCACTGCTTTCCTGGGCCTGCTGTGAGCTCCCTCTAGGACCC	120
Sbjct	61	TGTGGCCGCCTTGTGTGGTCACTGCTTTCCTGGGCCTGCTGTGAGCTCCCTCTAGGACCC	120
Query	121	CAGGCCTGTCTGGTGGGTCACTGTGACCACCACCTTGCACAGCACCTGGCGCGTGGCAGG	180
Sbjct	121	CAGGCCTGTCTGGTGGGTCACTGTGACCACCACCTTGCACAGCACCTGGCGCGTGGCAGG	180
Query	181	TGCTCAAACATTACTTGTTTTCGGAATGAACTTCATCTTGCTCTTGGCTTTTTGACTAATG	240
Sbjct	181	TGCTCAAACATTACTTGTTTTCGGAATGAACTTCATCTTGCTCTTGGCTTTTTGACTAATG	240
Query	241	CTGTGGAACATCTGACTAATTAGTGACTCTTTGGGGCCCCCAGTTTCCCAGCTATAAAGT	300
Sbjct	241	CTGTGGAACATCTGACTAATTAGTGACTCTTTGGGGCCCCCAGTTTCCCAGCTATAAAGT	300
Query	301	GGTAATATTAAGATAATAATTGCGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCAGC	360
Sbjct	301	GGTAATATTAAGATAATAATTGCGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCAGC	360
Query	361	ACTTTGGGAGGCCGAGGTGGGCAGATCACGAGGTCAGAAGATCGAGACCATCCTGGCTAA	420
Sbjct	361	ACTTTGGGAGGCCGAGGTGGGCAGATCACGAGGTCAGAAGATCGAGACCATCCTGGCTAA	420
Query	421	CACGGTGAAACCCCATCTCTACTAAAAATACAAAAAATTANCCGGGCGTGGTGGCGGGCG	480
Sbjct	421	CACGGTGAAACCCCATCTCTACTAAAAATACAAAAAATTANCCGGGCGTGGTGGCGGGCG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCTGTAGTCCCAGCTACTCANGAGGCTGANGCAGGAGAATGGTGTGAACCCGGGAGGCAG	540
Sbjct	481	CCTGTAGTCCCAGCTACTCANGAGGCTGANGCAGGAGAATGGTGTGAACCCGGGAGGCAG	540
Query	541	AGGTTGCAGTGAACCAAGATCGNNCCACTGCACTCCAGCCTGGGCAACAGAGCGAGACTC	600
Sbjct	541	AGGTTGCAGTGAACCAAGATCGNNCCACTGCACTCCAGCCTGGGCAACAGAGCGAGACTC	600
Query	601	CATCTTAAAAAA 612	
Sbjct	601	CATCTTAAAAAA 612	

Sequence 1449 matched with Sequence 485

Query= Sequence ID 1449
Length=362

SEQ ID NO: 485

ALIGNMENTS

Identities = 362/362 (100%), Gaps = 0/362 (0%)

Query	1	AATCAGGGCCG	CAGTGTGTTCTGCGCCTGCCCAGAGCTGACTCCTGATT	TAACCGCTGGC	60
Sbjct	1	AATCAGGGCCG	CAGTGTGTTCTGCGCCTGCCCAGAGCTGACTCCTGATT	TAACCGCTGGC	60
Query	61	GTAACCGCGGGTTGCACGCATGCGTGCTGAAAAGCCTTTT	CACCCTCACGTGGTTTCTTTT		120
Sbjct	61	GTAACCGCGGGTTGCACGCATGCGTGCTGAAAAGCCTTTT	CACCCTCACGTGGTTTCTTTT		120
Query	121	TTAACCGAGTCATCAAGCGAGGCTCGCGCGCAGGCCCGCGTTG	GGAAAATGGCGGGGAAGC		180
Sbjct	121	TTAACCGAGTCATCAAGCGAGGCTCGCGCGCAGGCCCGCGTTG	GGAAAATGGCGGGGAAGC		180
Query	181	TGAAACCTCTGAATGTGGAGGCGCCAGAAGCTGCTGAGGAGGCTGAAGGTAGTGAGGGCA			240
Sbjct	181	TGAAACCTCTGAATGTGGAGGCGCCAGAAGCTGCTGAGGAGGCTGAAGGTAGTGAGGGCA			240
Query	241	AGTGGGCTGCACTCCTTTCTCTCCAACCAGGGCAGAAAGGAGGGAGGATTCGTCCCATTA			300
Sbjct	241	AGTGGGCTGCACTCCTTTCTCTCCAACCAGGGCAGAAAGGAGGGAGGATTCGTCCCATTA			300
Query	301	CAATAATGAAATAATGATATTCTAAAttttttAAATAAAATGTTAAGCCTTTTGTTATTG			360
Sbjct	301	CAATAATGAAATAATGATATTCTAATTTTTTTAAATAAAATGTTAAGCCTTTTGTTATTG			360
Query	361	AA	362		
Sbjct	361	AA	362		

Sequence 1450 matched with Sequence 486

Query= Sequence ID 1450
Length=854

SEQ ID NO: 486

ALIGNMENTS

Identities = 851/851 (100%), Gaps = 0/851 (0%)

Query	1	GGAAANCATGAGGCTTCGGGAGCCGCTCCTGAGCGGCAGCGCCGCGATGCCAGGCGCGTC	60
Sbjct	1	GGAAANCATGAGGCTTCGGGAGCCGCTCCTGAGCGGCAGCGCCGCGATGCCAGGCGCGTC	60
Query	61	CCTACAGCGGGCCTGCCGCCTGCTCGTGGCCGTCTGCGCTCTGCACCTTGGCGTCACCCT	120
Sbjct	61	CCTACAGCGGGCCTGCCGCCTGCTCGTGGCCGTCTGCGCTCTGCACCTTGGCGTCACCCT	120
Query	121	CGTTTACTACCTGGCTGGCCGCGACCTGAGCCGCCTGCCCCAACTGGTCGGAGTCTCCAC	180
Sbjct	121	CGTTTACTACCTGGCTGGCCGCGACCTGAGCCGCCTGCCCCAACTGGTCGGAGTCTCCAC	180
Query	181	ACCGCTGCAGGGCGGCTCGAACAGTGCCGCCGCCATCGGGCAGTCCTCCGGGGAGCTCCG	240
Sbjct	181	ACCGCTGCAGGGCGGCTCGAACAGTGCCGCCGCCATCGGGCAGTCCTCCGGGGAGCTCCG	240
Query	241	GACCGGAGGGGCCCCGGCCGCCGCTCCTNTAGGCGCCTCCTCCCAGCCGCGCCCGGGTGG	300
Sbjct	241	GACCGGAGGGGCCCCGGCCGCCGCTCCTNTAGGCGCCTCCTCCCAGCCGCGCCCGGGTGG	300
Query	301	CGACTCCAGCCCAGTCGTGGATTCTGGCCCTGGCCCCGCTAGCAACTTGACCTCGGTCCC	360
Sbjct	301	CGACTCCAGCCCAGTCGTGGATTCTGGCCCTGGCCCCGCTAGCAACTTGACCTCGGTCCC	360
Query	361	AGTGCCCCACACCACCGCACTGTCGCTGCCCGCCTGCCCTGAGGAGTCCCCGCTGCTTGG	420
Sbjct	361	AGTGCCCCACACCACCGCACTGTCGCTGCCCGCCTGCCCTGAGGAGTCCCCGCTGCTTGG	420
Query	421	TAAGGACTCGGGTCGGCGCCAGTCGGAGGATTGGGAccccccGGATTTCCTCCGACAGGG	480
Sbjct	421	TAAGGACTCGGGTCGGCGCCAGTCGGAGGATTGGGACCCCCCGGATTTCCTCCGACAGGG	480

Query	481	TCCCCCANACATTCCCTCAGGCTGGCTCTTCTACGACAGCCAGCCTCCCTCTTCTGGATC	540
Sbjct	481	TCCCCCANACATTCCCTCAGGCTGGCTCTTCTACGACAGCCAGCCTCCCTCTTCTGGATC	540
Query	541	AGAGTTTTTAAATCCCANACAGAGGCTTGGGACTGGATGGGAGAGAAGGTTTGCGAGGTGG	600
Sbjct	541	AGAGTTTTTAAATCCCANACAGAGGCTTGGGACTGGATGGGAGAGAAGGTTTGCGAGGTGG	600
Query	601	GTCCCTGGGGAGTCCTGTTGGAGGCGTGGGGCCGGGACCGCACAGGGAAGTCCCGAGGCC	660
Sbjct	601	GTCCCTGGGGAGTCCTGTTGGAGGCGTGGGGCCGGGACCGCACAGGGAAGTCCCGAGGCC	660
Query	661	CCTCTAGCCCCAAAACCANAGAAGGCCTTGGAGACTTCCCTGCTGTGGCCCGAGGCTNAG	720
Sbjct	661	CCTCTAGCCCCAAAACCANAGAAGGCCTTGGAGACTTCCCTGCTGTGGCCCGAGGCTNAG	720
Query	721	GAAGTTTTTGGAGTTTTTGGGTCTGCTTANGGCTTCNAGCAGCCTTGCACTGAGAACTTTGG	780
Sbjct	721	GAAGTTTTTGGAGTTTTTGGGTCTGCTTANGGCTTCNAGCAGCCTTGCACTGAGAACTTTGG	780
Query	781	TAGGGACCTCGAGTAATCCACTCCNTTTTNNGGACTGACGTGAGGCTCCCGGTGGGGAAA	840
Sbjct	781	TAGGGACCTCGAGTAATCCACTCCNTTTTNNGGACTGACGTGAGGCTCCCGGTGGGGAAA	840
Query	841	GANACTGACCT	851
Sbjct	841	GANACTGACCT	851

Sequence 1453 matched with Sequence 487

Query= Sequence ID 1453

Length=843

SEQ ID NO: 487

ALIGNMENTS

Identities = 843/843 (100%), Gaps = 0/843 (0%)

Query	1	CCGACCTGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGG	60
Sbjct	1	CCGACCTGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGG	60
Query	61	AGGCTATCCAGCGTACTCCAAAGATTGAGTTTACTCACGTCATCCAGCAGAGAATGGAA	120
Sbjct	61	AGGCTATCCAGCGTACTCCAAAGATTGAGTTTACTCACGTCATCCAGCAGAGAATGGAA	120
Query	121	AGTCAAATTCCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAAGTTGACT	180
Sbjct	121	AGTCAAATTCCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAAGTTGACT	180
Query	181	TACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTGAGACTTGTCTTTCAGCAAGG	240
Sbjct	181	TACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTGAGACTTGTCTTTCAGCAAGG	240
Query	241	ACTGGTCTTCTATCTCTTGTACTACACTGAATTCACCCCCACTGAAAAAGATGAGTATG	300
Sbjct	241	ACTGGTCTTCTATCTCTTGTACTACACTGAATTCACCCCCACTGAAAAAGATGAGTATG	300
Query	301	CCTGCCGTGTGAACCATGTGACTTTGTACAGCCCAAGATAGTTAAGTGGGATCGAGACA	360
Sbjct	301	CCTGCCGTGTGAACCATGTGACTTTGTACAGCCCAAGATAGTTAAGTGGGATCGAGACA	360
Query	361	TGTAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTCCAAATTC	420
Sbjct	361	TGTAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTCCAAATTC	420
Query	421	TGCTTGCTTGCTTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACAAAATGTA	480
Sbjct	421	TGCTTGCTTGCTTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACAAAATGTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	GGGTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAGTGCTGTC	540
Sbjct	481	GGGTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAGTGCTGTC	540
Query	541	TCCATGTTTGATGTATCTGAGCAGGTTGCTCCACAGGTAGCTCTAGGAGGGCTGGCAACT	600
Sbjct	541	TCCATGTTTGATGTATCTGAGCAGGTTGCTCCACAGGTAGCTCTAGGAGGGCTGGCAACT	600
Query	601	TAGAGGTGGGGAGCAGAGAATTCTCTTATCCAACATCAACATCTTGGTCAGATTTGAACT	660
Sbjct	601	TAGAGGTGGGGAGCAGAGAATTCTCTTATCCAACATCAACATCTTGGTCAGATTTGAACT	660
Query	661	CTTCAATCTCTTGCACTCAAAGCTTGTTAAGATAGTTAAGCGTGCATAAGTTAACTTCCA	720
Sbjct	661	CTTCAATCTCTTGCACTCAAAGCTTGTTAAGATAGTTAAGCGTGCATAAGTTAACTTCCA	720
Query	721	ATTTACATACTCTGCTTAGAATTTGGGGGAAAATTTAGAAATATAATTGACAGGATTATT	780
Sbjct	721	ATTTACATACTCTGCTTAGAATTTGGGGGAAAATTTAGAAATATAATTGACAGGATTATT	780
Query	781	GGAAATTTGTTATAATGAATGAAACATTTTTGTCATATAAGATTCATATTTACTTCTTAT	840
Sbjct	781	GGAAATTTGTTATAATGAATGAAACATTTTTGTCATATAAGATTCATATTTACTTCTTAT	840
Query	841	ACA 843	
Sbjct	841	ACA 843	

Sequence 1454 matched with Sequence 488

Query= Sequence ID 1454
Length=578

SEQ ID NO: 488

ALIGNMENTS

Identities = 578/578 (100%), Gaps = 0/578 (0%)

Query	1	TAAATAGGGAATCCTTTCCCCATTGCTTGTTTTTCTCAGGTTTGTCAAAGATCAGATAGT	60
Sbjct	1	TAAATAGGGAATCCTTTCCCCATTGCTTGTTTTTCTCAGGTTTGTCAAAGATCAGATAGT	60
Query	61	TGTAGATATGCGACGTTATTTCTGAGGGCTCTGTTCTGTTCCATTGATCTATATCTCTGT	120
Sbjct	61	TGTAGATATGCGACGTTATTTCTGAGGGCTCTGTTCTGTTCCATTGATCTATATCTCTGT	120
Query	121	CACATGCACACGTATGTTTGTGTTGTGGCACTATTCACAGTGGCAAAGACTTGAACCAACC	180
Sbjct	121	CACATGCACACGTATGTTTGTGTTGTGGCACTATTCACAGTGGCAAAGACTTGAACCAACC	180
Query	181	CAAATGTCCAACAATGATAGACCGGGTTAAGAAAATGCGGCACATATACACCATGGAATA	240
Sbjct	181	CAAATGTCCAACAATGATAGACCGGGTTAAGAAAATGCGGCACATATACACCATGGAATA	240
Query	241	CTATGTAGCCATAAAAAATGATGAGTTCGTGTCCTTTGTAGGGACATGGATGAAATTGGA	300
Sbjct	241	CTATGTAGCCATAAAAAATGATGAGTTCGTGTCCTTTGTAGGGACATGGATGAAATTGGA	300
Query	301	AATCATCATTCTCAGTAAACTATCGCAGGAACAAAAACCAAACACTGCATATTCTCACT	360
Sbjct	301	AATCATCATTCTCAGTAAACTATCGCAGGAACAAAAACCAAACACTGCATATTCTCACT	360
Query	361	CATAGGTGGAATTGAACAGTGGGAACACATGGACACAGGAAGGGGAACATCACACTCTG	420
Sbjct	361	CATAGGTGGAATTGAACAGTGGGAACACATGGACACAGGAAGGGGAACATCACACTCTG	420
Query	421	AGGACTGTTGTGGGGTGGGGGGAGGGAGGAGGGATAGCATTGGGAGATATACCTAGTGCT	480
Sbjct	421	AGGACTGTTGTGGGGTGGGGGGAGGGAGGAGGGATAGCATTGGGAGATATACCTAGTGCT	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 GGATGACGAGTTAGTGGGTGCAGCGCACCAGCATGTCACATGTATACATATGTAAC TAAC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 GGATGACGAGTTAGTGGGTGCAGCGCACCAGCATGTCACATGTATACATATGTAAC TAAC 540

Query 541 CTGCACATTGTGCACATGTACCCTAAAAC TTAAGGTAT 578
          |||||||||||||||||||||||||||||
Sbjct 541 CTGCACATTGTGCACATGTACCCTAAAAC TTAAGGTAT 578
```


PATENT SEQUENCE ALIGNMENT

Query	481	TAGCTGGATGTGGTGGCGCATGCCTGTAGTCCCAGCTGCTCTAGGAGGCTGAGGCATGAG	540
Sbjct	481	TAGCTGGATGTGGTGGCGCATGCCTGTAGTCCCAGCTGCTCTAGGAGGCTGAGGCATGAG	540
Query	541	AATTGCTTGAACCTGGGAGGCAGAGGCTGCAGTGAGCCGAGATCGAGCCACTATACTCCA	600
Sbjct	541	AATTGCTTGAACCTGGGAGGCAGAGGCTGCAGTGAGCCGAGATCGAGCCACTATACTCCA	600
Query	601	GCCTGGTCAACAGAGTGAGACCCTGTCT	628
Sbjct	601	GCCTGGTCAACAGAGTGAGACCCTGTCT	628

Sequence 1460 matched with Sequence 490

Query= Sequence ID 1460

Length=612

SEQ ID NO: 490

ALIGNMENTS

Identities = 612/612 (100%), Gaps = 0/612 (0%)

Query	1	CCACAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGA	60
Sbjct	1	CCACAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGA	60
Query	61	GAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGC	120
Sbjct	61	GAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGC	120
Query	121	CCTGGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGGGA	180
Sbjct	121	CCTGGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGGGA	180
Query	181	TCTGTCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGT	240
Sbjct	181	TCTGTCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGT	240
Query	241	GCTCGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCAC	300
Sbjct	241	GCTCGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCAC	300
Query	301	ACTGAGTGAGCTGCACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGCTCCTGGG	360
Sbjct	301	ACTGAGTGAGCTGCACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGCTCCTGGG	360
Query	361	CAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCACCAAGTGCA	420
Sbjct	361	CAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCACCAAGTGCA	420
Query	421	GGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCCTGGCCCACAAGTATCACTA	480
Sbjct	421	GGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCCTGGCCCACAAGTATCACTA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGCTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTTCCCTTGTTCCCTAAGTCCAATA  540
          |||
Sbjct  481  AGCTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTTCCCTTGTTCCCTAAGTCCAATA  540

Query  541  CTAAACTGGGGGATATTATGAAGGGCCTTGAGCATCTGGATTCTGCCTAATAAAAAACAT  600
          |||
Sbjct  541  CTAAACTGGGGGATATTATGAAGGGCCTTGAGCATCTGGATTCTGCCTAATAAAAAACAT  600

Query  601  TTATTTTCATTG  612
          |||
Sbjct  601  TTATTTTCATTG  612
```

Sequence 1490 matched with Sequence 491

Query= Sequence ID 1490
Length=677

SEQ ID NO: 491

ALIGNMENTS

Identities = 677/677 (100%), Gaps = 0/677 (0%)

Query	1	ATGGGCATCTCTCGGGACAACCTGGCACAAGCGCCGCAAAACCGGGGGCAAGAGAAAGCCC	60
Sbjct	1	ATGGGCATCTCTCGGGACAACCTGGCACAAGCGCCGCAAAACCGGGGGCAAGAGAAAGCCC	60
Query	61	TACCACAAGAAGCGGAAGTATGAGTTGGGGCGCCCAGCTGCCAACACCAAGATTGGCCCC	120
Sbjct	61	TACCACAAGAAGCGGAAGTATGAGTTGGGGCGCCCAGCTGCCAACACCAAGATTGGCCCC	120
Query	121	CGCCGCATCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTG	180
Sbjct	121	CGCCGCATCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTG	180
Query	181	GACGTGGGGAATTTCTCCTGGGGCTCANAGTGTTGTACTCGTAAAAACAAGGATCATCGAT	240
Sbjct	181	GACGTGGGGAATTTCTCCTGGGGCTCANAGTGTTGTACTCGTAAAAACAAGGATCATCGAT	240
Query	241	GTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTACCAAGACCCTGGTGAAGAATTGC	300
Sbjct	241	GTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTACCAAGACCCTGGTGAAGAATTGC	300
Query	301	ATCGTGCTCATCGACAGCACACCGTACCGACAGTGGTACGAGTCCCACTATGCGCTGCCC	360
Sbjct	301	ATCGTGCTCATCGACAGCACACCGTACCGACAGTGGTACGAGTCCCACTATGCGCTGCCC	360
Query	361	CTGGGCCGCAAGAAGGGAGCCAAGCTGACTCCTGAGGAAGAAGAGATTTTaaacaaaaaa	420
Sbjct	361	CTGGGCCGCAAGAAGGGAGCCAAGCTGACTCCTGAGGAAGAAGAGATTTTAAACAAAAAA	420
Query	421	cgatctaaaaaaattcagaagaaatatgatgaaaggaaaaagaatgccaaaatCAGCAGT	480
Sbjct	421	CGATCTAAAAAAATTCAGAAGAAATATGATGAAAGGAAAAAGAATGCCAAAATCAGCAGT	480

PATENT SEQUENCE ALIGNMENT

```
Query 481 CTCCTGGAGGAGCAGTTCCAGCAGGGCAAGCTTCTTGCGTGCATCGCTTCAAGGCCGGGA 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 CTCCTGGAGGAGCAGTTCCAGCAGGGCAAGCTTCTTGCGTGCATCGCTTCAAGGCCGGGA 540

Query 541 CAGTGTGGCCGAGCAGATGGCTATGTGCTAGAGGGCAAAGAGTTGGAGTTCTATCTTAGG 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 CAGTGTGGCCGAGCAGATGGCTATGTGCTAGAGGGCAAAGAGTTGGAGTTCTATCTTAGG 600

Query 601 AAAATCAAGGCCCGCAAAGGCAAATAAATCCTTGTTTTGTCTTCACCCATGTAATAAAGG 660
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 AAAATCAAGGCCCGCAAAGGCAAATAAATCCTTGTTTTGTCTTCACCCATGTAATAAAGG 660

Query 661 TGTTTATTGTTTTTGT 677
      ||||||||||||
Sbjct 661 TGTTTATTGTTTTTGT 677
```

Sequence 1491 matched with Sequence 492

Query= Sequence ID 1491
Length=736

SEQ ID NO: 492

ALIGNMENTS

Identities = 736/736 (100%), Gaps = 0/736 (0%)

Query	1	CTTNCACATACTGATTGATGTCTCATGTCTCTCTAAAATGTGTAAAACCAAGCTGTGCCC	60
Sbjct	1	CTTNCACATACTGATTGATGTCTCATGTCTCTCTAAAATGTGTAAAACCAAGCTGTGCCC	60
Query	61	CAACCACCTTGGGNACATGTGGNGAGGACCTCCTGAGGCTGTGTCTCATGGGCACACCTTAA	120
Sbjct	61	CAACCACCTTGGGNACATGTGGNGAGGACCTCCTGAGGCTGTGTCTCATGGGCACACCTTAA	120
Query	121	CCCTGGGAAAAATAAACTTTCTAAACTGACTTGAGAGCTGTCTCAGATATTCTGAGCTTAC	180
Sbjct	121	CCCTGGGAAAAATAAACTTTCTAAACTGACTTGAGAGCTGTCTCAGATATTCTGAGCTTAC	180
Query	181	AGTTATTGTGAAATCATTTTAATTATAAAATTAAGTGGAGATTTACTTAAAATCATGTGTA	240
Sbjct	181	AGTTATTGTGAAATCATTTTAATTATAAAATTAAGTGGAGATTTACTTAAAATCATGTGTA	240
Query	241	GAAGTAGCCTGTGATATAGTCCTAGATACATACATTATCATCTTATGTATCTTCCCTCCC	300
Sbjct	241	GAAGTAGCCTGTGATATAGTCCTAGATACATACATTATCATCTTATGTATCTTCCCTCCC	300
Query	301	TCTTCCAGGTTCTGATAAAAAACAGATGAAATCTGAAAGACCATGACAGTAGTATTTTGAA	360
Sbjct	301	TCTTCCAGGTTCTGATAAAAAACAGATGAAATCTGAAAGACCATGACAGTAGTATTTTGAA	360
Query	361	AATGACAGTATTTGAAATTAAAAAATTGTAAGTGTCTGTTCTATCACTGCCAAAGGA	420
Sbjct	361	AATGACAGTATTTGAAATTAAAAAATTGTAAGTGTCTGTTCTATCACTGCCAAAGGA	420
Query	421	TAAGTTACAAATTGGTTCTTGAACGTAATATGTACTATGTGCTTGCTATTTAATAATTT	480
Sbjct	421	TAAGTTACAAATTGGTTCTTGAACGTAATATGTACTATGTGCTTGCTATTTAATAATTT	480

PATENT SEQUENCE ALIGNMENT

Query	481	ACCAGTCTTAGTCTTTTTTATTCAGACTAATTTTACCTtttttttAACCTATGACTCttta	540
Sbjct	481	ACCAGTCTTAGTCTTTTTTATTCAGACTAATTTTACCTTTTTTTAACCTATGACTCTTTA	540
Query	541	gttatagtagtacaaaaaagtagtttttagttatagtttttagttgtagtacaaaaaGCAT	600
Sbjct	541	GTTATAGTAGTACAAAAAAGTAGTTTTAGTTATAGTTTTAGTTGTAGTACAAAAAAGCAT	600
Query	601	TTTCTGTAAGCTTAATTTCTTTCCCTTCCCGCTTTCCAGTCAGATGACTTTAGTGATT	660
Sbjct	601	TTTCTGTAAGCTTAATTTCTTTCCCTTCCCGCTTTCCAGTCAGATGACTTTAGTGATT	660
Query	661	TGGAGTTGTGTGCTTTATAAGTGCATTCCTCAGAGGACTTAATATTACTAAGATTTTAGC	720
Sbjct	661	TGGAGTTGTGTGCTTTATAAGTGCATTCCTCAGAGGACTTAATATTACTAAGATTTTAGC	720
Query	721	AACNCTGAAATATGTT	736
Sbjct	721	AACNCTGAAATATGTT	736

Length=579

Identities = 579/579 (100%), Gaps = 0/579 (0%)

Query	1	TGTNCCTGTAGTCCTGTGTGGGAGGATTGCCTGAGCCTAGGAGCTCAAAGTTGCAGTGAG 	60
Sbjct	1	TGTNCCTGTAGTCCTGTGTGGGAGGATTGCCTGAGCCTAGGAGCTCAAAGTTGCAGTGAG	60
Query	61	CCCAGATCGNGNCATTGCAGTCCAGCCTGGGTGACAGAGTGAGACCCCATGTCAaaaaaa 	120
Sbjct	61	CCCAGATCGNGNCATTGCAGTCCAGCCTGGGTGACAGAGTGAGACCCCATGTCAAAAAAA	120
Query	121	aaaaaacaaaaaaCAGGGGCCTGCCTCANCCAGCAGGTGAGGTCTGCCACTGAGAGCACT 	180
Sbjct	121	AAAAAACAAAAAACAGGGGCCTGCCTCANCCAGCAGGTGAGGTCTGCCACTGAGAGCACT	180
Query	181	TCTAGCAGCAGGAACAGCCTCCACCCCCACACTGCAATCAAGTTTTTTGGGTGAGCCTTA 	240
Sbjct	181	TCTAGCAGCAGGAACAGCCTCCACCCCCACACTGCAATCAAGTTTTTTGGGTGAGCCTTA	240
Query	241	GGAGCTAANAAAGGGCCTAGTTTGNCTAAATAGCAGGAGTTATATCCAGGGATCTTCAGG 	300
Sbjct	241	GGAGCTAANAAAGGGCCTAGTTTGNCTAAATAGCAGGAGTTATATCCAGGGATCTTCAGG	300
Query	301	CCCAGGAATGCTAATGAGTAGGCATTCCATGGGCCCTGGGAATGGCTTTGTGTGCCANAA 	360
Sbjct	301	CCCAGGAATGCTAATGAGTAGGCATTCCATGGGCCCTGGGAATGGCTTTGTGTGCCANAA	360
Query	361	ATGATGGCCACAAAGGCCTTGCTGCCTTTTTTCAAAATGGCTGCATCCAGCTGAGTGCTC 	420
Sbjct	361	ATGATGGCCACAAAGGCCTTGCTGCCTTTTTTCAAAATGGCTGCATCCAGCTGAGTGCTC	420
Query	421	TCTGCCAAAGGGGanaanaaaaaTAAGTCTCCAGTGCATTTAGATTGGTCTCTCATCATCT 	480
Sbjct	421	TCTGCCAAAGGGGANANAANAATAAGTCTCCAGTGCATTTAGATTGGTCTCTCATCATCT	480

Query	481	CTCTCCTTTTTGTTTTATTAGTCTCCTTAACCAAAACTGCCAAGAAAGGCTTGGAATTG	540
Sbjct	481	CTCTCCTTTTTGTTTTATTAGTCTCCTTAACCAAAACTGCCAAGAAAGGCTTGGAATTG	540
Query	541	AAACAAAACCTGATANAANAGGTAAGAGGTTGTTCTTTT	579
Sbjct	541	AAACAAAACCTGATANAANAGGTAAGAGGTTGTTCTTTT	579

Sequence 1493 matched with Sequence 494

Query= Sequence ID 1493
Length=752

SEQ ID NO: 494

ALIGNMENTS

Identities = 752/752 (100%), Gaps = 0/752 (0%)

Query	1	TGTNTCaaaaaaaaaaaaaGAACGGNAATGTACTGGAGATGTATTTGATAACCAAGGNT	60
Sbjct	1	TGTNTCAAAAAAAAAAAAAAGAACGGNAATGTACTGGAGATGTATTTGATAACCAAGGNT	60
Query	61	TTAGGTAAATTTTCACCAGTATTAGTTNTATTTGCAAAC TGAAAAATGTTGTAGGCTTAA	120
Sbjct	61	TTAGGTAAATTTTCACCAGTATTAGTTNTATTTGCAAAC TGAAAAATGTTGTAGGCTTAA	120
Query	121	TATAAAATAACCACATTAGTGAACATTATATCTCTTAGAAGAAAGGCCATATTTTGCTCC	180
Sbjct	121	TATAAAATAACCACATTAGTGAACATTATATCTCTTAGAAGAAAGGCCATATTTTGCTCC	180
Query	181	TGCTTCTGTAAAAATATTATTTGTTTGAAGGGGAAATAATGGTAGTGTGACCTTTCACTT	240
Sbjct	181	TGCTTCTGTAAAAATATTATTTGTTTGAAGGGGAAATAATGGTAGTGTGACCTTTCACTT	240
Query	241	AATTCCTACTCCCTTAATGTGAGAGAGACAAAATGAGCTGAAGAAGGAAAATTCTGGAGT	300
Sbjct	241	AATTCCTACTCCCTTAATGTGAGAGAGACAAAATGAGCTGAAGAAGGAAAATTCTGGAGT	300
Query	301	TACTCTCCACAACCTTGAACATACTGACGGACATCTCTGTTTTGACAACGATTTCTCCAT	360
Sbjct	301	TACTCTCCACAACCTTGAACATACTGACGGACATCTCTGTTTTGACAACGATTTCTCCAT	360
Query	361	GCCACCCATGCTNTAATGCCTTGTGGATCACGGACAACCCTCTTTGCACAAGCTACAGCA	420
Sbjct	361	GCCACCCATGCTNTAATGCCTTGTGGATCACGGACAACCCTCTTTGCACAAGCTACAGCA	420
Query	421	TCAGCGATGTTATCTTGCAGCAAAGCACTGCAGGATAAATGACAGGCATTAAGTCTCCT	480
Sbjct	421	TCAGCGATGTTATCTTGCAGCAAAGCACTGCAGGATAAATGACAGGCATTAAGTCTCCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GGGGTTTTGCCATCATTACACCAGTAGCGGCTATTGATCTGAAATATCCCATAATCAGTG	540
Sbjct	481	GGGGTTTTGCCATCATTACACCAGTAGCGGCTATTGATCTGAAATATCCCATAATCAGTG	540
Query	541	CTTCTGTCTCCAGCATTGTAGTTTGTAGCTCGTGTGTTGTAACCACTCTCCCATTG	600
Sbjct	541	CTTCTGTCTCCAGCATTGTAGTTTGTAGCTCGTGTGTTGTAACCACTCTCCCATTG	600
Query	601	AAACACATCCAGTTTGCTAGGCTGATTCCCCTGTAGCCATCCATTCCCAATCTTTTCAGA	660
Sbjct	601	AAACACATCCAGTTTGCTAGGCTGATTCCCCTGTAGCCATCCATTCCCAATCTTTTCAGA	660
Query	661	GTTCTGGCCAACTCACACCTTTCAAAGACCTTGGCCCTGGACCGTAACAGAAAGGAGGACA	720
Sbjct	661	GTTCTGGCCAACTCACACCTTTCAAAGACCTTGGCCCTGGACCGTAACAGAAAGGAGGACA	720
Query	721	AGCCCCAGAACAATGAGAGCCTTCATGTTGAC	752
Sbjct	721	AGCCCCAGAACAATGAGAGCCTTCATGTTGAC	752

Sequence 1494 matched with Sequence 495

Query= Sequence ID 1494
Length=414

SEQ ID NO: 495

ALIGNMENTS

Identities = 414/414 (100%), Gaps = 0/414 (0%)

Query	1	TTGGTACCCGGGAAATTCTTTGCCGCGTCGACGGCCGGTGAGGCAGATCACCTGAGCCCA	60
Sbjct	1	TTGGTACCCGGGAAATTCTTTGCCGCGTCGACGGCCGGTGAGGCAGATCACCTGAGCCCA	60
Query	61	GGAGTTCAGGACCAGCCTGGGCAGCATACCGGGATTCCATCTNNACTAAAAACAGTAGGC	120
Sbjct	61	GGAGTTCAGGACCAGCCTGGGCAGCATACCGGGATTCCATCTNNACTAAAAACAGTAGGC	120
Query	121	TGGGTGTGGTGGCTCATGTCTGTAAGCTCAGGACTTTGGAAGGCCAAGATGGGAGGATCA	180
Sbjct	121	TGGGTGTGGTGGCTCATGTCTGTAAGCTCAGGACTTTGGAAGGCCAAGATGGGAGGATCA	180
Query	181	CTTGAGCCTGGGAGTTTGACACCAGCTTGAGCATCGTAGCCAGGCCCTGACTCTACAAAA	240
Sbjct	181	CTTGAGCCTGGGAGTTTGACACCAGCTTGAGCATCGTAGCCAGGCCCTGACTCTACAAAA	240
Query	241	AAGTGAAATAATTAGCCGAGTGTGGTGGTTCACACCTGTAATCCCAGCTGCTCAGGAGGC	300
Sbjct	241	AAGTGAAATAATTAGCCGAGTGTGGTGGTTCACACCTGTAATCCCAGCTGCTCAGGAGGC	300
Query	301	TGAGGTAGGAGAATCATTTGAACCCGGGAGGTGGAGGTTGCAGTTAGCCGAGATCACGCC	360
Sbjct	301	TGAGGTAGGAGAATCATTTGAACCCGGGAGGTGGAGGTTGCAGTTAGCCGAGATCACGCC	360
Query	361	ATTGCACTCCGGCCTGGGCGATAAAGCGAGACTCTGTCTCaaaaaaaaaaaaaaaaa	414
Sbjct	361	ATTGCACTCCGGCCTGGGCGATAAAGCGAGACTCTGTCTCAAAAAAAAAAAAAAAAAA	414

Sequence 1495 matched with Sequence 496

Query= Sequence ID 1495

Length=670

SEQ ID NO: 496

ALIGNMENTS

Identities = 670/670 (100%), Gaps = 0/670 (0%)

Query	1	ATTCGGGCCGAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCT	60
Sbjct	1	ATTCGGGCCGAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCT	60
Query	61	GGCCTGGAGGCTATCCAGCGTACTCCAAAGATTCAAGTTTACTCACGTCATCCAGCAGAG	120
Sbjct	61	GGCCTGGAGGCTATCCAGCGTACTCCAAAGATTCAAGTTTACTCACGTCATCCAGCAGAG	120
Query	121	AATGGAAAGTCAAATTTCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAA	180
Sbjct	121	AATGGAAAGTCAAATTTCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAA	180
Query	181	GTTGACTTACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAAGCTTGTCTTTC	240
Sbjct	181	GTTGACTTACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAAGCTTGTCTTTC	240
Query	241	AGCAAGGACTGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCCCACTGAAAAAGAT	300
Sbjct	241	AGCAAGGACTGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCCCACTGAAAAAGAT	300
Query	301	GAGTATGCCTGCCGTGTGAACCATGTGACTTTGTACAGCCCAAGATAGTTAAGTGGGAT	360
Sbjct	301	GAGTATGCCTGCCGTGTGAACCATGTGACTTTGTACAGCCCAAGATAGTTAAGTGGGAT	360
Query	361	CGAGACATGTAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTC	420
Sbjct	361	CGAGACATGTAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTC	420
Query	421	CAAATTCTGCTTGCTTGCTTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACA	480
Sbjct	421	CAAATTCTGCTTGCTTGCTTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACA	480

PATENT SEQUENCE ALIGNMENT

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Query  481  AAATGTAGGGTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AAATGTAGGGTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAG  540

Query  541  TGCTGTCTCCATGTTTGATGTATCTGAGCAGGTTGCTCCACAGGTAGCTCTAGGAGGGCT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGCTGTCTCCATGTTTGATGTATCTGAGCAGGTTGCTCCACAGGTAGCTCTAGGAGGGCT  600

Query  601  GGCACCTTAGAGGTGGGGAGCAGAGAATTCTCTTATCCAACATCAACATCTTGGTCAGAT  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  GGCACCTTAGAGGTGGGGAGCAGAGAATTCTCTTATCCAACATCAACATCTTGGTCAGAT  660

Query  661  TTGAACTCTT  670
          |||||||||
Sbjct  661  TTGAACTCTT  670
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Sequence G6 matched with Sequence 497

Query= Sequence ID G6
Length=489

SEQ ID NO: 497

ALIGNMENTS

Identities = 489/489 (100%), Gaps = 0/489 (0%)

Query	1	GGATTTTTGGTCCGCACGCTCCTGCTCCTGACTCACCGCTGTTGCTCTCGCCGAGGAAC	60
Sbjct	1	GGATTTTTGGTCCGCACGCTCCTGCTCCTGACTCACCGCTGTTGCTCTCGCCGAGGAAC	60
Query	61	AAGTCGGTCAGGAAGCCCGCGCGCAACAGCCATGGCTTTTAAGGATACCGGAAAAACACC	120
Sbjct	61	AAGTCGGTCAGGAAGCCCGCGCGCAACAGCCATGGCTTTTAAGGATACCGGAAAAACACC	120
Query	121	CGTGGAGCCGGAGGTGGCAATTCACCGAATTCGAATCACCTAACAAGCCGCAACGTAAA	180
Sbjct	121	CGTGGAGCCGGAGGTGGCAATTCACCGAATTCGAATCACCTAACAAGCCGCAACGTAAA	180
Query	181	ATCCTTGAAAAAGGTGTGTGCTGACTTGATAAGAGGCGCAAAAGAAAAGAATCTCAAAGT	240
Sbjct	181	ATCCTTGAAAAAGGTGTGTGCTGACTTGATAAGAGGCGCAAAAGAAAAGAATCTCAAAGT	240
Query	241	GAAAGGACCAGTTCGAATGCCTACCAAGACTTTGAGAATCACTACAAGAAAACTCCTTG	300
Sbjct	241	GAAAGGACCAGTTCGAATGCCTACCAAGACTTTGAGAATCACTACAAGAAAACTCCTTG	300
Query	301	TGGTGAAGGTTCTAAGACGTGGGATCGTTTCCAGATGAGAATTCACAAGCGACTCATTGA	360
Sbjct	301	TGGTGAAGGTTCTAAGACGTGGGATCGTTTCCAGATGAGAATTCACAAGCGACTCATTGA	360
Query	361	CTTGACAGTCCTTCTGAGATTGTTAAGCAGATTACTTCCATCAGTATTGAGCCAGGAGT	420
Sbjct	361	CTTGACAGTCCTTCTGAGATTGTTAAGCAGATTACTTCCATCAGTATTGAGCCAGGAGT	420
Query	421	TGAGGTGGAAGTCACCATTGCAGATGCTTAAGTCAACTATTTTAATAAATTGATGACCAG	480
Sbjct	421	TGAGGTGGAAGTCACCATTGCAGATGCTTAAGTCAACTATTTTAATAAATTGATGACCAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTGTTAAAA	489
Sbjct	481	TTGTTAAAA	489

Sequence 61 matched with Sequence 498

Query= Sequence ID - 61
Length=362

SEQ ID NO: 498

ALIGNMENTS

Identities = 362/362 (100%), Gaps = 0/362 (0%)

Query	1	CTTATTGAAAATTTTACTAATTTCTTACTTTTTAGGTTTTAGGAGAATACTTTTGGATAA	60
Sbjct	1	CTTATTGAAAATTTTACTAATTTCTTACTTTTTAGGTTTTAGGAGAATACTTTTGGATAA	60
Query	61	TTGACTAGCCTCACATTATATTGATAGAGGTTCTTGAAAACTTTAATGCCAATTCATGTA	120
Sbjct	61	TTGACTAGCCTCACATTATATTGATAGAGGTTCTTGAAAACTTTAATGCCAATTCATGTA	120
Query	121	TCTTATGACTAAAATAGATAATCCATTTAGAAATTTAAGTCATTCTTGCGTGCTTGATAT	180
Sbjct	121	TCTTATGACTAAAATAGATAATCCATTTAGAAATTTAAGTCATTCTTGCGTGCTTGATAT	180
Query	181	GTGTCAGCACTATCCAAGTTGCTAGGGGATACAATGGTGAAGTGAAAATATCAGCTAGGT	240
Sbjct	181	GTGTCAGCACTATCCAAGTTGCTAGGGGATACAATGGTGAAGTGAAAATATCAGCTAGGT	240
Query	241	GCCGGTGGCTCACACCTGTTATCCCAACAGTTTGGGAGGCCAGGGTGGGAGGATCACTCA	300
Sbjct	241	GCCGGTGGCTCACACCTGTTATCCCAACAGTTTGGGAGGCCAGGGTGGGAGGATCACTCA	300
Query	301	AGCACANGCGTTTCACACCAGCCTGGACAACATACAAGACCCCATCTTTACCAAAAGTTA	360
Sbjct	301	AGCACANGCGTTTCACACCAGCCTGGACAACATACAAGACCCCATCTTTACCAAAAGTTA	360
Query	361	AG	362
Sbjct	361	AG	362

Sequence 77 matched with Sequence 499

Query= Sequence ID - 77
Length=464

SEQ ID NO: 499

ALIGNMENTS

Identities = 464/468 (99%), Gaps = 4/468 (0%)

Query	1	GCGGCTGCTGTTGGTTGGGGCCGTCCCGCTCCTAAGGCAGGAAGATGGTGGCCGCAAAG	60
Sbjct	1	GCGGCTGCTGTTGGTTGGGGCCGTCCCGCTCCTAAGGCAGGAAGATGGTGGCCGCAAAG	60
Query	61	AAGACGAAAAAGTCGCTGGAGTCGATCAACTCTAGGCTCCAACCTCGTTATGAAAAGTGGG	120
Sbjct	61	AAGACGAAAAAGTCGCTGGAGTCGATCAACTCTAGGCTCCAACCTCGTTATGAAAAGTGGG	120
Query	121	AAGTACGTCCTGGGGTACAAGCAGACTCTGAAGATGATCAGACAAGGCAAAGCGAAATTG	180
Sbjct	121	AAGTACGTCCTGGGGTACAAGCAGACTCTGAAGATGATCAGACAAGGCAAAGCGAAATTG	180
Query	181	GTCATTCTCGCTAACAACTGCCCAGCTTTGAGGAAATCTGAAATAGAGTACTATGCTATG	240
Sbjct	181	GTCATTCTCGCTAACAACTGCCCAGCTTTGAGGAAATCTGAAATAGAGTACTATGCTATG	240
Query	241	TTGGCTAAAACTGGTGTCCATCACTACAGTGGCAATAATATTGAACTGGGCACAGCA---	297
Sbjct	241	TTGGCTAAAACTGGTGTCCATCACTACAGTGGCAATAATATTGAACTGGGCACAGCAGCA	300
Query	298	TGCGGAAAAATACTACAGAGTGTGCACACTGGCTATCATTGATCCAGGTGACTCTGACATC	357
Sbjct	301	TGCGGAAAAATACTACAGAGTGTGCACACTGGCTATCATTGATCCAGGTGACTCTGACATC	360
Query	358	ATTAGAAGCATGCCAGAACAGACTGGTGAAAAGTA-AACCTTTTCACCTACAAAATTTCA	416
Sbjct	361	ATTAGAAGCATGCCAGAACAGACTGGTGAAAAGTANAACCTTTTCACCTACAAAATTTCA	420
Query	417	CCTGCAAACCTTAAACCTGCAAAATTTTCCTTTAATAAAAATTTGCTTG	464
Sbjct	421	CCTGCAAACCTTAAACCTGCAAAATTTTCCTTTAATAAAAATTTGCTTG	468

Sequence 490 matched with Sequence 500

Query= Sequence ID - 490
Length=382

SEQ ID NO: 500

ALIGNMENTS

Identities = 382/382 (100%), Gaps = 0/382 (0%)

Query	1	TTTTCTTAGAACTTTATTTTTTCTGGCCAGGCGCAGTGGCTCACACCTGTAATCCCAGCA	60
Sbjct	1	TTTTCTTAGAACTTTATTTTTTCTGGCCAGGCGCAGTGGCTCACACCTGTAATCCCAGCA	60
Query	61	CTTTGGGAGGCCAAGGCAGGTCGATCACCTGAGGTCAGGAGCTCAAGACCAGCCTGGCCA	120
Sbjct	61	CTTTGGGAGGCCAAGGCAGGTCGATCACCTGAGGTCAGGAGCTCAAGACCAGCCTGGCCA	120
Query	121	ACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGCGCATG	180
Sbjct	121	ACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGCGCATG	180
Query	181	CCTGTAATCCCANCTACTCAGGAGGCTGAGGCAGGAGAATTGTTTGAACCCGGGAGGCGG	240
Sbjct	181	CCTGTAATCCCANCTACTCAGGAGGCTGAGGCAGGAGAATTGTTTGAACCCGGGAGGCGG	240
Query	241	AGGTTGCANTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAGAGCGAAACTC	300
Sbjct	241	AGGTTGCANTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAGAGCGAAACTC	300
Query	301	CATCTCaaaaaaaaaaaaaaaaaaaaCAACCTTTATTTTTTCTGATTTTAAAAGTAATAACT	360
Sbjct	301	CATCTCAAAAAAAAAAAAAAAAAAAAAACACCTTTATTTTTTCTGATTTTAAAAGTAATAACT	360
Query	361	AGTTTGTAGAAACATTTAAAAGT	382
Sbjct	361	AGTTTGTAGAAACATTTAAAAGT	382

Length=556

SEQ ID NO: 501

Identities = 556/556 (100%), Gaps = 0/556 (0%)

Query	1	TCTTTCGGAAGCGCGCCTTGTGTTGGTACCCGGGAATTCGCGGCCGCGTCGACGCGGTTCG	60
Sbjct	1	TCTTTCGGAAGCGCGCCTTGTGTTGGTACCCGGGAATTCGCGGCCGCGTCGACGCGGTTCG	60
Query	61	TAAGGGCTGAGGATTTTTGGTCCGCACGCTCCTGCTCCTGACTACCGCTGTTTCGCTCTC	120
Sbjct	61	TAAGGGCTGAGGATTTTTGGTCCGCACGCTCCTGCTCCTGACTACCGCTGTTTCGCTCTC	120
Query	121	GCCGAGGAACAAGTCGGTCAGGAAGCCCGCGCGCAACAGCCATGGCTTTTAAGGATACCG	180
Sbjct	121	GCCGAGGAACAAGTCGGTCAGGAAGCCCGCGCGCAACAGCCATGGCTTTTAAGGATACCG	180
Query	181	GAAAAACACCCGTGGAGCCGGAGGTGGCAATTCACCGAATTCGAATCACCTAACAAGCC	240
Sbjct	181	GAAAAACACCCGTGGAGCCGGAGGTGGCAATTCACCGAATTCGAATCACCTAACAAGCC	240
Query	241	GCAACGTAAAATCCTTGAAAAAGGTGTGTGCTGACTTGATAAGAGGCGCAAAAGAAAAGA	300
Sbjct	241	GCAACGTAAAATCCTTGAAAAAGGTGTGTGCTGACTTGATAAGAGGCGCAAAAGAAAAGA	300
Query	301	ATCTCAAAGTGAAAGGACCAGTTCGAATGCCTACCAAGACTTTGAGAATCACTACAAGAA	360
Sbjct	301	ATCTCAAAGTGAAAGGACCAGTTCGAATGCCTACCAAGACTTTGAGAATCACTACAAGAA	360
Query	361	AAACTCCTTGTGGTGAAGGTTCTAAGACGTGGGATCGTTTCCAGATGAGAATTCACAAGC	420
Sbjct	361	AAACTCCTTGTGGTGAAGGTTCTAAGACGTGGGATCGTTTCCAGATGAGAATTCACAAGC	420
Query	421	GACTCATTGACTTGACACAGTCCTTCTGAGATTGTTAAGCAGATTACTTCCATCAGTATTG	480
Sbjct	421	GACTCATTGACTTGACACAGTCCTTCTGAGATTGTTAAGCAGATTACTTCCATCAGTATTG	480

PATENT SEQUENCE ALIGNMENT

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Query  481  AGCCAGGAGTTGAGGTGGAAGTCACCATTGCAGATGCTTAAGTCAACTATTTTAATAAAT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGCCAGGAGTTGAGGTGGAAGTCACCATTGCAGATGCTTAAGTCAACTATTTTAATAAAT  540

Query  541  TGATGACCAGTTGTTT  556
          |||||||||||||||
Sbjct  541  TGATGACCAGTTGTTT  556
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